

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:12 ; Search time 7204 Seconds

(without alignments)
11124.552 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctagagcgcgcgtacatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl:
1: gb_da:
2: gb_hcg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pac:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sv:
13: gb_un:
14: gb_vl:
15: em_da:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pac:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_hcg_hum:
31: em_hcg_inv:
32: em_hcg_other:
33: em_hcg_mus:
34: em_hcg_pln:
35: em_hcg_rod:
36: em_hcg_mam:
37: em_hcg_vrt:
38: em_sy:
39: em_hcgo_hum:
40: em_hcgo_mus:
41: em_hcgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1849	100.0	AR252489	AR252489 Sequence
2	1849	100.0	AX092290	AX092290 Sequence
3	1849	100.0	AX376066	AX376066 Sequence
4	1849	100.0	AX403270	AX403270 Sequence
5	1849	100.0	AX358576	AX358576 Homo sapi
6	1824.4	98.7	BC039573	BC039573 Homo sapi
7	1811.6	98.0	AX879640	AX879640 Sequence
8	1811.6	98.0	BD157945	BD157945 Primer fo
9	1811.6	98.0	AK022704	AK022704 Homo sapi
10	1684.4	91.1	AX880746	AX880746 Sequence
11	1684.4	91.1	BD158566	BD158566 Primer fo
12	1684.4	91.1	AK023676	AK023676 Homo sapi
13	1193.4	64.5	AC098014	AC098014 Homo sapi
14	1191.4	64.4	AC012280	AC012280 Homo sapi
15	1125	60.8	AX881436	AX881436 Sequence
16	1125	60.8	BD159031	BD159031 Primer fo
17	1125	60.8	AK021582	AK021582 Homo sapi
18	1015.2	54.9	AC096768	AC096768 Homo sapi
19	944.8	51.1	AC124242	AC124242 Homo sapi
20	943.4	51.0	AB020868	AB020868 Homo sapi
21	943.4	51.0	AP006203	AP006203 Homo sapi
22	942.4	51.0	AP006208	AP006208 Homo sapi
23	770.2	41.7	BC029845	BC029845 Mus muscu
24	681.8	36.9	AX867484	AX867484 Sequence
25	681.8	36.9	BD147546	BD147546 Primer fo
26	568.4	30.7	AX870066	AX870066 Sequence
27	568.4	30.7	BD150128	BD150128 Primer fo
28	536.2	29.0	AX870976	AX870976 Sequence
29	536.2	29.0	BD151038	BD151038 Primer fo
30	519.2	28.1	AF220172S1	AF220172 Homo sapi
31	482.6	26.1	AC018406	AC018406 Homo sapi
32	454.6	24.6	AR414220	AR414220 Sequence
33	454.6	24.6	BD107973	BD107973 EST and e
34	414.2	22.4	BD076179	BD076179 5' EST of
35	337.4	18.2	G30051	G30051 human STS S
36	306.4	16.6	AX071613	AX071613 Sequence
37	213.2	11.5	AC107774	AC107774 Mus muscu
38	197.4	10.7	BC008999	BC008999 Homo sapi
39	195.4	10.6	D63877	D63877 Human mRNA
40	194	10.5	G22972	G22972 human STS W
41	188.2	10.2	AC106280	AC106280 Rattus no
42	188.2	10.2	AC103333	AC103333 Rattus no
43	172	9.3	BC016905	BC016905 Homo sapi
44	147.8	8.0	BC063225	BC063225 Silurana
45	138.4	7.5	AC111301	AC111301 Rattus no

ALIGNMENTS

RESULT 1
LOCUS AR252489
DEFINITION Sequence 157 from patent US 64/8825.
ACCESSION AR252489
VERSION AR252489.1 GI:27300397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1849)
Winterbottom J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 64/8825-A 157 12-NOV-2002;

Not in date

REFERENCE
AUTHORS
1 Baton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, M.I.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0116318-A 21 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
1..1849
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGGTAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 60
QY 61 CGGCGGCTCGCTTCCAGACCTCTCAACGACCTCGGCAAGGAGTTCTCTTGG 120
DB 61 CGGCGGCTCGCTTCCAGACCTCTCAACGACCTCGGCAAGGAGTTCTCTTGG 120
QY 121 GGAAGTAAAGGTGAAGCAGAACAGCATTACTGATTCGCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAGAACAGCATTACTGATTCGCAATGATGATGTAAGT 180
QY 181 TGTATTACATTGACATTCAGAAATATATTCATGCTATCAAGCTTTTAACTTTATPA 240
DB 181 TGTATTACATTGACATTCAGAAATATATTCATGCTATCAAGCTTTTAACTTTATPA 240
QY 241 TTTTTCAGGGAAGTAAATGAGCAGACCTGAAGAAATATATTCGCAATGATGTAAGT 300
DB 241 TTTTTCAGGGAAGTAAATGAGCAGACCTGAAGAAATATATTCGCAATGATGTAAGT 300
QY 241 TTTTTCAGGGAAGTAAATGAGCAGACCTGAAGAAATATATTCGCAATGATGTAAGT 300
DB 241 TTTTTCAGGGAAGTAAATGAGCAGACCTGAAGAAATATATTCGCAATGATGTAAGT 300
QY 301 TGTGTAGTGTGTGTACAAATTCGCTGCTCATTCAGATCATGACGTTTAAAGAG 360
DB 301 TGTGTAGTGTGTGTACAAATTCGCTGCTCATTCAGATCATGACGTTTAAAGAG 360
QY 361 GGTGCTTCACAAACCTTCAGAGGACATTTTCAACCAAGACCTGTTTCTCTAT 420
DB 361 GGTGCTTCACAAACCTTCAGAGGACATTTTCAACCAAGACCTGTTTCTCTAT 420
QY 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATGACGTGAACATTCCTTATPA 480
DB 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATGACGTGAACATTCCTTATPA 480
QY 481 AACTCAAAAGGACCTTTTCAAGGCTACCTTAAAGTGTGCAATCTGGGAGATGCTGA 540
DB 481 AACTCAAAAGGACCTTTTCAAGGCTACCTTAAAGTGTGCAATCTGGGAGATGCTGA 540
QY 541 ACAACTGGGTTATTAACAGTATCAGGTTCTGTATGCTCACTGTTTAAAGCGAGT 600
DB 541 ACAACTGGGTTATTAACAGTATCAGGTTCTGTATGCTCACTGTTTAAAGCGAGT 600
QY 601 ACAACACACAGCTCTTAATTTTGAAGAGTGAATCTTAAAGAGGTACATPAAT 660
DB 601 ACAACACACAGCTCTTAATTTTGAAGAGTGAATCTTAAAGAGGTACATPAAT 660
QY 661 AAATGAAATGTATGCTTCAATTAAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720
DB 661 AAATGAAATGTATGCTTCAATTAAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAGCAGTATTAATCTAGTAAAGATGTTAAACAGATTTAAACGAAATTTGA 780
DB 721 CAGTGAACAGCAGTATTAATCTAGTAAAGATGTTAAACAGATTTAAACGAAATTTGA 780
QY 781 GAAAGAGAGAGGACAGATTGAGGAGAGAGAGAAATCATCAAAAAGACCTCA 840

DB 781 GAAAGAGAGAGGACAGATTGAGGAGAGAGAGAAATCATCAAAAAGACCTCA 840
QY 841 GGAAACATTTTCTTTGTGAGGATTAAGGACCTTTTTCGAATCTGAATTTCTTCA 900
DB 841 GGAAACATTTTCTTTGTGAGGATTAAGGACCTTTTTCGAATCTGAATTTCTTCA 900
QY 901 TTCAATGTATGTCTTTTAAATAAGACATGTTCTTAAAGTGTAGTACTGACACCA 960
DB 901 TTCAATGTATGTCTTTTAAATAAGACATGTTCTTAAAGTGTAGTACTGACACCA 960
QY 961 CCATCTGATGTATGATCAATCTGACCTTAAAGTGTGAACACATGACATTCCTGAGC 1020
DB 961 CCATCTGATGTATGATCAATCTGACCTTAAAGTGTGAACACATGACATTCCTGAGC 1020
QY 1021 TAGTCCAGCTAGTACACACCAATCATTTAAGATTAAGGCTTGAATGATGACATG 1080
DB 1021 TAGTCCAGCTAGTACACACCAATCATTTAAGATTAAGGCTTGAATGATGACATG 1080
QY 1081 GCAATTCAGAGATCTCGTGTGTAGATACACAAGACAAACGATCTTAAACCAATCTGG 1140
DB 1081 GCAATTCAGAGATCTCGTGTGTAGATACACAAGACAAACGATCTTAAACCAATCTGG 1140
QY 1141 TAGTATGATCCAGATTAAGATCCAAATGAGGCGGCAAGACAGATGAGAAATTTGA 1200
DB 1141 TAGTATGATCCAGATTAAGATCCAAATGAGGCGGCAAGACAGATGAGAAATTTGA 1200
QY 1201 AAAGATGAAGGCTTTGTGATATTCAGGCTCTCTACATTTTGAATCCTTTAACTTA 1260
DB 1201 AAAGATGAAGGCTTTGTGATATTCAGGCTCTCTACATTTTGAATCCTTTAACTTA 1260
QY 1261 CAAGAGATTTTATTTATTTGGCTGATGAGTAAAGCCAAATCTTCTTATTTACTAT 1320
DB 1261 CAAGAGATTTTATTTATTTGGCTGATGAGTAAAGCCAAATCTTCTTATTTACTAT 1320
QY 1321 GTTACGCTACTGAGTAAAGTCTTGTGTTTACTATGTTTCACTGCTTTGAGTAAATAC 1380
DB 1321 GTTACGCTACTGAGTAAAGTCTTGTGTTTACTATGTTTCACTGCTTTGAGTAAATAC 1380
QY 1381 ACAATTAATCTTATGATCTTATTTACTTCAAAAGTACTTTTCAAACTGAGATCTTTA 1440
DB 1381 ACAATTAATCTTATGATCTTATTTACTTCAAAAGTACTTTTCAAACTGAGATCTTTA 1440
QY 1441 TTTCCAAACCTTTTTCACCTTCACTAAGTTGTGAGGGAAGGCTTACACAGACA 1500
DB 1441 TTTCCAAACCTTTTTCACCTTCACTAAGTTGTGAGGGAAGGCTTACACAGACA 1500
QY 1501 TTTCTTGAATTTGAAAAGTGAACACAGGACACAGTGTCTCAACCTGTAAATCCAGACT 1560
DB 1501 TTTCTTGAATTTGAAAAGTGAACACAGGACACAGTGTCTCAACCTGTAAATCCAGACT 1560
QY 1561 TAGGAAAGACAGTCAAGAGATTTGATTGAAGCTAGAGTTAGAGACCACTGGGGAAC 1620
DB 1561 TAGGAAAGACAGTCAAGAGATTTGATTGAAGCTAGAGTTAGAGACCACTGGGGAAC 1620
QY 1621 GTATTGAGACCATGCTATTAATAAATTAAGAAAAGCAAGATGCTTATTTTCAA 1680
DB 1621 GTATTGAGACCATGCTATTAATAAATTAAGAAAAGCAAGATGCTTATTTTCAA 1680
QY 1681 AATATGAAAAGAAATTTATATGAATAATTTATCTGAGCTATTAATCTCTTAAAGTAT 1740
DB 1681 AATATGAAAAGAAATTTATATGAATAATTTATCTGAGCTATTAATCTCTTAAAGTAT 1740
QY 1741 ACTTTTGAAGTACATTAATGCTAGAGTGTCCAGATTAATGCTGATATCATGCAAT 1800
DB 1741 ACTTTTGAAGTACATTAATGCTAGAGTGTCCAGATTAATGCTGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAAACATCATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1849
DB 1801 AAATTTGCAAAAACATCATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1849

RESULT 3
AM376066

LOCUS AX376066 1849 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 133 from Patent WO0168848.
ACCESSION AX376066
VERSION AX376066.1 GI:19170425
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, D., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 133 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1..1849
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGGCGGCGGTAGCAGTGGAGGGGAGAGTACGTGCGGCGTCTCGGGCTTTGTGCT 60
Db 1 CTGAGGCGGCGGTAGCAGTGGAGGGGAGAGTACGTGCGGCGTCTCGGGCTTTGTGCT 60
QY 61 CCGGCGACCTGCTTTCCAGACCTCAACACGAGCTGGACACAGGAGTTTCTTCTTG 120
Db 61 CCGGCGACCTGCTTTCCAGACCTCAACACGAGCTGGACACAGGAGTTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCCAAAGACGATTAAGTCCCAATGATGATGTTGAAGT 180
Db 121 GGAAGTAAAGGTGAAGCCAAAGACGATTAAGTCCCAATGATGATGTTGAAGT 180
QY 181 TGTATTACATTTGACATTCAGAAATATTCATGCTATCAGCTTTTAACTTTATA 240
Db 181 TGTATTACATTTGACATTCAGAAATATTCATGCTATCAGCTTTTAACTTTATA 240
QY 241 TTCTTCAGCGAGATTAATGAGCAAGCACTGAGAAATATTAATGCTCAAAAAGA 300
Db 241 TTCTTCAGCGAGATTAATGAGCAAGCACTGAGAAATATTAATGCTCAAAAAGA 300
QY 301 TGTGTAGTGTGTGACAAATTCGTCGTCATTCAGATCAGATCAGATCGTTTGAAGAG 360
Db 301 TGTGTAGTGTGTGACAAATTCGTCGTCATTCAGATCAGATCAGATCGTTTGAAGAG 360
QY 361 GGTGCTTCAAAAACCTGAGAGAGATTTTCAAAACCAAGACCTGTTTGTGCTAT 420
Db 361 GGTGCTTCAAAAACCTGAGAGAGATTTTCAAAACCAAGACCTGTTTGTGCTAT 420
QY 421 AACACCAAGTATATAACAGAAAGCTGCTACTCATCGACTGAAACATCTCTATATA 480
Db 421 AACACCAAGTATATAACAGAAAGCTGCTACTCATCGACTGAAACATCTCTATATA 480
QY 481 ACCCTCAAAAAGATTTTTCAGAGGATCCTTTAGTGTGCTCAACTGCGGCAATGCTGA 540
Db 481 ACCCTCAAAAAGATTTTTCAGAGGATCCTTTAGTGTGCTCAACTGCGGCAATGCTGA 540
QY 541 ACAACGTGGTTATTAACCTGATCAGGTTCCTGATGTCACATGTTTAAAGCGAGCA 600
Db 541 ACAACGTGGTTATTAACCTGATCAGGTTCCTGATGTCACATGTTTAAAGCGAGCA 600
QY 601 ACAACGACAGCTCTAATTTTGAAGAGATGATCCTTAAAGAGATTAATAGAT 660
Db 601 ACAACGACAGCTCTAATTTTGAAGAGATGATCCTTAAAGAGATTAATAGAT 660
QY 661 AATGAATGATGCTCATTAACAAGAGAAATTAAGATATAGCAAAAAGCTGGAAGA 720

Db 661 AATGAATGATGCTCATTAACAAGAGAAATTAAGATATAGCAAAAAGCTGGAAGA 720
QY 721 CAGTGAACAAGCAGTATATAACCTGATTAAGATGTTAAAGATTAAGAGAAATGA 780
Db 721 CAGTGAACAAGCAGTATATAACCTGATTAAGATGTTAAAGATTAAGAGAAATGA 780
QY 781 GAAAGAGAGAGAGACAGATTCAGGAGAGAGAGAGAGAGATCCAAAAGACCTCA 840
Db 781 GAAAGAGAGAGAGACAGATTCAGGAGAGAGAGAGAGAGATCCAAAAGACCTCA 840
QY 841 GGAAGACATTTTCTTTGTCAGAGGATTAAGGACCTTTTCCAAATCTGAATTTCTCA 900
Db 841 GGAAGACATTTTCTTTGTCAGAGGATTAAGGACCTTTTCCAAATCTGAATTTCTCA 900
QY 901 TTCAATGTTATGCTTTTAAATAATAGACATGTTTCTTAAAGATGCTGTAATCAACA 960
Db 901 TTCAATGTTATGCTTTTAAATAATAGACATGTTTCTTAAAGATGCTGTAATCAACA 960
QY 961 CCATCTGATGTAGTACACATCTGACCTTAATGTTGAACACATGACATTCCTGAAGC 1020
Db 961 CCATCTGATGTAGTACACATCTGACCTTAATGTTGAACACATGACATTCCTGAAGC 1020
QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAAGCCTTAGACTTAGATGACAGATG 1080
Db 1021 TAGTCCAGCTAGTACACCAAAATCATTAAAGCCTTAGACTTAGATGACAGATG 1080
QY 1081 GCAATTCAGAGATCTCGGTTGTTAGATCAACAAGACAAACGATCTAAAGCAATATCG 1140
Db 1081 GCAATTCAGAGATCTCGGTTGTTAGATCAACAAGACAAACGATCTAAAGCAATATCG 1140
QY 1141 TAGATGATACCAATTAAGATCCAAATAGAGAGCCAGAAACAGATGAAGAAATGA 1200
Db 1141 TAGATGATACCAATTAAGATCCAAATAGAGAGCCAGAAACAGATGAAGAAATGA 1200
QY 1201 AAGAGTGAAGGTTTGTGTAATTCACGCTCTCAATTTTGAATCCTTTAACTTA 1260
Db 1201 AAGAGTGAAGGTTTGTGTAATTCACGCTCTCAATTTTGAATCCTTTAACTTA 1260
QY 1261 CAAGAGATTTTCTTATTTGGCTGATGAGTAAAGCCAAACATTCATGTTTAACTAT 1320
Db 1261 CAAGAGATTTTCTTATTTGGCTGATGAGTAAAGCCAAACATTCATGTTTAACTAT 1320
QY 1321 GTTGAAGTCTTGAAGTATTCATTTGTTTCTATGTTCACTGCTTTGACATATAC 1380
Db 1321 GTTGAAGTCTTGAAGTATTCATTTGTTTCTATGTTCACTGCTTTGACATATAC 1380
QY 1381 ACAAGTATCTGTAGTCAATTTTCAAAAGTATTTTCAAAACATCAGATGCTTTTA 1440
Db 1381 ACAAGTATCTGTAGTCAATTTTCAAAAGTATTTTCAAAACATCAGATGCTTTTA 1440
QY 1441 TTTCCAAACTTTTTCACCTTTCACTAAGTTGTTAGGGGAAGGCTTACACAGACA 1500
Db 1441 TTTCCAAACTTTTTCACCTTTCACTAAGTTGTTAGGGGAAGGCTTACACAGACA 1500
QY 1501 TTCTTTAATTTGAAAAAGTGAACAGGACACATGCTCACACCTTAATCCAGACT 1560
Db 1501 TTCTTTAATTTGAAAAAGTGAACAGGACACATGCTCACACCTTAATCCAGACT 1560
QY 1561 TAGGGAACACAGTCAAGAGATGATGAAGCTTAGAGGATTAAGAGACAGCTGGGCAAC 1620
Db 1561 TAGGGAACACAGTCAAGAGATGATGAAGCTTAGAGGATTAAGAGACAGCTGGGCAAC 1620
QY 1621 GTATTGAGACATGCTCTTAAATAATTAAGTAAAGCAAGATGCTTAATTTTCAA 1680
Db 1621 GTATTGAGACATGCTCTTAAATAATTAAGTAAAGCAAGATGCTTAATTTTCAA 1680
QY 1681 AATATGAAAGAAATTTATGAAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1740
Db 1681 AATATGAAAGAAATTTATGAAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1740
QY 1741 ACTTTTGAAGATGATTAATGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1800

QY 1621 GATATGAGACCATGTCTATTAAAAATAAATGAGAAAGACAGATAGCTTATTTTCAA 1680
DB 1621 GATATGAGACCATGTCTATTAAAAATAAATGAGAAAGACAGATAGCTTATTTTCAA 1680
QY 1681 AATATGGAAGAAATTTATATGAAAAATTTCTGAGCATTAAATTCCTTAAGTAT 1740
DB 1681 AATATGGAAGAAATTTATATGAAAAATTTCTGAGCATTAAATTCCTTAAGTAT 1740
QY 1741 ACTTTTATGAGATACATTATGAGTGAAGTGCAGATTAATATGCTGATATCATCAAT 1800
DB 1741 ACTTTTATGAGATACATTATGAGTGAAGTGCAGATTAATATGCTGATATCATCAAT 1800
QY 1801 AATTTGCAAAACATCTCTTAATTTAAAAAATTTAAAAAATTTAAAAA 1849
DB 1801 AATTTGCAAAACATCTCTTAATTTAAAAAATTTAAAAAATTTAAAAA 1849

RESULT 5
AY358576 1849 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DN56410 EGES496 (UNQ496) mRNA, complete cds.
DEFINITION AY358576
ACCESSION AY358576.1 GI:37182273
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 1849)
Clark, H.F., Gurey, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Dowd, P., Bacon, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robie, B., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Weiland, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, M.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 1849)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
Source
1. 1849
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DN56410"
1. 1849
/locus_tag="UNQ496"
17. 1246
/locus_tag="UNQ496"
/note="PRO1013"
/codon_start=1
/product="EGES496"
/protein_id="AAO88938.1"
/db_xref="GI:37182273"
/translation="MEGSTSAVUSGVLCALAFQHLNTSDTEGFLIGVKEAKNS
ITDSQMDVEVYITIDIQKTPCYQLSPFNSSGEVQALKILSVKAVGWKIF
RRSDQIMTFERLMEKLEHFNODLVFLPLPSITTSCTHREHSLVYKQKL
FHRVPLVAVNGEMLQKTVSGSCWSTGSRVAVQHTSSKFEEDGSLKVKINEM
YASLOEILKSI CKKVEDSEAVDKLVKDVRLKREIKRGAQICAAERENIQDPE
NIFLCAALTFEENSEPLHSCVMSLKRVHKSCTVNHHLVDVDTLWVETDIE
ASPASTPQITIKHKLIDLDNRQFKSRILDTODRSKXANTSSNQDASMSSEPTDE
ELEKMGEGEYSRSTP"

ORIGIN

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGGATGATGAGAGGAGAGATAGCTCCGCGGTGCTCCGCGCTTTGTGCT 60
DB 1 CTGAGCGCGGATGATGAGAGGAGAGATAGCTCCGCGGTGCTCCGCGCTTTGTGCT 60
QY 61 CGGCGACTCGCTTTCCAGCACTTCACAGGATCCGACACGGAAGTTTCTCTGG 120
DB 61 CGGCGACTCGCTTTCCAGCACTTCACAGGATCCGACACGGAAGTTTCTCTGG 120
QY 121 GGAAGTAAAGGTAGAGCAAGACAGATCTGATTCCTCAATGATGATGAGT 180
DB 121 GGAAGTAAAGGTAGAGCAAGACAGATCTGATTCCTCAATGATGATGAGT 180
QY 181 TGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 TGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 TTCTTCAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 TTCTTCAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 TGTGTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 TGTGTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GGTGTTTCAAAAACCTTGACAGGAGCTTTTCAACCAACCTGTTTCTGCTAT 420
DB 361 GGTGTTTCAAAAACCTTGACAGGAGCTTTTCAACCAACCTGTTTCTGCTAT 420
QY 421 AACACCAATATATATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 AACACCAATATATATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 ACCTGAAAAAGACCTTTTTCACAGGATCTTTTCAACCAACCTGTTTCTGCTAT 540
DB 481 ACCTGAAAAAGACCTTTTTCACAGGATCTTTTCAACCAACCTGTTTCTGCTAT 540
QY 541 ACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 ACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 ACACCAACACGCTTTTATTTTGAAGAGATGATGATGATGATGATGATGAT 660
DB 601 ACACCAACACGCTTTTATTTTGAAGAGATGATGATGATGATGATGATGAT 660
QY 661 AATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 AATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 CAGTGAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 CAGTGAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 GAAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GAAAAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GAGAAACATTTTCTTTGTCAGGCAATGAGACCTTTTCCAAATTCGAATTTCTCA 900
DB 841 GAGAAACATTTTCTTTGTCAGGCAATGAGACCTTTTCCAAATTCGAATTTCTCA 900
QY 901 TTCATGTTATGCTTTTAAAAATGACATGTTCTAAAGTACGTATACACCA 960
DB 901 TTCATGTTATGCTTTTAAAAATGACATGTTCTAAAGTACGTATACACCA 960
QY 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1021 TAGTCCAGCTAGTACCAACCAATCATTAAGCATTAAGCCTTAGACTAGATGACAGATG 1080
 Db 1021 TAGTCCAGCTAGTACCAACCAATCATTAAGCATTAAGCCTTAGACTAGATGACAGATG 1080
 QY 1081 GCAATTCAGAGATTCGGGTGTGATGATGACCAAGCAAAAGATCTTAAGCAATCTCG 1140
 Db 1081 GCAATTCAGAGATTCGGGTGTGATGATGACCAAGCAAAAGATCTTAAGCAATCTCG 1140
 QY 1141 TAGTAGTACCAAGATTAAGCATTAAGCATTAAGCCTTAGACTAGATGACAGATG 1200
 Db 1141 TAGTAGTACCAAGATTAAGCATTAAGCATTAAGCCTTAGACTAGATGACAGATG 1200
 QY 1201 AAAGATGAAGGTTTGGTGAATATTCAGCGCTCTCTCACTTTGATCTTTTAACTTA 1260
 Db 1201 AAAGATGAAGGTTTGGTGAATATTCAGCGCTCTCTCACTTTGATCTTTTAACTTA 1260
 QY 1261 CAAGAGATTTTATTTATTTGGCTGATGGGTAAAGCAAACTTTCTATTGTTTAACTAT 1320
 Db 1261 CAAGAGATTTTATTTATTTGGCTGATGGGTAAAGCAAACTTTCTATTGTTTAACTAT 1320
 QY 1321 GTTAGACTACTTGAGATTAAGTCAATTTGTTTATCTATGTTCACTGTTTGCAGTAATAC 1380
 Db 1321 GTTAGACTACTTGAGATTAAGTCAATTTGTTTATCTATGTTTCACTGTTTGCAGTAATAC 1380
 QY 1381 ACAGATTAAGCTTGTGATGATTTACTTACCAAGATCTTTTCAAAATCTGATGCTTTTA 1440
 Db 1381 ACAGATTAAGCTTGTGATGATTTACTTACCAAGATCTTTTCAAAATCTGATGCTTTTA 1440
 QY 1441 TTTCCAAACCTTTTTCACCTTTTCACTTAAGTGTGAGGGGAGGCTTACACAGACACA 1500
 Db 1441 TTTCCAAACCTTTTTCACCTTTTCACTTAAGTGTGAGGGGAGGCTTACACAGACACA 1500
 QY 1501 TTCTTTAGATTTGGAAGAAGTGAACCAAGCAAGTGGCTCACTCTGTAATCCAGACT 1560
 Db 1501 TTCTTTAGATTTGGAAGAAGTGAACCAAGCAAGTGGCTCACTCTGTAATCCAGACT 1560
 QY 1561 TAGGGAAGACCAAGTCAAGAGATGATTAAGTGAAGTGAAGTGAAGACCAAGCTGGGCAAC 1620
 Db 1561 TAGGGAAGACCAAGTCAAGAGATGATTAAGTGAAGTGAAGTGAAGACCAAGCTGGGCAAC 1620
 QY 1621 GTATTGAGACCATCTTATTAAAAATTAATGGAAGCAAGATAGCTTTATTTTCA 1680
 Db 1621 GTATTGAGACCATCTTATTAAAAATTAATGGAAGCAAGATAGCTTTATTTTCA 1680
 QY 1681 AATATGGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
 Db 1681 AATATGGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
 QY 1741 ACTTTTGTAGAGTACATTAATGCTAGAGTTGCCAGATTAATGCTGATATCATGCAAT 1800
 Db 1741 ACTTTTGTAGAGTACATTAATGCTAGAGTTGCCAGATTAATGCTGATATCATGCAAT 1800
 QY 1801 AAATTTGCAAAACATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1849
 Db 1801 AAATTTGCAAAACATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1849

RESULT 6
 BC039573
 LOCUS
 DEFINITION Homo sapiens hypothetical protein FLJ13614, mRNA (cDNA clone
 WGC:48664 IMAGE:6045433), complete cds.
 ACCESSION BC039573
 VERSION BC039573.1 GI:24660389
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 2649)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 REMARK
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb-re@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansys@systemsbiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES
 source
 1..2649
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="WGC:48664 IMAGE:6045433"
 /tissue_type="testis embryonal carcinoma"
 /clone_id="NIH_MGC_92"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
 1..2649
 /gene="FLJ13614"
 /note="synonyms: FLJ11520, FLJ12642"
 /db_xref="locusid:84142"
 340..1242
 /codon_start=1
 /product="FLJ13614 protein"
 /protein_id="AAH39573.1"
 /db_xref="gi:24660390"
 /db_xref="locusid:84142"
 /translation="MTPREPLIKNLEHPENODLVLLTPSTTESCTHRLHSL
 VKPKGLFHRVPIVYANIGMSHQGYTVSSCSSTFSBAYVCHSSKPREDSIKE
 VAKINEMFASLOEELKSI CKVEDSEQAVDLVADVAVKSLREIKRGAQIQARBEK
 IQKQDENIFLQALRTFPNSERLHSCVSLKRVHKSCKNNEHDVDVNTLLW
 EHTDIPASPASTPQIIKHKALDLDWQFRRSLDTPDKRSADYDGSNSQDASAK
 SSPETDEIERMKGFGEYSRSPF"

ORIGIN
 Query Match 98.7%, Score 1824.4, DB 9; Length 2649;

Source 1. .2663
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
379. .1281
/note="unnamed protein product"
/codon_start=1
/protein_id="CAE90598.1"
/db_xref="GI:40034377"
/translation="WTFPERLHKNIQEPHSNODLVFLITPSIITESCSTRLEHSL
YKPKGLFHRVPLVANLQMSQEQAVKTVSGMSVGFRAVQTHSKFEEDGSLKE
VHKINENYASLQBELKSIICKYVDESOAVKLVNRLKREIKERGAQIQDAEIK
IQKDPENIFLCOALRFFENPFLHSVMSLKNRYSKSSCNVNHLDVNTLMY
EHTIDPEASPASTPOIIKKHTLDDRWQPKSRLLDQDKSKADTGSNDKXSKM
SSPTEBEIKMKGFGEYKSRPTF"

ORIGIN

Query Match 98.0%; Score 1811.6; DB 6; Length 2663;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1825; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

1 CTGAGGCGGCGGTAGCATGAGGCGGAGAGTAGTGGCGGTGCTCGCGCTTTGCT 60
36 CTGAGGCGGCGGTAGCATGAGGCGGAGAGTAGTGGCGGTGCTCGCGCTTTGCT 95
61 CGGCGCATCGCTTCCAGCACTCAACAGGACTCGGACACGGAAGTTTCTCTTG 120
96 CGGCGCATCGCTTCCAGCACTCAACAGGACTCGGACACGGAAGTTTCTCTTG 155
121 GGAAGTAAAGGTGAGGCCAAGACAGCATTTACTGATTCGCAATGATGATGAT 180
156 GGAAGTAAAGGTGAGGCCAAGACAGCATTTACTGATTCGCAATGATGATGAT 215
181 TGTATATACATGACATTCAGAAATATATTCATCATCTAGCTTTTATGATTA 240
216 TGTATATACATGACATTCAGAAATATATTCATCATCTAGCTTTTATGATTA 275
241 TTTTTCAGCGAAGTAATGAGCAAGCATGAAAGAAATTTTCATATGTCAGAAA 300
276 TTTTTCAGCGAAGTAATGAGCAAGCATGAAAGAAATTTTCATATGTCAGAAA 335
301 TGTGATAGTTGATACAAATTCGCTGCTCATTCAGATCATGATGATGATGAT 360
336 TGTGATAGTTGATACAAATTCGCTGCTCATTCAGATCATGATGATGATGAT 395
361 GGTGCTTACAAAACCTTGAGAGGATTTTCAACCAAGACCTTGTCTGCTAT 420
396 GGTGCTTACAAAACCTTGAGAGGATTTTCAACCAAGACCTTGTCTGCTAT 455
421 AATACCAAGTATATACAGAAAGCTGCTACTCATTCAGATGAGCAATTCCTTA 480
456 AATACCAAGTATATACAGAAAGCTGCTACTCATTCAGATGAGCAATTCCTTA 515
481 ACCTCAAAAAGGACTTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 540
516 ACCTCAAAAAGGACTTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 575
541 ACCTCAAAAAGGACTTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 600
576 ACCTCAAAAAGGACTTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 635
601 ACAACACACAGCTTAAATTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 660
636 ACAACACACAGCTTAAATTTTTCAGAGGATCTTTAGTGTGCTCAATCTGCGCAT 695
661 AATGTAATGTATGCTTCATTAACAAGGATTTAAAGATATATGCAAAAAAGTGA 720
696 AATGTAATGTATGCTTCATTAACAAGGATTTAAAGATATATGCAAAAAAGTGA 755
721 CAGTGAACAGAGTATGATTAACATGATTAAGATGATTAACAGATTAACAGAAAT 780
756 CAGTGAACAGAGTATGATTAACATGATTAAGATGATTAACAGATTAACAGAAAT 815

781 GAAAAGAGAGAGACAGATTTCAAGCGAGCAAGAGAGAGACATCCCAAAAGACCTCA 840
816 GAAAAGAGAGAGACAGATTTCAAGCGAGCAAGAGAGAGAGACATCCCAAAAGACCTCA 875
841 GAGAGACATTTTCTTTGTCAGGATTAACGACCTTTTTCATTAATCTGATTTCTTCA 900
876 GAGAGACATTTTCTTTGTCAGGATTAACGACCTTTTTCATTAATCTGATTTCTTCA 935
901 TTGATGTATATGCTTTTAAAAAATAGATGTTTCTTAAAGTATGCTATCTACACCA 960
936 TTGATGTATATGCTTTTAAAAAATAGATGTTTCTTAAAGTATGCTATCTACACCA 995
961 CCATTCGATGATGAGCAATCTGACCTTATGATGAGCAACATGATCTTAAAGCAAT 1020
996 CCATTCGATGATGAGCAATCTGACCTTATGATGAGCAACATGATCTTAAAGCAAT 1055
1021 TAGTCAGCTAGTACACCAAAATCATTAGCATTAAGCTTTAGATGATGACATG 1080
1056 TAGTCAGCTAGTACACCAAAATCATTAGCATTAAGCTTTAGATGATGACATG 1115
1081 GCAATTCAGAGATCTGCTGTTGATGATGACCAAGACCAAGATCTTAAAGCAATCTG 1140
1116 GCAATTCAGAGATCTGCTGTTGATGATGACCAAGACCAAGATCTTAAAGCAATCTG 1175
1141 TAGTATGACCAAGATTAAGCATCCAAATAGAGACCCAGAAACAGATGAAGAAATGA 1200
1176 TAGTATGACCAAGATTAAGCATCCAAATAGAGACCCAGAAACAGATGAAGAAATGA 1235
1201 AAGATGAAGGTTTGGTGAATTTCAAGCTTCCTCAATTTGATCTTTTAACTTA 1260
1236 AAGATGAAGGTTTGGTGAATTTCAAGCTTCCTCAATTTGATCTTTTAACTTA 1295
1261 CAAGAGATTTTATTTATGCTGATGAGTAAAGCAAACTTTCTATTTTACTAT 1320
1296 CAAGAGATTTTATTTATGCTGATGAGTAAAGCAAACTTTCTATTTTACTAT 1355
1321 GTTACGCTACTTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1356 GTTACGCTACTTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1415
1381 AAGATTAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1416 AAGATTAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1475
1441 TTTCCAAACCTTTTTCACCTTCACTTAAGTTGTTGAGGGAAGGCTTACAGACCA 1500
1476 TTTCCAAACCTTTTTCACCTTCACTTAAGTTGTTGAGGGAAGGCTTACAGACCA 1534
1501 TTTCTTGAATTTGAAAAAGTGAACAGGACAGTGGCTCACCTGTAATCCAGACCT 1560
1535 TTTCTTGAATTTGAAAAAGTGAACAGGACAGTGGCTCACCTGTAATCCAGACCT 1594
1561 TAGGAGACCAAGTCAAGAGATGATTAAGCTTGAAGGTTGAGACCAAGCTTGGGCA 1620
1595 TAGGAGACCAAGTCAAGAGATGATTAAGCTTGAAGGTTGAGACCAAGCTTGGGCA 1654
1621 GTATTTGAGACCAAGTCAAGAGATGATTAAGCTTGAAGGTTGAGACCAAGCTTGGGCA 1680
1655 GTATTTGAGACCAAGTCAAGAGATGATTAAGCTTGAAGGTTGAGACCAAGCTTGGGCA 1714
1681 AATATGAGAAAGAAATTAATGAAGAAATTAATGAAGAAATTAATGAAGAAAT 1740
1715 AATATGAGAAAGAAATTAATGAAGAAATTAATGAAGAAATTAATGAAGAAAT 1774
1741 ACTTTTGAAGAAAGAAATTAATGAAGAAATTAATGAAGAAATTAATGAAGAAAT 1800
1775 ACTTTTGAAGAAAGAAATTAATGAAGAAATTAATGAAGAAATTAATGAAGAAAT 1834
1801 AATTTGCAAAACATCATCTTAAATTTTAA 1830
1835 AATTTGCAAAACATCATCTTAAATTTTAA 1864

LOCUS	BD157945	2663 bp	DNA	linear	PAT 17-JAN-2003
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.				
ACCESSION	BD157945.1	GI:27863703			
VERSION	BD157945.1	GI:27863703			
KEYWORDS	JP 2002191363-A/12788.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 2663)				
TITLE	Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Makamatsu,A., Nagai,K. and Otsuki,T.				
JOURNAL	Primer for synthesizing full-length cDNA and use thereof				
COMMENT	Patent: JP 2002191363-A/12788 09-JUL-2002; HELIX RESEARCH INSTITUTE				
PS	Homo sapiens (human)				
PN	JP 2002191363-A/12788				
PD	09-JUL-2002				
PF	28-JUL-2000 JP 2000280990				
PI	TOSHIO OCA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,				
PI	JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI MAKAMATSU,				
PI	KEIICHI NAGAI, TETSUJI OTSUKI				
PC	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N5/00, C12N5/00 CC				
FT	CDS	Location/Qualifiers			
FEATURES	source	1..2663			
		/organism="Homo sapiens"			
		/mol_type="genomic DNA"			
		/db_xref="taxon:9606"			
ORIGIN	Query Match	98.0%; Score 1811.6; DB 6; Length 2663;			
	Best Local Similarity	99.7%; Pred. No. 0;			
	Matches 1825; Conservative	0; Mismatches 4; Indels 1; Gaps 1			
QY	1 CTGAGCGCGCGGTAGCATGGAGGGGAGAGTACGTGGCGGTCTCGCGCTTTGTGCT	60			
DB	36 CTGAGCGCGCGGTAGCATGGAGGGGAGAGTACGTGGCGGTCTCGCGCTTTGTGCT	95			
QY	61 CGGCCGACCTCGCTTTCAGACACCTCAACAGGACTCGGACAGGAAGTTTCTCTGG	120			
DB	96 CGGCCGACCTCGCTTTCAGACACCTCAACAGGACTCGGACAGGAAGTTTCTCTGG	155			
QY	121 GGAAGTAAAGGTGAAGCCAGAACGACTTACTGATTCCTCAATGGATGTTGAAGT	180			
DB	156 GGAAGTAAAGGTGAAGCCAGAACGACTTACTGATTCCTCAATGGATGTTGAAGT	215			
QY	181 TGTATTATCAATTGACATTCAGAAATATTCAGTCTGACGTTTATAGCTTTATTA	240			
DB	216 TGTATTATCAATTGACATTCAGAAATATTCAGTCTGACGTTTATAGCTTTATTA	275			
QY	241 TTCTTCAGCGCAAGTAAATGAGCACTGAAGAAATATTATCAATAGTCAAAAAGA	300			
DB	276 TTCTTCAGCGCAAGTAAATGAGCACTGAAGAAATATTATCAATAGTCAAAAAGA	335			
QY	301 TGTGTAGGTGGTACAAATCCGTGTCATTCAGATCAGATCAGATGATTTAGAGAG	360			
DB	336 TGTGTAGGTGGTACAAATCCGTGTCATTCAGATCAGATCAGATGATTTAGAGAG	395			
QY	361 GCGGCTTCAAAAACTTGAGAGGATTTTCAACCAAGACCTGTTTCTGCTATT	420			
DB	396 GCGGCTTCAAAAACTTGAGAGGATTTTCAACCAAGACCTGTTTCTGCTATT	455			
QY	421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATA	480			

D	456	AAACAACAAGTATATAACAGAAAGCTGCTCTACTCATCACTGGAACATTCCTATATATAA	515
Q	481	ACCTCMAAAGAGACTTTTTCACAGGGATACCTTTTAGTGGTTGCCAATCTGGGCATGCTG	540
D	516	ACCTCAAAAAGAGACTTTTTCACAGGGATACCTTTTAGTGGTTGCCAATCTGGGCATGCTG	575
Q	541	ACAACCTGGGTATATAAAGTATGATAGAGTCTCTGATGTCACAGGTTTTCAGCGAGCAGT	600
D	576	ACAACCTGGGTATATAAAGTATGATAGAGTCTCTGATGTCACAGGTTTTCAGCGAGCAGT	635
Q	601	ACAAACAACAAGCTCTAAATTTTTCAGAAAGATGATCCTTAAAGAGGTACATAAGAT	660
D	636	ACAAACAACAAGCTCTAAATTTTTCAGAAAGATGATCCTTAAAGAGGTACATAAGAT	695
Q	661	AAATGAATATGATGCTCATTTACAAAGAGATTTAAAGATATATGCAAAAAAGTGAAGA	720
D	696	AAATGAATATGATGCTCATTTACAAAGAGATTTAAAGATATATGCAAAAAAGTGAAGA	755
Q	721	CAGTGAACAAGACAGTATAGTAAACTAGTAAAGATGTAAACAGATTTAAACGAGAAATG	780
D	756	CAGTGAACAAGACAGTATAGTAAACTAGTAAAGATGTAAACAGATTTAAACGAGAAATG	815
Q	781	GAAAAAGAGAGACACAGATTCAGGAGACAGAGAAAGAAACATCCAAAAAGACCTCA	840
D	816	GAAAAAGAGAGACACAGATTCAGGAGACAGAGAAAGAAACATCCAAAAAGACCTCA	875
Q	841	GAAGAACATTTTCTTTGTGTCAGGATTAACGACCTTTTTCAAATTCGTAATTCCTCA	900
D	876	GAAGAACATTTTCTTTGTGTCAGGATTAACGACCTTTTTCAAATTCGTAATTCCTCA	935
Q	901	TTTCATGTGTATGTCCTTTTAAAAAATAGACATGTTTCTTAAAGTACGTATCTCAACCA	960
D	936	TTTCATGTGTATGTCCTTTTAAAAAATAGACATGTTTCTTAAAGTACGTATCTCAACCA	995
Q	961	CCATCTGATGATAGTATGACATCTGACCTTATAGTATGAGAACACACTGACATCTCTGAAGC	1020
D	996	CCATCTGATGATAGTATGACATCTGACCTTATAGTATGAGAACACACTGACATCTCTGAAGC	1055
Q	1021	TAGTCACCTTAGTACACCAACCAATCATTTAGCATTAAGCCTTAGACTAGTACAGATG	1080
D	1056	TAGTCACCTTAGTACACCAACCAATCATTTAGCATTAAGCCTTAGACTAGTACAGATG	1115
Q	1081	GCAATTCAGAGATCTGGTGGTGTATGATACAAAGACAAAGATCTAAAGCAATACTG	1140
D	1116	GCAATTCAGAGATCTGGTGGTGTATGATACAAAGACAAAGATCTAAAGCAATACTG	1175
Q	1141	TAGTAGTACCAAGATTAAGATCCAAATGAGCAGCCACAGAAACAGATGAAGAAATTGA	1200
D	1176	TAGTAGTACCAAGATTAAGATCCAAATGAGCAGCCACAGAAACAGATGAAGAAATTGA	1235
Q	1201	AAAGATGAAGGTTTGTGTGAATATTCACGGTCTCCATCATTTGATCCTTTTAACTTA	1260
D	1236	AAAGATGAAGGTTTGTGTGAATATTCACGGTCTCCATCATTTGATCCTTTTAACTTA	1295
Q	1261	CAAGAGATTTTTTTTATTTGGCTGATGGTAAAGCCAAACATTTCTATGTTTTACTAT	1320
D	1296	CAAGAGATTTTTTTTATTTGGCTGATGGTAAAGCCAAACATTTCTATGTTTTACTAT	1355
Q	1321	GTTGAGCTACTTCGATGATAGTTCAATTTGTTTTTACTATGTTTCACTGTTTGCAAGTAATAC	1380
D	1356	GTTGAGCTACTTCGATGATAGTTCAATTTGTTTTTACTATGTTTCACTGTTTGCAAGTAATAC	1415
Q	1381	ACAGATTAAGCTCTAGTGAATTTACTTCAAAAGTACTTTTCAACATCAAGATGCTTTTA	1440
D	1416	ACAGATTAAGCTCTAGTGAATTTACTTCAAAAGTACTTTTCAACATCAAGATGCTTTTA	1475
Q	1441	TTTCCAAACCTTTTTTCACTTTTCACTAAAGTGTGAGGGGAAAGGCTTACACACACA	1500
D	1476	TTTCCAAACCTTTTTTCACTTTTCACTAAAGTGTGAGGGGAAAGGCTTACACACACA	1535
Q	1501	TTCTTTAGATTTGAAAAAGTGAACACAGACACAGGCTCAACCTGTAACTCCAGCACT	1560
D	1536	TTCTTTAGATTTGAAAAAGTGAACACAGACACAGGCTCAACCTGTAACTCCAGCACT	1595

QY 1561 TAGGGAAGACAGTACAGAGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGGCAAC 1620
 Db 1595 TAGGGAAGACAGTACAGAGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGGCAAC 1654
 QY 1621 GATATGAGACATGTCATTAATAAATTAATAAGAAAGCAAGATAGCTTATTTTCA 1680
 Db 1655 GTATGAGACATGTCATTAATAAATTAATAAGAAAGCAAGATAGCTTATTTTCA 1714
 QY 1681 AATATGAGAAAGAAATTAATAAGAAATTAATCTGAGTCATTAATAATCTCTTAAGTAT 1740
 Db 1715 AATATGAGAAAGAAATTAATAAGAAATTAATCTGAGTCATTAATAATCTCTTAAGTAT 1774
 QY 1741 ACTTTTAAAGTACATTTAGCTAGAGTGGCAATTAATAAGCTGATATATGATCAT 1800
 Db 1775 ACTTTTAAAGTACATTTAGCTAGAGTGGCAATTAATAAGCTGATATATGATCAT 1834
 QY 1801 AATTTGCAAAACATCATCTTAATTTAA 1830
 Db 1835 AATTTGCAAAACATCATCTGAATTTAA 1864

RESULT 9
 AK022704 2663 bp mRNA linear PRI 01-AUG-2002
 LOCUS Homo sapiens cDNA FLJ12642 fis, clone NTZRM4001965.
 DEFINITION AK022704 GI:10434253
 VERSION oligo capping; fis (full insert sequence).
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1
 1 Isogai,T., Ota,T., Hayaashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagaizawa,M., Hosotani,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Matanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuno,Y., Ninomiya,K. and Iwayanagi,T.
 NEDO human cDNA sequencing project
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 2663)
 REFERENCE Isogai,T. and Otsuki,T.
 AUTHORS Direct Submission
 JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3586) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

COMMENT
 FEATURES
 source
 1.2663
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NTZRM4001965"
 /cell_line="NT2"
 /cell_type="teratocarcinoma"
 /clone_id="NTZRM4"
 /note="cloning vector: pXELISFL3-mRNA from uninduced NT2 neuronal precursor cells."
 379.1281
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BABI4189.1"
 /db_xref="GI:10434254"
 /translation="MTFRRLHKNIQEHFSNODLVFLLLPSITTESCSRLRLHSL

ORIGIN
 Query Match 98.0%; Score 1811.6; DB 9; Length 2663;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1825; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 YKPKGLFHRVPLVANLGMSEDLGYTVSGSCKSTGFSAPVQTHSSKFEEDGSLKE
 VHKINEMVASLOEELKSI CKKVEDSEAVKLVADVRLKREIEKRAQIOARBN
 IORDPBNIFLCALRTFPPNSERBSLKNRHSVCNHNHLDVQDNTLWY
 EHTDIPASPASTPOI IKHKTLDLDDEWQFRSLDTPQKRSAVDTGSSNODKASKM
 SSPTDEIEEMKGFGEYSRSPTE"

QY 1 CTGAGGCGCGGTGATGAGAGGAGAGATGCGCGGTGCTCGGCGCTTGCT 60
 Db 36 CTGAGGCGCGGTGATGAGAGGAGAGATGCGCGGTGCTCGGCGCTTGCT 95
 QY 61 CGGCGACTGCTTCCAGACCTCAACACGAGTGGAGACGGAAGTTTCTTTGG 120
 Db 96 CGGCGACTGCTTCCAGACCTCAACACGAGTGGAGACGGAAGTTTCTTTGG 155
 QY 121 GGAAGTAAAGGTAAAGCAAGACAGATACGATTTCCAAATGATGATGAGT 180
 Db 156 GGAAGTAAAGGTAAAGCAAGACAGATACGATTTCCAAATGATGATGAGT 215
 QY 181 TGTATATCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 216 TGTATATCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 275
 QY 241 TTCTTCAGGCGAAGTAAATGAGACAGTGAAGAAATATTAATCAATGTC 300
 Db 276 TTCTTCAGGCGAAGTAAATGAGACAGTGAAGAAATATTAATCAATGTC 335
 QY 301 TGTGTAGTGTGTGATCAAAATCCCTGCTCATTCAGATCAGATCAGTGA 360
 Db 336 TGTGTAGTGTGTGATCAAAATCCCTGCTCATTCAGATCAGATCAGTGA 395
 QY 361 GCTGCTTACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTTC 420
 Db 396 GCTGCTTACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTTC 455
 QY 421 AACACCAAGTAAATTAACAGAACTGCTACATCAGATGAGACATTCCTAT 480
 Db 456 AACACCAAGTAAATTAACAGAACTGCTACATCAGATGAGACATTCCTAT 515
 QY 481 ACTCTAAAAGACCTTTTCAAGAGGATACCTTATGAGTGGCAATCTGGAG 540
 Db 516 ACTCTAAAAGACCTTTTCAAGAGGATACCTTATGAGTGGCAATCTGGAG 575
 QY 541 ACAACCTGGCTATTAACCTGATCAGGTCCTGATGATGATGATGATGAT 600
 Db 576 ACAACCTGGCTATTAACCTGATCAGGTCCTGATGATGATGATGATGAT 635
 QY 601 ACAACCAAGCTCTTAATTTTGAAGAAGATGATCTTAAAGAGGATCAAT 660
 Db 636 ACAACCAAGCTCTTAATTTTGAAGAAGATGATCTTAAAGAGGATCAAT 695
 QY 661 AAATGAAGTGAATGATCTTATTAAGAGAAATTAAGATTAAGAAAGTGA 720
 Db 696 AAATGAAGTGAATGATCTTATTAAGAGAAATTAAGATTAAGAAAGTGA 755
 QY 721 CAGTGAACAGCAATGATTAATCTGATTAAGATGATTAAGATTAAGAGAT 780
 Db 756 CAGTGAACAGCAATGATTAATCTGATTAAGATGATTAAGATTAAGAGAT 815
 QY 781 GAAAGAGAGAGACACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 816 GAAAGAGAGAGACACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 875
 QY 841 GGAAGACATTTTCTTTGTCAGGATTAAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 876 GGAAGACATTTTCTTTGTCAGGATTAAGAGAGAGAGAGAGAGAGAGAGAG 935
 QY 901 TTCAATGCTATGCTTTTAAATTAAGATGATGATGATGATGATGATGAT 960

Db 936 TTCATGCTTATGCTTTTAAAAATAGACATGTTCTTAAAGTAGCTGTATCAACCA 995
 QY 961 CCATCTGATGTAGTACCAATCTGACCTTAATGTTGAAACACATGACATTCCTGAGC 1020
 Db 996 CCATCTGATGTATGATACCAATCTGACCTTAATGTTGAAACACATGACATTCCTGAGC 1055
 QY 1021 TAGTCCAGCTGTACACCAACCAATCTTAAGCATTAAGCCTTGAAGCTTAAGTACAGATG 1080
 Db 1056 TAGTCCAGCTGTACACCAACCAATCTTAAGCATTAAGCCTTGAAGCTTAAGTACAGATG 1115
 QY 1081 GCAATTCAGAGATCTGGTGTGTAATACACAAAGACAAACGATCTAAGCAAAATCTG 1140
 Db 1116 GCAATTCAGAGATCTGGTGTGTAATACACAAAGACAAACGATCTAAGCAAAATCTG 1175
 QY 1141 TAGTAGTACCAAGATTAAGCATCAAAATGAGCAGCCAGAAACAGATGAGAAATTTGA 1200
 Db 1176 TAGTAGTACCAAGATTAAGCATCAAAATGAGCAGCCAGAAACAGATGAGAAATTTGA 1235
 QY 1201 AAAGATGAAAGGTTTGGTGAATATCAAGGCTCTCTACATTTTGTATCTTTAACCTTA 1260
 Db 1236 AAAGATGAAAGGTTTGGTGAATATCAAGGCTCTCTACATTTTGTATCTTTAACCTTA 1295
 QY 1261 CAAGGATTTTGTATTTGTCGATAGGTTAAAGCCAAACATTTCTAATGTTTCTAT 1320
 Db 1296 CAAGGATTTTGTATTTGTCGATAGGTTAAAGCCAAACATTTCTAATGTTTCTAT 1355
 QY 1321 GTTAGAGCTTGTGAGTAAAGTCAATTTGTTTACTAATGTTCACTGTTTGCAGTAAAC 1380
 Db 1356 GTTAGAGCTTGTGAGTAAAGTCAATTTGTTTACTAATGTTCACTGTTTGCAGTAAAC 1415
 QY 1381 ACAATTAATCTTGTAGTCAATTTACTCAAAAGTCAATTTTCAAAACATGAGTCTTTA 1440
 Db 1416 ACAATTAATCTTGTAGTCAATTTACTCAAAAGTCAATTTTCAAAACATGAGTCTTTA 1475
 QY 1441 TTTCCAAACCTTTTTCACCTTCACTAATGTTGAGGGGAAAGCTTACACAGACACA 1500
 Db 1476 TTTCCAAACCTTTTTCACCTTCACTAATGTTGAGGGGAAAGCTTACACAGACACA 1534
 QY 1501 TTCTTTAGATTTGAAAGTGAACACAGCAGTGGTCTCACACCTGTAATCCAGACACT 1560
 Db 1535 TTCTTTAGATTTGAAAGTGAACACAGCAGTGGTCTCACACCTGTAATCCAGACACT 1594
 QY 1561 TAGGGAAGACAGTCAAGGATGATGAGAGCTAGAGTTAGAGACAGCCTGGGCAAC 1620
 Db 1595 TAGGGAAGACAGTCAAGGATGATGAGAGCTAGAGTTAGAGTTAGAGACAGCCTGGGCAAC 1654
 QY 1621 GTATTGAGACCAATGCTTATTAATAAATGAATAAAGCAAGATAGCTTATTTTCAA 1680
 Db 1655 GTATTGAGACCAATGCTTATTAATAAATGAATAAAGCAAGATAGCTTATTTTCAA 1714
 QY 1681 AATATGAAAGAAATTTATGAAATTTATCTGATCAATTAATCTCTTAAGTAT 1740
 Db 1715 AATATGAAAGAAATTTATGAAATTTATCTGATCAATTAATCTCTTAAGTAT 1774
 QY 1741 ACTTTTATGAAAGTCAATTTAGTGTAGAGTTGCCAGATTAATCTGGATATCTGCAAT 1800
 Db 1775 ACTTTTATGAAAGTCAATTTAGTGTAGAGTTGCCAGATTAATCTGGATATCTGCAAT 1834
 QY 1801 AAATTTGCAAAACATCATCTTAATTTAA 1830
 Db 1835 AAATTTGCAAAACATCATCTGAAATTTAA 1864

RESULT 10

AX880746

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

2719 bp. DNA

linear PAT 17-DEC-2003

Sequence 15651 from Patent EP1074617.

AX880746

AX880746.1 GI:40035482

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS TITLE JOURNAL FEATURES source

CDS

ORIGIN

Query Match 91.1%; Score 1684.4; DB 6; Length 2719;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 1762; Conservative 0; Mismatches 1; Indels 67; Gaps 1;

1 CTGAGGCGCGGTAGCATGAGGAGGAGAGTACGTCGCGGTGCTCTCGGCTTTGTCCT 60
 Db 17 CTGAGGCGCGGTAGCATGAGGAGGAGAGTACGTCGCGGTGCTCTCGGCTTTGTCCT 76
 QY 61 CGGCGACTCGCTTTCCAGACCTCAACAACGAGCTCGACACGGAAGGTTTCTCTGG 120
 Db 77 CGGCGACTCGCTTTCCAGACCTCAACAACGAGCTCGACACGGAAGGTTTCTCTGG 136
 QY 121 GGAAGTAAAGGTGAAGCAAGACAGATTAATCCCAATGATGATGTTGAAGT 180
 Db 137 GGAAGTAAAGGTGAAGCAAGACAGATTAATCCCAATGATGATGTTGAAGT 196
 QY 181 TGTATATCAATGACATTCAGAAATATTCATGATGATGATGATGATGATGATGATGAT 240
 Db 197 TGTATATCAATGACATTCAGAAATATTCATGATGATGATGATGATGATGATGATGAT 245
 QY 241 TTCTTCAGCGCAAGTAATGAGCAAGCACTGAGAAATATTAATCAATATGCAAAAGAA 300
 Db 246 -----AGAA 249
 QY 301 TGTGTAGGTGTGTAATAATTCGTCATTCATGATGATGATGATGATGATGATGATGATGAT 360
 Db 250 TGTGTAGGTGTGTAATAATTCGTCATTCATGATGATGATGATGATGATGATGATGATGAT 309
 QY 361 GCTGCTTCACAAAACCTTGACAGAGCATTTTCAACCAAGCCTGTTTCTGCTAT 420
 Db 310 GCTGCTTCACAAAACCTTGACAGAGCATTTTCAACCAAGCCTGTTTCTGCTAT 369
 QY 421 AACACAAATATATACAGAAAGTGTCTACTCATGATGATGATGATGATGATGATGATGATGAT 480
 Db 370 AACACAAATATATACAGAAAGTGTCTACTCATGATGATGATGATGATGATGATGATGAT 429
 QY 481 ACTCTAAAAGACATTTTCAAGAGTACCTTTAGTGTGTCATCTGGGAGATGATGATGATGAT 540
 Db 430 ACTCTAAAAGACATTTTCAAGAGTACCTTTAGTGTGTCATCTGGGAGATGATGATGATGAT 489
 QY 541 ACACTGGGTATTAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 490 ACACTGGGTATTAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
 QY 601 ACAACACACAGCTCTAAATTTTGTGAAGAAATGATGATGATGATGATGATGATGATGATGAT 660
 Db 550 ACAACACACAGCTCTAAATTTTGTGAAGAAATGATGATGATGATGATGATGATGATGATGAT 609

QY	661	AAATGAATGATGCTCTTCAATTAACAAGAAATTAAGGTATATGCAAAAAAGTGAAGA	720
Db	610	AAATGAATGATGCTCTTCAATTAACAAGAAATTAAGGTATATGCAAAAAAGTGAAGA	669
QY	721	CAGTGAACAAGCATAGATTAACCTAGTAAAGGATGTAAACAGATTAAACGAAATTTGA	780
Db	670	CAGTGAACAAGCATAGATTAACCTAGTAAAGGATGTAAACAGATTAAACGAAATTTGA	729
QY	781	GAAAAAGAGAGAGACAGATTCAAGGAGCAAGAGAAAGAAATCCAAAAAGACCTTCA	840
Db	730	GAAAAAGAGAGAGACAGATTCAAGGAGCAAGAGAAAGAAATCCAAAAAGACCTTCA	789
QY	841	GGAGAACATTTTCTTTGTCAAGGCAATTAACGACCTTTTCCAAATTCGAATTTCTTCA	900
Db	790	GGAGAACATTTTCTTTGTCAAGGCAATTAACGACCTTTTCCAAATTCGAATTTCTTCA	849
QY	901	TTCATGTGTATGCTTTTAAAAAATAGACATGTTCTTAAAGTAGCTGTAACTACACCA	960
Db	850	TTCATGTGTATGCTTTTAAAAAATAGACATGTTCTTAAAGTAGCTGTAACTACACCA	909
QY	961	CCATCTCGATGTAGTACAAATCTCACTTATGTTAGAACACATGACATTCCTGGAAGC	1020
Db	910	CCATCTCGATGTAGTACAAATCTCACTTATGTTAGAACACATGACATTCCTGGAAGC	969
QY	1021	TAGTCCAGCTAGTACACCAAAATCATTAAAGCATTAAGCCTTAGACTTAGATGACAGATG	1080
Db	970	TAGTCCAGCTAGTACACCAAAATCATTAAAGCATTAAGCCTTAGACTTAGATGACAGATG	1029
QY	1081	GCAATTCAGAGATCTCGGTTGTTAGATACAAACAAAGATTAAGAAATATGAG	1140
Db	1030	GCAATTCAGAGATCTCGGTTGTTAGATACAAACAAAGATTAAGAAATATGAG	1089
QY	1141	TAGTAGTACCAAGATTAAGCATCCAAATAGAGCAGCCAGAAACAGATGAGAAATTTGA	1200
Db	1090	TAGTAGTACCAAGATTAAGCATCCAAATAGAGCAGCCAGAAACAGATGAGAAATTTGA	1149
QY	1201	AAAGATGAAGGCTTTTGGTGAATATTCACGGTCTCTCATTTTGATCTCTTTAACTTAA	1260
Db	1150	AAAGATGAAGGCTTTTGGTGAATATTCACGGTCTCTCATTTTGATCTCTTTAACTTAA	1209
QY	1261	CAAGGAGATTTTAAATTTGGCTGATGGTTAAAGCAAAATTTCTATTTGTTTAACTAT	1320
Db	1210	CAAGGAGATTTTAAATTTGGCTGATGGTTAAAGCAAAATTTCTATTTGTTTAACTAT	1269
QY	1321	GTTAGACTACTTGCAGTAAAGTTCAATTTGTTTAACTATGTTCACTGTTTGCAGTAATAC	1380
Db	1270	GTTAGACTACTTGCAGTAAAGTTCAATTTGTTTAACTATGTTCACTGTTTGCAGTAATAC	1329
QY	1381	ACAGATTAACCTTATAGTGAATTACTTCACAAAGTACTTTTCAAACATCAAGATGGTTTAA	1440
Db	1330	ACAGATTAACCTTATAGTGAATTACTTCACAAAGTACTTTTCAAACATCAAGATGGTTTAA	1389
QY	1441	TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAAGGGAAGGCTTACACACACACA	1500
Db	1390	TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAAGGGAAGGCTTACACACACACA	1449
QY	1501	TTCTTTTGAATTTGGAAAAGTAGACACAGGCAAGTGGCTCAACCTGTAAATCCAGACACT	1560
Db	1450	TTCTTTTGAATTTGGAAAAGTAGAGACAGGCAAGTGGCTCAACCTGTAAATCCAGACACT	1509
QY	1561	TAGGGAAGACAAAGTCAGAGAGATGATTGAAGCTAGAGTTAGAGACACAGGCTGGGCAAC	1620
Db	1510	TAGGGAAGACAAAGTCAGAGAGATGATTGAAGCTAGAGTTAGAGACACAGGCTGGGCAAC	1569
QY	1621	GTATTGAGACCATGTCTATTTAAAAATTAATGAAAAAGCAAGATTAACCTTATTTTCAA	1680
Db	1570	GTATTGAGACCATGTCTATTTAAAAATTAATGAAAAAGCAAGATTAACCTTATTTTCAA	1629
QY	1681	AAATGGAAGAAATTTATATGAAAAATTTATCTGAGTCAATTAATAATTTCTCTTAAGTAT	1740
Db	1630	AAATGGAAGAAATTTATATGAAAAATTTATCTGAGTCAATTAATAATTTCTCTTAAGTAT	1689
QY	1741	ACTTTTTTAGAAGTACATTAATGCTAGAGTTTCCAGATTAATAATGCTGGATATCATGCAAT	1800

[illegible]

Db 250 TGTGTAGTGTGTACAAATTCGTCGTCAATCGATCGATGACGTTTAGAGAG 309
 QY 361 GCTGCTTCACAAAATCTGAGAGCATTTTTCACCAAGACCTGTGTTGCTAT 420
 Db 310 GCTGCTTCACAAAATCTGAGAGCATTTTTCACCAAGACCTGTGTTGCTAT 369
 QY 421 AACCCAAAGTATTAACAGAAAGCTGCTACTCATGCACTGGAACTCTTATATA 480
 Db 370 AACCCAAAGTATTAACAGAAAGCTGCTACTCATGCACTGGAACTCTTATATA 429
 QY 481 ACCCTCAAAAAGGACTTTTTCACAGAGTACCTTGTAGTGGCAATCGGCACTGTGA 540
 Db 430 ACCCTCAAAAAGGACTTTTTCACAGAGTACCTTGTAGTGGCAATCGGCACTGTGA 489
 QY 541 ACAATGGGTTATAAACTGTATCAAGTTCCTGTATGTCACTGGTTTAGCCGAGCAGT 600
 Db 490 ACAATGGGTTATAAACTGTATCAAGTTCCTGTATGTCACTGGTTTAGCCGAGCAGT 549
 QY 601 ACAAAACACAGCTCTAAATTTTTCAGAAAGATGATCCTTAAAGGAGTACATAAGAT 660
 Db 550 ACAAAACACAGCTCTAAATTTTTCAGAAAGATGATCCTTAAAGGAGTACATAAGAT 609
 QY 661 AAATGAAATGTATGCTTCATTACAGAGAAATTAAAGATATATGCAAAAAAGTGAAGA 720
 Db 610 AAATGAAATGTATGCTTCATTACAGAGAAATTAAAGATATATGCAAAAAAGTGAAGA 669
 QY 721 CAGTGAACAAAGCATATGATTAACATTAAGTAAAGATGTTAAAGATTAAGAGAAATTGA 780
 Db 670 CAGTGAACAAAGCATATGATTAACATTAAGTAAAGATGTTAAAGATTAAGAGAAATTGA 729
 QY 781 GAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAGAGATCCCAAAAGACCTCA 840
 Db 730 GAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAGAGATCCCAAAAGACCTCA 789
 QY 841 GGAAGAACTTTTCTTTGTCAAGGATTAACGACCTTTTTCACAAATCTGATTTCTCA 900
 Db 790 GGAAGAACTTTTCTTTGTCAAGGATTAACGACCTTTTTCACAAATCTGATTTCTCA 849
 QY 901 TTCAATGTATGTCTTTTAAATAATAGCATGTTCTTAAAGATGATGATTAACAACA 960
 Db 850 TTCAATGTATGTCTTTTAAATAATAGCATGTTCTTAAAGATGATGATTAACAACA 909
 QY 961 CCAATCTGATGTATGACCAATCTGACCTTATGTGTGAACACACTGACATTCCTGAAGC 1020
 Db 910 CCAATCTGATGTATGACCAATCTGACCTTATGTGTGAACACACTGACATTCCTGAAGC 969
 QY 1021 TAGTCCAGCTGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATG 1080
 Db 970 TAGTCCAGCTGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATG 1029
 QY 1081 GCAATTCAGAGATCTCGGTTGTATGATACCAAGACAAACGATCTAAAGCAAAATCTGG 1140
 Db 1030 GCAATTCAGAGATCTCGGTTGTATGATACCAAGACAAACGATCTAAAGCAAAATCTGG 1089
 QY 1141 TAGTAGTACCAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1200
 Db 1090 TAGTAGTACCAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1149
 QY 1201 AAAAGTGAAGGTTTGTGTGAATATCAACGCTCTCTACATTTTGTATGATCCTTTAACTTA 1260
 Db 1150 AAAAGTGAAGGTTTGTGTGAATATCAACGCTCTCTACATTTTGTATGATCCTTTAACTTA 1209
 QY 1261 CAAGAGATTTTATTTTATTTGCTATGAGGTAAAGCCAAACATTTCTATGTTTATATAT 1320
 Db 1210 CAAGAGATTTTATTTTATTTGCTATGAGGTAAAGCCAAACATTTCTATGTTTATATAT 1269
 QY 1321 GTTAGAGTACTTGAAGTATGATTTGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 1380
 Db 1270 GTTAGAGTACTTGAAGTATGATTTGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 1329
 QY 1381 ACAAGTAACTCTTATGATGATTTACTTCAAAAGTACTTTTTCACAAATCGATGCTTTTA 1440
 Db 1330 ACAAGTAACTCTTATGATGATTTACTTCAAAAGTACTTTTTCACAAATCGATGCTTTTA 1389

QY 1441 TTTCCAAACTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCAC 1500
 Db 1390 TTTCCAAACTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCAC 1449
 QY 1501 TTTCCTTAATTTGGAAGATGAGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGAC 1560
 Db 1450 TTTCCTTAATTTGGAAGATGAGACCAAGGACCAAGGACCAAGGACCAAGGACCAAGGAC 1509
 QY 1561 TAGGAGACCAAGTCCAGAGATTTGATTTGAAGCTTAGAGATTTAGAGACCAAGGCTGGCAAC 1620
 Db 1510 TAGGAGACCAAGTCCAGAGATTTGATTTGAAGCTTAGAGATTTAGAGACCAAGGCTGGCAAC 1569
 QY 1621 GTATTGAGACCAAGTCTTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
 Db 1570 GTATTGAGACCAAGTCTTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1629
 QY 1681 AATATGGAAGAAATTTATGATAAATTTATCTGATGATTTAAATTTCTCTTAAGTAT 1740
 Db 1630 AATATGGAAGAAATTTATGATAAATTTATCTGATGATTTAAATTTCTCTTAAGTAT 1689
 QY 1741 ACTTTTATGAGATCATTTATGCTTAGAGTTCAGGATTAATGCTGATATTCATGAT 1800
 Db 1690 ACTTTTATGAGATCATTTATGCTTAGAGTTCAGGATTAATGCTGATATTCATGAT 1749
 QY 1801 AAATTTGCAAAACATCATCTAAATTTTAA 1830
 Db 1750 AAATTTGCAAAACATCATCTAAATTTTAA 1779

RESULT 12
 AK023676 2719 bp mRNA linear PRI 01-AUG-2002
 LOCUS Homo sapiens cDNA FLJ13614 f18, clone PLACE1010857.
 DEFINITION AK023676
 ACCESSION AK023676.1 GI:10435671
 VERSION Oligo capting; f18 (full insert sequence).
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 1 Isogai, T., Oca, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sato, H., Sugino, S., Ishibashi, T.,
 Fujimori, K., Tanai, H., Kimata, M., Matsumoto, M., Hiraoka, S.,
 Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
 Nakamura, Y., Nagahara, K., Masuko, Y. and Kanehori, K.
 NEDO human cDNA sequencing project
 TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 2719)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kasarazu, Chiba 292-0812, Japan
 (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing and clone selection;
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.

FEATURES
 source
 1. 2719
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="PLACE1010857"
 /cissue_type="Placenta"
 /clone_lib="PLACE1"
 /note="Cloning vector: pME18FLJ3"
 2477248
 /note="67 bases segment is present in AK022704."

misc_feature
 2477248
 /note="67 bases segment is present in AK022704."

CDS

293..1195
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB14635.1"
/db_xref="GI:10435672"
/translation="MTPRERLHKNLOEHSNODIVFLLTPSITTESGSTRLEHSL
YKPKGLFHRVPLVYVANTGKSEQLGYTTSQSCMSTGFSAVTHSKPFEEGSLKE
VHKINEMTASLQEBLKSICKVEDSEGVAKLVADNVRLEKREIKERGAQIQAREKN
IQKDPENIFLQCALRTFPNSFLHSCVSLNRRYKSSCNHLLVDVNLTLNV
EHTDIPASPASTPOIKHKALDLDRMOKRSRLDTPKRSKADTGSNODKSKM
SSPETDEIRIKMKGFGEYSRSPTF"

Query Match 91.1%; Score 1684.4; DB 9; Length 2719;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 1; Indels 67; Gaps 1;

QY 1 CTGAGCGCGCGGTAGCATGAGGGGAGAGATCGTCGGCGGTGCTCTCGGGCTTTGTGCT 60
DB 17 CTGAGCGCGCGGTAGCATGAGGGGAGAGATCGTCGGCGGTGCTCTCGGGCTTTGTGCT 76
QY 61 CGGCGCACTGCGCTTCCAGCACTCAACACGCACTGGACACGGAAGTTCCTTCTTG 120
DB 77 CGGCGCACTGCGCTTCCAGCACTCAACACGCACTGGACACGGAAGTTCCTTCTTG 136
QY 121 GGAAGTAAAGGTGAAGCAAGACAGCATTAAGTCCCAANTGATGATGAT 180
DB 137 GGAAGTAAAGGTGAAGCAAGACAGCATTAAGTCCCAANTGATGATGATGAT 196
QY 181 TGTATTACAAATTGACATTCAGAAATATATTCATGCTATGACCTTTTGTATTATA 240
DB 197 TGTATTACAAATTGACATTCAGAAATATATTCATGCTATGACCTTTTGTATTATA 245
QY 241 TTCTTCAGGGAAGTAATGAGCAAGCACTGAAGAAATATTTCAATGTCAAAAAGAA 300
DB 246 -----AGAA 249
QY 301 TGTGTAGGTGTGATCAAAATTCGTCGTCATTCAGATCAGATCATGCTTTAGAGAG 360
DB 250 TGTGTAGGTGTGATCAAAATTCGTCGTCATTCAGATCAGATCATGCTTTAGAGAG 309
QY 361 GCTGCTTCAAAAACTTGGAGAGCATTTTCAAACCAAGACCTTGTGTTTCTGCTATT 420
DB 310 GCTGCTTCAAAAACTTGGAGAGCATTTTCAAACCAAGACCTTGTGTTTCTGCTATT 369
QY 421 AACCAAGTATTAATACAGAAAGTCTCTACATCGATCGATGGAACATCTTATATA 480
DB 370 AACCAAGTATTAATACAGAAAGTCTCTACATCGATCGATGGAACATCTTATATA 429
QY 481 ACCTCAAAAAGACCTTTTCAACAGGATACCTTATAGTGTGCAATCTGGGCATGCTGA 540
DB 430 ACCTCAAAAAGACCTTTTCAACAGGATACCTTATAGTGTGCAATCTGGGCATGCTGA 489
QY 541 ACAACTGGGTATTAATCTGATCAGGTCTCTGATGTCACATCGTGTGACCGACAGT 600
DB 490 ACAACTGGGTATTAATCTGATCAGGTCTCTGATGTCACATCGTGTGACCGACAGT 549
QY 601 ACAAAACACAGCTCTAAATTTTGAAGAAAGTGAATCCTTAAAGAGGTACATTAAGT 660
DB 550 ACAAAACACAGCTCTAAATTTTGAAGAAAGTGAATCCTTAAAGAGGTACATTAAGT 609
QY 661 AAAAGAAATGTATGCTTCAATTAACAGAGGAATTAAGAGTATATGCAAAAAATGGAAG 720
DB 610 AAAAGAAATGTATGCTTCAATTAACAGAGGAATTAAGAGTATATGCAAAAAATGGAAG 669
QY 721 CAGTGAACAAGCAGTAGATAAATCTAGTAAGATGTAAACAGATTAAACGAGAAATTGA 780
DB 670 CAGTGAACAAGCAGTAGATAAATCTAGTAAGATGTAAACAGATTAAACGAGAAATTGA 729
QY 781 GAAAAAGAGAGAGCAGATTCAGGCAAGAGAGAGAAACATCCAAAAACCTCTCA 840
DB 730 GAAAAAGAGAGAGCAGATTCAGGCAAGAGAGAGAAACATCCAAAAACCTCTCA 789

QY 841 GGAGAACATTTTCTCTTGTACAGCATTAACGACCTTTTTCCAAATCTGATTTCTTCA 900
DB 790 GGAGAACATTTTCTCTTGTACAGCATTAACGACCTTTTTCCAAATCTGATTTCTTCA 849
QY 901 TTCAATGTATATGCTTTTAAAAAATGACATGTTTCTAAAGTAGCTTAATCAACCA 960
DB 850 TTCAATGTATATGCTTTTAAAAAATGACATGTTTCTAAAGTAGCTTAATCAACCA 909
QY 961 CCATCTCATGTAGTAGCAATCTGACCTTAAAGTAGAGACACACTGACATTCCTGAAGC 1020
DB 910 CCATCTCATGTAGTAGCAATCTGACCTTAAAGTAGAGACACACTGACATTCCTGAAGC 969
QY 1021 TAGTCCAGTGTACACCACAATATTTAAGCATTAAGCCTTTAGATGATGACAGATG 1080
DB 970 TAGTCCAGTGTACACCACAATATTTAAGCATTAAGCCTTTAGATGATGACAGATG 1029
QY 1081 GCAATTCAGAGATCTCGTGTGTAGTAGACAAAGACAAAGATTAAGCAAAATACG 1140
DB 1030 GCAATTCAGAGATCTCGTGTGTAGTAGACAAAGACAAAGATTAAGCAAAATACG 1089
QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAATAGACGCCCAAGAACAGATGAAGAAATTGA 1200
DB 1090 TAGTAGTAACCAAGATTAAGCATCCAAATAGACGCCCAAGAACAGATGAAGAAATTGA 1149
QY 1201 AAAGATGAAGGTTTGTGAATATTCAGGCTTCCTCATTTGATTCCTTTAACCTTA 1260
DB 1150 AAAGATGAAGGTTTGTGAATATTCAGGCTTCCTCATTTGATTCCTTTAACCTTA 1209
QY 1261 CAAGAGATTTTATTTATGCTGATGAGTAAAGCAACATTTCTATGTTTTACTAT 1320
DB 1210 CAAGAGATTTTATTTATGCTGATGAGTAAAGCAACATTTCTATGTTTTACTAT 1269
QY 1321 GTTGAAGTACTGAGTAGTATGATTTTCTATAGTCACTGTTGACAGTAATAC 1380
DB 1270 GTTGAAGTACTGAGTAGTATGATTTTCTATAGTCACTGTTGACAGTAATAC 1329
QY 1381 ACAGATTAATCTGTATGATTTACTTCAAAAGTACTTTTCAACATCAGATGCTTTTA 1440
DB 1330 ACAGATTAATCTGTATGATTTACTTCAAAAGTACTTTTCAACATCAGATGCTTTTA 1389
QY 1441 TTTCCAAACCTTTTTCACCTTTCACTAATGTTGTAGGGGAAAGCTTAACACAGACA 1500
DB 1390 TTTCCAAACCTTTTTCACCTTTCACTAATGTTGTAGGGGAAAGCTTAACACAGACA 1449
QY 1501 TTCTTAAGATTTGAAAGTAGACACAGGCAACAGTGTCTCACCTGTAAATCCAGCACT 1560
DB 1450 TTCTTAAGATTTGAAAGTAGACACAGGCAACAGTGTCTCACCTGTAAATCCAGCACT 1509
QY 1561 TAGGAGAACAGTCAAGAGATGATTAAGCTTAGAGATTAGACACAGCTGGGCAAC 1620
DB 1510 TAGGAGAACAGTCAAGAGATGATTAAGCTTAGAGATTAGACACAGCTGGGCAAC 1569
QY 1621 GATTAAGAACATGCTATTAATAAATAAATGAGAAAGCAAGATAGCTTATTTTCAA 1680
DB 1570 GATTAAGAACATGCTATTAATAAATAAATGAGAAAGCAAGATAGCTTATTTTCAA 1629
QY 1681 AATATGAAGAAATTTATGAAATTTATCTGATGATTAATTTCTCTTAAGTAT 1740
DB 1630 AATATGAAGAAATTTATGAAATTTATCTGATGATTAATTTCTCTTAAGTAT 1689
QY 1741 ACTTTTGAAGATGATTAAGGCTAGAGTGCAGATTAAGTGTGATTCATGCAAT 1800
DB 1690 ACTTTTGAAGATGATTAAGGCTAGAGTGCAGATTAAGTGTGATTCATGCAAT 1749
QY 1801 AAATTTGCAAAACATCATCTAAATTTAA 1830
DB 1750 AAATTTGCAAAACATCATCTAAATTTAA 1779

RESULT 13
AC080014/c AC080014 163111 bp DNA linear PRI 25-FEB-2003
LOCUS Homo sapiens 3 BAC RP11-301G23 (Rowe) Park Cancer Institute Human
DEFINITION


```
repeat_region complement(9671..,10122)
/rpc_family="MER45B"
repeat_region 10124..,10873
/rpc_family="L1P4"
repeat_region complement(10879..,11461)
/rpc_family="MER45B"
repeat_region 12515..,12659
/rpc_family="MIR"
repeat_region 12671..,12948
/rpc_family="AluJb"
repeat_region 13292..,13603
/rpc_family="AluY"
repeat_region 13825..,13965
/rpc_family="L1P"
repeat_region 13961..,15866
/rpc_family="L1P7"
repeat_region complement(16016..,16132)
/rpc_family="FLAM_C"
SMS
17586..,17734
/standard_name="6896"
repeat_region 17735..,17762
/rpc_family="(A)n"
repeat_region 19317..,19411
/rpc_family="L2"
repeat_region 20418..,20620
/rpc_family="MER45C"
repeat_region 20906..,21227
/rpc_family="MER45C"
repeat_region 21963..,22111
/rpc_family="MIR"
repeat_region 23721..,23816
/rpc_family="(CCCA)n"
repeat_region 24296..,24443
/rpc_family="MIR"
repeat_region complement(25826..,25871)
/rpc_family="MIR"
repeat_region complement(25872..,26178)
/rpc_family="AluSg1"
repeat_region complement(26179..,26349)
/rpc_family="MIR"
repeat_region 27742..,27968
/rpc_family="MLT1D"
repeat_region 27969..,28051
/rpc_family="(ATG3TG)n"
repeat_region 28052..,28320
/rpc_family="MLT1D"
repeat_region 29166..,29312
/rpc_family="L1MC5"
repeat_region 29437..,30077
/rpc_family="L1MC5"
repeat_region 30866..,30890
/rpc_family="(TTTA)n"

Query Match 64.5%; Score 1193; DB 9; Length 163111;
Best Local Similarity 85.6%; Prid. No. 2,3e-236;
Matches 1535; Conservative 0; Mismatches 190; Indels 68; Gaps 16;
```

```
QY 241 TTCTTCAGCGCAAGTAAATGAGCACTGAGAAATATTAATCAATGCAAAAAGAA 300
DB 17424 TTCTTCAGTGAATTAATGAGCACTGAGAAATATTAATGCAAAAAGAA 17365
QY 301 TGTGTAGTTGGTGAATTCCTGCTCATTCAGATCAATCAAGCTTTAGAGAG 360
DB 17364 TGTATAGTTGGTGAATTCCTGCTCATTCAGATCAATCAAGCTTTAGAGAG 17305
QY 361 GTCCTTCACAAAAGTGGAGAGCAATTTTCAACCAAGACCTGTTTTCTGATTT 420
DB 17304 GTCCTTCACAAAAGTGGAGAGCAATTTTCAACCAAGACCTTATTTTCTGATTT 17245
QY 421 AACCAAGTATATTAACAGAAAGCTGCTACTCATCGACTGACATTCCTTATATA 480
DB 17244 AACCAAGTATATTAACAGAAAGCTGCTACTCATCGACTGACATTCCTTATATA 17188
QY 481 ACCCTCAAAAAGCACTTTTTCACAGGTAACCTTAGTGTTGCCAATCTGGGCATGCTGA 540
DB 17187 ACCCTCAAAAAGCACTTTTTCACAGGTAACCTTAGTGTTGCCAATCTGATATTTCTGA 17128
QY 541 ACAACTGGTTATATAAATGATCAGGTTCTGTATGTCACCTGTTTTAGCCGAGCAGT 600
DB 17127 ACAACTGGTTATATAAATGATCAGGTTCTGTATGTCACCTGTTTTAGCCGAGCAGT 17068
QY 601 ACAACACACAGCTCTTAATTTTGAAGAAAGATGATCCTTAAGAGGTATCAATAGT 660
DB 17067 AAAACACACAGCTCTTAATTTTGAAGAAAGATGATCCTTAAGAGGTATCAATAGT 17008
QY 661 AATGAATGTATGCTCATTCACAGAGAAATTAAGATATGTC--AAAAAGTGA 718
DB 17007 AATGAATGTATGCTCATTCACAGAGAAATTAAGATATGTC--AAAAAGTGA 16949
QY 719 GACAGTGAACAGAGATGATTAATCTGTAAAGATGTAACGATTTAAACGGAATTT 778
DB 16948 AACATGAACAGAGATGATTAATCTGTAAAGATGTAACGATTTAAACGGAATTT 16889
QY 779 -GAGAAAGAGAGAGACAGATTCAGGACAGCAAGAGAGAAATCCAAAAGAGCC 837
DB 16888 GAGAAAGAGAGAGAGACAGATTCAGGACAGCAAGAGAGAAATCCAAAAGAGCC 16829
QY 838 TCAGAGAAATTTTCTTTGTGACGATTAACGACTTTTTCGAATTTCTGAATTTCT 897
DB 16828 TCAGAGAAATTTTCTTTGTGACGATTAACGACTTTTTCGAATTTCTGAATTTCT 16769
QY 898 TCATTCAGTGTATGCTTTTAAATATGATCAATGTTCTTAAAGTGTGATCTCA 957
DB 16768 TCATTCAGTGTATGCTTTTAAATATGATCAATGTTCTTAAAGTGTGATCTCA 16712
QY 958 CCACCATCTGATGTATGATCAATCTGACCTTAATGTAAGAACACACTGATCTCTGA 1017
DB 16711 CCACCATCTGATGTATGATCAATCTGACCTTAATGTAAGAACACACTGATCTCTGA 16652
QY 1018 AGCTAGTCCAGTATGATCAACCAAAATCAATTAAGCAATTAAGCTTTAGTGAAG 1077
DB 16651 AGCTAGTCCAGTATGATCAACCAAAATCAATTAAGCAATTAAGCTTTAGTGAAG 10712
QY 1078 ATGCAATTCAGAGATCTGAGTGTGTATGATACACAGCAAAATGATCTTAAGCAAT 1137
DB 16531 ATGCAATTCAGAGATCTGAGTGTGTATGATACACAGCAAAATGATCTTAAGCAAT 11317
QY 1138 TGTATAGTATGATCAACCAATTAAGATCAAAATGAGAGCCGGAACCAATGAAGAA 1197
DB 16531 TGTATAGTATGATCAACCAATTAAGATCAAAATGAGAGCCGGAACCAATGAAGAA 11917
QY 1198 TGAAGATGAAGGTTTGTGATATATCAAGGTTCTCTCAATTTGATCTTTTAAAC 1257
DB 16471 TGAAGATGAAGGTTTGTGATATATCAAGGTTCTCTCAATTTGATCTTTTAAAC 16414
QY 1258 TTAACA--AGGAGATTTTATTTTGGCTGATGGGTAAAGCCAA-----CATTTCAAT 1309
DB 16413 TTAAGAGAGATTTTATTTTATTTTGGGATGGGTAAAGCCAAATTTTCAATTTT 16354
QY 1310 GTTTTACTATGTTGAGCTACTTGA-----GTAAGTCAATTTGTTTACTATGT 1360
```



```

Db      16353 G|TTTACATGTTGGAGCTTGCCTTAATACAGTAAATTCATTGTTTACTATAT 16294
QY      1361 TCACCTGTTGAGATATACAGATACCTTAGTACTTACTTCAAGACTTTT 1420
Db      16293 TCCCTGTTGAGATATACAGATACCTTAGTACTTACTTCAAGACTTTT 16234
QY      1421 TCACATCATGATGCTTTTATTTTCCAACTTTTTCACCTTTCACTAAGTGTGAGG 1480
Db      16233 TCACATCATGATGCTTTTATTTTCAAAATC-TTTTTCACATTTCACTAAGTGTGAGG 16175
QY      1481 GGAAGGCTTACACAGACACTTCTTAGAATGGAAGGAGACAGAGCACTGGCTC 1540
Db      16174 GAAAGGCTTACACACTGCTTCTTTTATTTTACGAAAAGTGAAGCCGGGACAGTGGCTC 16115
QY      1541 ACACCTGTATCCACACACTTACGGAAGACAACTGAGAGATGATGAGCTAGAGT 1600
Db      16114 ACACCTGTATCCACACACTTACGGAAGACAACTGAGAGATGATGAGCTAGAGT 16055
QY      1601 TAGAGACCACTGGGCAAGCTATGAGC-----CATGCTATTAATAAATTAATG 1654
Db      16054 TAGAGACCACTGGGCAAGCTATGAGC-----CATGCTATTAATAAATTAATG 15995
QY      1655 AAAAGCAAGATAG-----CCTTATTTTCAAAATATGGAAGAAATTTATATG 1702
Db      15994 AAAAGCAAGATAG-----CCTTATTTTCAAAATATGGAAGAAATTTATATG 15935
QY      1703 AAAA-----TTTATCTAGTATTAATTTCTCTTAAAGTACTTTT 1748
Db      15934 AAAATTTACTTTTATTCGAAGTCAATTAATTTCTCTTAAAGTACTTTT 15882

```

RESULT 14

LOCUS AC012280/c 192819 bp DNA 1linear HTG 26-MAY-2000
 DEFINITION Homo sapiens chromosome 3 clone RP11-49H3 map 3, WORKING DRAFT
 SEQUENCE 21 unordered pieces.

ACCESSION AC012280
 VERSION AC012280.3 GI:7107766
 KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 192819)
 AUTHORS Birren, B., Linton, J., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Batra, N., Beckert, R., Boguslavsky, L., Boultinger, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., D'Arrellano, K., Dewar, K., Domiano, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karasik, A., Klein, J., Lebeck, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGuck, A., McKernan, K., McLaughlin, J., Melidini, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 192819)
 AUTHORS Birren, B., Linton, J., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Batra, N., Beckert, R., Boguslavsky, L., Boultinger, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., D'Arrellano, K., Dewar, K., Domiano, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karasik, A., Klein, J., Lebeck, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGuck, A., McKernan, K., McLaughlin, J., Melidini, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 192819)
 AUTHORS Birren, B., Linton, J., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Batra, N., Beckert, R., Boguslavsky, L., Boultinger, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., D'Arrellano, K., Dewar, K., Domiano, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Heath, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karasik, A., Klein, J., Lebeck, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGuck, A., McKernan, K., McLaughlin, J., Melidini, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
 JOURNAL Unpublished

TITLE Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 JOURNAL On Feb 26, 2000 this sequence version replaced gi:5524236.
 COMMENT All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

FEATURES

source

```

-----
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
-----
Project Information
Center project name: 49 H_3
Center clone name: 11791
-----
Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.967731
Consensus quality: 14855 bases at least Q40
Consensus quality: 171402 bases at least Q20
Consensus quality: 183678 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 190819; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1308: contig of 1308 bp in length
* 1309 1408: gap of 100 bp
* 1409 2850: contig of 1442 bp in length
* 2851 2950: gap of 100 bp
* 2951 4183: contig of 1233 bp in length
* 4184 4283: gap of 100 bp
* 4283 6838: contig of 2555 bp in length
* 6839 6937: gap of 100 bp
* 6937 9037: contig of 1999 bp in length
* 9038 9037: gap of 100 bp
* 9037 13593: contig of 4556 bp in length
* 13594 14693: gap of 100 bp
* 14693 18456: contig of 4763 bp in length
* 18457 18556: gap of 100 bp
* 18557 24027: contig of 5471 bp in length
* 24028 24127: gap of 100 bp
* 24128 29146: contig of 5019 bp in length
* 29147 29246: gap of 100 bp
* 29247 35149: contig of 5903 bp in length
* 35150 35249: gap of 100 bp
* 35250 41614: contig of 6365 bp in length
* 41615 41714: gap of 100 bp
* 41715 51640: contig of 9926 bp in length
* 51641 51740: gap of 100 bp
* 51741 59644: contig of 7904 bp in length
* 59645 59744: gap of 100 bp
* 59745 60013: contig of 9287 bp in length
* 60014 60131: gap of 100 bp
* 60132 79011: contig of 9880 bp in length
* 79012 79111: gap of 100 bp
* 79112 91883: contig of 12772 bp in length
* 91884 91983: gap of 100 bp
* 91984 105714: contig of 13731 bp in length
* 105715 105814: gap of 100 bp
* 105815 121426: contig of 15612 bp in length
* 121427 121527: gap of 100 bp
* 121528 138809: contig of 17283 bp in length
* 138810 138909: gap of 100 bp
* 138910 161154: contig of 22245 bp in length
* 161155 161254: gap of 100 bp
* 161255 192819: contig of 31565 bp in length.
-----
Location/Qualifiers
1. 192819
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3"

```



```
/clone="RP11-49H3"
/clone.lib="RP11 Human Male BAC"
1..1308
misc_feature
  /note="assembly_fragment"
  1409..2850
misc_feature
  /note="assembly_fragment"
  2951..4183
misc_feature
  /note="assembly_fragment"
  4284..6838
misc_feature
  /note="assembly_fragment"
  6939..8937
misc_feature
  /note="assembly_fragment"
  clone_end:Spe
  vector_side:left"
9038..13593
misc_feature
  /note="assembly_fragment"
  13694..18456
misc_feature
  /note="assembly_fragment"
  18557..24027
misc_feature
  /note="assembly_fragment"
  24128..29146
misc_feature
  /note="assembly_fragment"
  29247..35149
misc_feature
  /note="assembly_fragment"
  35250..41614
misc_feature
  /note="assembly_fragment"
  41715..51640
misc_feature
  /note="assembly_fragment"
  51741..59644
misc_feature
  /note="assembly_fragment"
  clone_end:T7
  vector_side:right"
59745..69031
misc_feature
  /note="assembly_fragment"
  69132..79011
misc_feature
  /note="assembly_fragment"
  79112..91883
misc_feature
  /note="assembly_fragment"
  91984..105714
misc_feature
  /note="assembly_fragment"
  105815..121426
misc_feature
  /note="assembly_fragment"
  121527..138809
misc_feature
  /note="assembly_fragment"
  138910..161154
misc_feature
  /note="assembly_fragment"
  161255..192819
  /note="assembly_fragment"
```

ORIGIN

```
Query Match      64.4%; Score 1191.4; DB 2; Length 192819;
Best Local Similarity 85.6%; Pred. No. 4.9e-236;
Matches 153; Conservative 0; Mismatches 191; Indels 68; Gaps 16;

QY      1 CTGAGCGCGCGGTAGCATGAGGCGGAGAGTACGTGCGCGGTCTCGGCGCTTTGTGCT 60
DB      41191 CTGAGCGCGAGCGAGCAGAGGGGTAAAGACA-----GGTGTCTTGGCGCTTGTG-T 41140

QY      61 CGGCGCACTCGCTTTCAGACCTCAACGAGACTCGACACGAGAGTCTTTCTTTGG 120
DB      41139 TGAACAGCTTGCTCTTACACACCCAGCACTGTCTGGACACGAGAGTGTCTTTTAA 41080

QY      121 GGAAGTAAAGGTGAAGCCAGAAACGACATTACTGATCTCCAAATGATGATGTTGAAGT 180
DB      41079 GGAAGTAAAGGTGAAGGCAAGATGACATTACTGATCTCCAAATGATGATGTTGAAGT 41020

QY      181 TGTATTACCAATTGACATTGACAAATATATTCCATGCTACACTTTTAGCTTTATATA 240
DB      41019 TGTATTACCAATTGACATTGACAAATATATTCCATGCT-----TTTTTAGCTTTTATA 40965

QY      241 TTCTTCAGCGCAAGTAATAGCAAGCACTGAAAGAAATATTTATCAATGTCAAAAAGAA 300
DB      40964 TTCTTCAGGTGAAGTAATAGCAAGCACTGAAAGAAATATTTCTCAATGTCAAAAAGAA 40905
```

```
QY      301 TGTGTAGGTGTGTACAAATTCGCTGCTCATTCAGATCAGATCAGTACGTTTAGAGAG 360
DB      40904 TGTATATAGTTGGTACAAATTCGTGTGCTCATTCAGATCAGATCAGTACGTTTAGAGAG 40845

QY      361 GCTGCTTCACAAAAACCTTGACAGAGCATTTTTCAAAACCAAGACCTGTTTCTGCTATT 420
DB      40844 GCTGCTTCACAAAAACCTTGACAGAGCATTTTTCAAAACCAAGACCTTATTTTCTGCTATT 40785

QY      421 AACACCAAGTATATATAACAGAAAGCTGCTACTCATCGACTGACATTCCTTATATAA 480
DB      40784 AACACCAAGTATATATAACAGAAAGCTGCTACTCATCGACTGACATTCCTTATATAA 40728

QY      481 ACCTCAAAAAGACCTTTTTCACAGGGTACCTTTTAGTGTGTGCCAATGTGGCATGTCTGA 540
DB      40727 ACCTCAAAAAGACCTTTTTCACAGGGTACCTTTTAGTGTGTGCCAATGTGTATTTCTGA 40668

QY      541 ACAACTGGGTTATATAAAGTATCAGGTTCCGTATGCTCACTGTTTACCCGAGCAGT 600
DB      40667 ACAACTAGTTTATATAAAGTATCAGGTTCCGTATGCTCACTGTTTACCCGAGCAGT 40608

QY      601 ACAACACACAGCTCTAAATTTTGTGAAGATGATCCTTTAAGAGAGTACATAAGAT 660
DB      40607 AAAAACACACAGCTCTAAATTTTGTGAAGATGATCCTTTAAGAGAGTACATAAGAT 40548

QY      661 AATGAATGTATGCTTCATTACAAAGAGATTAAAGATATATGC--AAAAAGTGGAA 718
DB      40547 AATGAATGT--ATGCTTCATTACAAAGAGATTAAAGATATATGCAAAAAAGTGGAA 40489

QY      719 GACAGTGAACAGCAGATAGATATAAAGTAAAGATGTAAACAGATTAAACGAAATTT 778
DB      40488 AACATGACACAGCAATATAAAGTAAAGATGTAAAGATGTAAACAGATTAAACGAAATTT 40429

QY      779 -GAGAAAAGAGAGAGACACAGATTTCAGGACAGAGAGAGAGAGAACATCCAAAAGAGCCC 837
DB      40428 GGAAGAAAAGAGAGAGATAGATTTCAGGAGCTGAGAGAGAGATTTCTNAAAAGAGCCC 40369

QY      838 TCAGAGAGACATTTTCTTTGTCCAGCATTAACGACCTTTTTCGAAATTTCTGAATTTCT 897
DB      40368 TCAGAGAGACATTTTCTTTGTCCAGCATTAACGACCTTTTATTCAGATTTCTGAATTTCT 40309

QY      898 TCATTATGCTGTATGCTTTTAAATAAGACATGTTTCTTAAAGTACGCTACTACAA 957
DB      40308 TCATTGCTGTGTGCTTTTAAATAAGACATGTTTCTTAA--AGCTGTAAACAA 40252

QY      958 CCACCATCTGATGTAGTACATCTGACCTTAATGATGAGACACACATGACATTCCTGA 1017
DB      40251 CCTCCACCTGATGTAGTACATCTGACCTTAATGATGAGACACACATGACATTCCTGA 40192

QY      1018 AGTATGTCAGCTAGTACACCAACATCATTAAGCATTAAGCCTTACATGATGACAG 1077
DB      40191 AGTATGTCAGCTAGTACACCAACATCATTAAGCATTAAGCCTTACATGATGACAG 40132

QY      1078 ATGGCAATTAAGAGATCGGTTGTAGATACACAAGACAAAGATCTAAAGCAATATC 1137
DB      40131 ATGCAATTAAGAGATCGGTTGTAGATACACAAGATCTAAAGCAATATGATGATC 40072

QY      1138 TGTATGATGAACCAAGATTAAGATCCAAATGATGAGACGCCGAGAAACATGAGAAAT 1197
DB      40071 TGTATGATGAACCAAGATTAAGATCTACATGATGAGACGCCGAGAAATGATGAGAAAT 40012

QY      1198 TGAAGAAATGAAGGTTTGTGTAATTTCAAGGTTCTCATTTTGTATGATCTTTTAAAC 1257
DB      40011 TGAAGAAATGAAGGATCTATGATATCA--GTTCCTTCATCTGATCTTTTAAAC 39954

QY      1258 TTACA--AGGAGATTTTATTTTGTGCTGATGAGTAAAGCCAA--CATTTCTATT 1309
DB      39953 TAAAGAGATTTTATTTTTCATTTGGCGAGATGGGTAAGCCCAACATTTCTATCTATT 39894

QY      1310 GTTTTACTATGTAGAGTACTGCA-----GTAAGTCAATTTGTTTACTATGT 1360
DB      39893 GTTTTACTATGTAGAGTACTGCACTAATACAGATTAATTCATTTGTTTACTATAT 39834
```

QY 1361 TCACCTGTTGGAGTAATACAGATTAACCTTGTGATTTACTTCACAAAGTCTTT 1420
 Db 39833 TCCCTGTTGGAGTAATACAGATTAACCTTGTGATTTACTTCACAAAGTCTTT 39774
 QY 1421 TCACATCAAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACAAAGTGTGAGG 1480
 Db 39773 TCACATCAAGATGCTTTTATTTCCAAATC-TTTTTCACATTTCACTAAGTTGTGAGG 39715
 QY 1481 GGAGGCTTACACAGACATCTTTAGAAATGAAAAGTGAACAGCAGTGTGCTC 1540
 Db 39714 GAAAGCTTACACTGACATCTTTTAACTGAAAAGTGAAGCCGAGGACAGTGTGCTC 39655
 QY 1541 ACACTGTATCCACAGACTTGAAGAAACAAGTCAAGAGATTTGATTTGAAGTGTGAGT 1600
 Db 39654 ACACCTGTATTTCCACACTTGAAGAAACAAGTCAAGAGATTTGATTTGAAGTGTGAGT 39595
 QY 1601 TAGAGACCAAGCCGAGCAAGTGTGAGAC-----CATGTCTATTTAAAAATTAATG 1654
 Db 39594 TAGAGACCAAGCCGAGCAAGTGTGAGACCATCTCTATTTTAAAAATTAATG 39535
 QY 1655 AAAAGCAAGATG-----CCTATTTTAAAAATTTGAAAAGATTTATATG 1702
 Db 39534 AAAAGCAAGATGAAAAGATTTATTTTTCACACGATGAAGAAATTTGTATG 39475
 QY 1703 AAAA-----TTATCTGAGTCAATAAATCTCCTTAAGTATCTTTT 1748
 Db 39474 AAAATTTACTTTTATTTAGATTAATAATCTCCTTAAGTATCTTTT 39422

RESULT 15

AX881436 1896 bp DNA linear PAT 17-DEC-2003
 LOCUS AX881436
 DEFINITION Sequence 16341 from Patent EP1074617.
 ACCESSION AX881436
 VERSION AX881436.1 GI:40036172
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesizing full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 16341 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES
 source
 1..1896
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 790..1512
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CA831279.1"
 /db_xref="GI:40036173"
 /translation="MSEQLGKTVSGSCMTGSRVQTHSSKFFEDGSLKWKHN
 EMVASIQEELKSIKVDSEQAVDKLVKQVNLKRETERKAQIQDAEKKIQDP
 QENIFLCALTFPNSBFLHSCVMSLKNHVSNSVNHLDVNDLTLWEHTDI
 PEASPASTPOIIRKHTLDRMQFKRSRLDLDKLSKADTSSNDKRSXSSPET
 DEIEKKMGFEYSRPTFSF"

ORIGIN

Query Match 60.8%; Score 1125; DB 6; Length 1896;
 Best Local Similarity 99.5%; Pred. No. 3.6e-222;
 Matches 1139; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 496 TTTTACAGGATCTTATGATGCTGCAATCTGGGCACTGTCTGAACAACCTGGTTATA 555
 Db 753 TTTTACAGGATCTTATGATGCTGCAATCTGGGCACTGTCTGAACAACCTGGTTATA 812
 QY 556 AACTGTATCAGGTTCTCTGATGTCACATGCTTTTACCGAGACAGTACAAACACAGCTC 615

Db 813 AACTGTATCAGGTTCTCTGATGTCACATGCTTTTACCGAGACAGTACAAACACAGCTC 872
 QY 616 TAAATTTTGAAGAAAGATGATCTTTAAAGAGGTACATAGATTAATGAATGTATGC 675
 Db 873 TAAATTTTGAAGAAAGATGATCTTTAAAGAGGTACATAGATTAATGAATGTATGC 932
 QY 676 TTGATTAACAAGAAATTTAAAGATATGACAAAAGTGAAGACAGTGAACAGT 735
 Db 933 TTGATTAACAAGAAATTTAAAGATATGACAAAAGTGAAGACAGTGAACAGT 992
 QY 736 AGATTAACCTAGTAAAGATGTAAACAGATTAACAGAAATTTGAAGAAAGAGAGC 795
 Db 993 AGATTAACCTAGTAAAGATGTAAACAGATTAACAGAAATTTGAAGAAAGAGAGC 1052
 QY 796 ACAGATTCAGGACGACAGAGAGAGAGAGAGATCCAAAAGACCTCAGAGAACTTTTCT 855
 Db 1053 ACAGATTCAGGACGACAGAGAGAGAGAGATCCAAAAGACCTCAGAGAACTTTTCT 1112
 QY 856 TTGTCAAGCATTAAGACCTTTTTCCAAATTTGAAATTTCTTCAATGCTATGTC 915
 Db 1113 TTGTCAAGCATTAAGACCTTTTTCCAAATTTGAAATTTCTTCAATGCTATGTC 1172
 QY 916 TTTAAAAATTAAGACATGTTTCTAAAGTACGTTAATAACACACATCTCGATGAT 975
 Db 1173 TTTAAAAATTAAGACATGTTTCTAAAGTACGTTAATAACACACATCTCGATGAT 1232
 QY 976 AGACATCTGACCTTAAATGTGAGAACACACTGACATTTCTGAAGCTATGTCAGTATAC 1035
 Db 1233 AGACATCTGACCTTAAATGTGAGAACACACTGACATTTCTGAAGCTATGTCAGTATAC 1292
 QY 1036 ACCACAAATCTTAAAGATTAAGCTTGAAGTGAAGACAGATGGCAATTCAGAGATC 1095
 Db 1293 ACCACAAATCTTAAAGATTAAGCTTGAAGTGAAGACAGATGGCAATTCAGAGATC 1352
 QY 1096 TCGGTTGTATGATACACAGACAAACATCTAAAGCAATCTGTATGTATTAACAAGA 1155
 Db 1353 TCGGTTGTATGATACACAGACAAACATCTAAAGCAATCTGTATGTATTAACAAGA 1412
 QY 1156 TAAAGCATCCAAAATGAGACCCCAAGAACAGATGAAGAAATTAAGAAAGTGAAGGTT 1215
 Db 1413 TAAAGCATCCAAAATGAGACCCCAAGAACAGATGAAGAAATTAAGAAAGTGAAGGTT 1472
 QY 1216 TGGTAAATATTCAGGCTCTCTACATTTTGAATCTTTTAACTTACAGAGATTTT 1275
 Db 1473 TGGTAAATATTCAGGCTCTCTACATTTTGAATCTTTTAACTTACAGAGATTTT 1532
 QY 1276 ATTGGCTGATGGTAAAGCCAAACATTTCTATTTTACTATGTGACTCTGCA 1335
 Db 1533 ATTGGCTGATGGTAAAGCCAAACATTTCTATTTTACTATGTGACTCTGCA 1592
 QY 1336 GTAAATGATTTGTTTACTATGTTTACCTGTTGACGATATCACAGATTAAGT 1395
 Db 1593 GTAAATGATTTGTTTACTATGTTTACCTGTTGACGATATCACAGATTAAGT 1652
 QY 1396 TGCATTTACTTCAAAAGTACTTTTGAACATGATGCTTTTATTTCCAAACCTTTT 1455
 Db 1653 TGCATTTACTTCAAAAGTACTTTTGAACATGATGCTTTTATTTCCAAACCTTTT 1712
 QY 1456 TTCACTTCACTAGTGTGAGGGAAGGTTTACACAGACACATTTAGATTTGA 1515
 Db 1713 TTCACTTCACTAGTGTGAGGGAAGGTTTACACAGACACATTTAGATTTGA 1771
 QY 1516 AAGTGAACAGGACAGTGTGCTGACCTGTAATCCAGACCTTAGGAAAGACAAATC 1575
 Db 1772 AAGTGAACAGGACAGTGTGCTGACCTGTAATCCAGACCTTAGGAAAGACAAATC 1831
 QY 1576 AGAGATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1635
 Db 1832 AGAGATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1891
 QY 1636 CTATT 1640
 Db 1892 CTATT 1896

Mon Apr 19 12:46:08 2004

us-10-063-523-21.rge

Page 21

Search completed: April 17, 2004, 23:03:42
Job time : 7224 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 149 Seconds

(without alignments) updates/sec
6886.605 Million cell

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ccgagggcgcggtacgcatcg.....aaaaaaaaaaaaaaaaaaaaa 1849

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 10

Total number of hits satisfying chosen parameters: 314562

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

Issued Patents NA: *
1: /cgm2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgm2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgm2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgm2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgm2_6/prodata/2/ina/PCOTUS_COMB.seq:*
6: /cgm2_6/prodata/2/ina/backfillseq1.seq:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	454	24.6	480	4 US-09-621-976-57	Sequence 57, Appl
2	37	2.0	314	4 US-09-621-976-14078	Sequence 14078, A
3	37	2.0	323	4 US-09-621-976-12896	Sequence 12896, A
4	37	2.0	330	4 US-09-621-976-13508	Sequence 13508, A
5	37	2.0	335	4 US-09-621-976-12895	Sequence 12895, A
6	37	2.0	446	4 US-09-621-976-9200	Sequence 9200, Ap
7	37	2.0	464	4 US-09-621-976-14241	Sequence 14241, A
8	37	2.0	2455	4 US-09-685-166A-881	Sequence 881, App
9	37	2.0	2455	4 US-09-685-166A-882	Sequence 882, App
10	37	2.0	5590	4 US-09-050-159-129	Sequence 129, App
11	37	2.0	22255	4 US-09-616-889-51	Sequence 51, Appl
12	37	2.0	33982	4 US-09-820-824-3	Sequence 3, Appl
13	37	2.0	48763	4 US-09-916-104-3	Sequence 3, Appl
14	37	2.0	53526	3 US-08-658-136-2	Sequence 2, Appl
15	37	2.0	53577	3 US-08-658-136-1	Sequence 1, Appl
16	37	2.0	63588	4 US-09-873-404-3	Sequence 3, Appl
17	37	2.0	74962	4 US-09-685-853A-3	Sequence 3, Appl
18	37	2.0	162450	4 US-09-345-882-1	Sequence 1, Appl
19	37	2.0	174493	4 US-09-864-971A-3	Sequence 3, Appl
20	37	2.0	174493	4 US-10-238-709-3	Sequence 3, Appl
21	36	1.9	481	4 US-09-702-705-583	Sequence 583, App
22	36	1.9	481	4 US-09-736-457-583	Sequence 583, App
23	36	1.9	481	4 US-09-614-124B-583	Sequence 583, App
24	36	1.9	481	4 US-09-671-325-583	Sequence 583, App
25	36	1.9	481	4 US-09-589-184-583	Sequence 583, App
26	34	1.8	293	4 US-09-621-976-12021	Sequence 12021, A
27	34	1.8	302	4 US-09-621-976-12333	Sequence 12333, A

28	34	1.8	309	4 US-09-621-976-11582	Sequence 11582, A
29	34	1.8	322	4 US-09-621-976-11620	Sequence 11620, A
30	34	1.8	479	4 US-09-621-976-24825	Sequence 2482, Ap
31	34	1.8	494	4 US-09-621-976-18845	Sequence 18845, A
32	34	1.8	498	4 US-09-621-976-14555	Sequence 14555, A
33	34	1.8	503	4 US-09-621-976-14219	Sequence 14219, A
34	34	1.8	601	4 US-09-811-825A-11	Sequence 10, Appl
35	34	1.8	601	4 US-09-811-825A-11	Sequence 10, Appl
36	34	1.8	601	4 US-09-811-825A-12	Sequence 12, Appl
37	34	1.8	601	4 US-09-811-825A-13	Sequence 13, Appl
38	34	1.8	1762	4 US-09-443-184-35	Sequence 35, Appl
39	34	1.8	6623	2 US-08-687-080-68	Sequence 68, Appl
40	34	1.8	7050	4 US-09-976-594-683	Sequence 683, App
41	34	1.8	12047	2 US-09-022-461-1	Sequence 1, Appl
42	34	1.8	12047	4 US-09-033-556-3	Sequence 3, Appl
43	34	1.8	12047	4 US-09-474-699-11	Sequence 11, Appl
44	34	1.8	12047	4 US-09-151-376-3	Sequence 3, Appl
45	34	1.8	12565	3 US-09-345-217-3	Sequence 3, Appl
46	34	1.8	14796	3 US-08-975-080-35	Sequence 3, Appl
47	34	1.8	14796	3 US-09-630-706-10	Sequence 10, Appl
48	34	1.8	14796	4 US-09-496-694B-3	Sequence 3, Appl
49	34	1.8	16595	4 US-09-146-053-7	Sequence 7, Appl
50	34	1.8	18000	4 US-09-657-346A-17	Sequence 17, Appl
51	34	1.8	18554	4 US-09-811-825A-3	Sequence 3, Appl
52	34	1.8	40000	4 US-08-780-949-18	Sequence 18, Appl
53	34	1.8	87350	3 US-08-781-991-79	Sequence 79, Appl
54	34	1.8	87350	4 US-09-618-166-79	Sequence 79, Appl
55	34	1.8	87543	4 US-09-791-211-3	Sequence 3, Appl
56	34	1.8	92139	4 US-09-918-686-1	Sequence 1, Appl
57	34	1.8	162450	4 US-09-345-882-1	Sequence 1, Appl
58	34	1.8	565	4 US-09-621-976-11747	Sequence 11747, A
59	33	1.8	3464	3 US-08-318-448-30	Sequence 30, Appl
60	33	1.8	87350	3 US-08-781-991-19	Sequence 79, Appl
61	33	1.8	87350	4 US-09-618-166-79	Sequence 79, Appl
62	33	1.8	87543	4 US-09-791-211-3	Sequence 3, Appl
63	33	1.8	99500	4 US-09-798-096-10	Sequence 10, Appl
64	32	1.7	530	4 US-09-621-976-1934	Sequence 1934, Ap
65	32	1.7	31571	1 US-08-323-443B-1	Sequence 1, Appl
66	32	1.7	117132	4 US-09-741-150-3	Sequence 3, Appl
67	32	1.7	117132	4 US-10-160-187-3	Sequence 3, Appl
68	31	1.7	405	4 US-09-621-976-14833	Sequence 14833, A
69	31	1.7	456	4 US-09-621-976-1688	Sequence 1688, Ap
70	31	1.7	526	4 US-09-621-976-3286	Sequence 3286, Ap
71	31	1.7	601	4 US-09-691-861A-19	Sequence 19, Appl
72	31	1.7	8133	4 US-09-659-791A-10	Sequence 10, Appl
73	31	1.7	9862	4 US-09-691-861A-13	Sequence 3, Appl
74	31	1.7	392000	4 US-10-027-983-11	Sequence 11, Appl
75	30	1.6	271	4 US-09-643-557-265	Sequence 265, App
76	30	1.6	271	4 US-09-480-884A-265	Sequence 265, App
77	30	1.6	271	4 US-09-542-615A-265	Sequence 265, App
78	30	1.6	271	4 US-09-606-421B-265	Sequence 265, App
79	30	1.6	322	4 US-09-621-976-13274	Sequence 13274, A
80	30	1.6	390	4 US-09-621-976-14200	Sequence 14200, A
81	30	1.6	400	4 US-09-621-976-18294	Sequence 18294, A
82	30	1.6	466	4 US-09-621-976-3263	Sequence 263, Ap
83	30	1.6	468	4 US-09-621-976-619	Sequence 219, App
84	30	1.6	468	4 US-09-621-976-14057	Sequence 14057, A
85	30	1.6	485	4 US-09-621-976-17711	Sequence 17711, A
86	30	1.6	489	4 US-09-621-976-17517	Sequence 17517, A
87	30	1.6	492	4 US-09-621-976-16439	Sequence 16439, A
88	30	1.6	505	4 US-09-621-976-10635	Sequence 10635, A
89	30	1.6	514	4 US-09-621-976-10635	Sequence 6254, Ap
90	30	1.6	595	4 US-09-621-976-3654	Sequence 3654, Appl
91	30	1.6	998	4 US-09-227-357-62	Sequence 274, App
92	30	1.6	1001	4 US-09-671-317-274	Sequence 37, Appl
93	30	1.6	1154	4 US-09-539-333D-37	Sequence 110, App
94	30	1.6	1247	3 US-09-177-776-110	Sequence 110, App
95	30	1.6	1289	3 US-09-247-155-138	Sequence 138, App
96	30	1.6	1289	3 US-09-539-333D-36	Sequence 36, Appl
97	30	1.6	1301	4 US-09-539-333D-40	Sequence 40, Appl
98	30	1.6	1366	4 US-09-620-312D-743	Sequence 743, App
99	30	1.6	2091	4 US-08-381-691-17	Sequence 17, Appl
100	30	1.6	2119	2	

101	30	1.6	2229	4	US-09-439-313-469	Sequence 469, App	174	30	1.6	319608	4	US-09-679-409-1	Sequence 1, Appl1
102	30	1.6	2229	4	US-09-352-616A-69	Sequence 469, App	175	29	1.6	404	4	US-09-621-976-18360	Sequence 18360, A
103	30	1.6	2229	4	US-09-636-215-469	Sequence 469, App	176	29	1.6	442	4	US-09-621-976-14429	Sequence 14429, A
104	30	1.6	2229	4	US-09-685-166A-469	Sequence 469, App	177	29	1.6	487	4	US-09-621-976-14071	Sequence 14071, A
105	30	1.6	2229	4	US-09-439-313-470	Sequence 470, App	178	29	1.6	517	3	US-09-085-199B-27	Sequence 27, Appl
106	30	1.6	2226	4	US-09-352-616A-470	Sequence 470, App	179	29	1.6	655	3	US-09-385-982-301	Sequence 301, App
107	30	1.6	2426	4	US-09-636-215-470	Sequence 470, App	180	29	1.6	788	4	US-09-659-845A-25	Sequence 25, Appl
108	30	1.6	2426	4	US-09-685-166A-470	Sequence 470, App	181	29	1.6	2040	4	US-09-659-845A-25	Sequence 33, Appl
109	30	1.6	2501	3	US-08-787-739-58	Sequence 58, Appl	182	29	1.6	2045	3	US-09-069-023-33	Sequence 1, Appl1
110	30	1.6	2501	3	US-09-178-115-58	Sequence 58, Appl	183	29	1.6	2119	2	US-09-227-357-48	Sequence 48, Appl
111	30	1.6	2501	3	US-09-177-776-58	Sequence 58, Appl	184	29	1.6	3061	2	US-08-692-787-47	Sequence 47, Appl
112	30	1.6	2886	2	US-08-687-080-55	Sequence 55, Appl	185	29	1.6	3061	3	US-09-097-199-47	Sequence 3, Appl1
113	30	1.6	3425	3	US-09-800-971-1	Sequence 90, Appl1	186	29	1.6	3365	1	US-08-578-649-3	Sequence 6, Appl
114	30	1.6	3425	3	US-08-787-739-90	Sequence 90, Appl1	187	29	1.6	4220	2	US-08-532-883-66	Sequence 66, Appl
115	30	1.6	3532	3	US-09-178-115-90	Sequence 90, Appl1	188	29	1.6	4220	2	US-08-632-877-66	Sequence 10, Appl
116	30	1.6	3532	3	US-09-177-776-90	Sequence 90, Appl1	189	29	1.6	2600	4	US-09-843-976-10	Sequence 16, Appl
117	30	1.6	4174	4	US-09-845-716A-1	Sequence 1, Appl1	190	29	1.6	43950	4	US-09-735-934A-3	Sequence 3, Appl1
118	30	1.6	9704	4	US-09-814-951A-3	Sequence 3, Appl1	191	29	1.6	5152	4	US-10-060-332-3	Sequence 30, Appl1
119	30	1.6	10898	2	US-08-481-658B-5	Sequence 5, Appl1	192	29	1.6	5152	4	US-09-733-294A-30	Sequence 3, Appl1
120	30	1.6	10898	2	US-08-477-504A-5	Sequence 5, Appl1	193	29	1.6	6467	4	US-09-803-671E-3	Sequence 3, Appl1
121	30	1.6	10898	2	US-08-486-756A-5	Sequence 5, Appl1	194	29	1.6	75395	4	US-09-884-890-3	Sequence 11, Appl
122	30	1.6	10898	2	US-08-485-862B-5	Sequence 5, Appl1	195	29	1.6	32000	4	US-10-027-983-11	Sequence 8420, App
123	30	1.6	10898	3	US-08-787-739-5	Sequence 5, Appl1	196	28	1.5	67	4	US-09-621-976-8420	Sequence 11997, A
124	30	1.6	10898	3	US-08-487-077A-5	Sequence 5, Appl1	197	28	1.5	121	4	US-09-621-976-11997	Sequence 268, App
125	30	1.6	10898	3	US-08-485-863A-5	Sequence 5, Appl1	198	28	1.5	223	4	US-09-643-597-268	Sequence 268, App
126	30	1.6	10898	3	US-08-485-863A-5	Sequence 5, Appl1	199	28	1.5	223	4	US-09-480-884A-268	Sequence 268, App
127	30	1.6	10898	3	US-09-178-115-5	Sequence 5, Appl1	200	28	1.5	223	4	US-09-582-615A-268	Sequence 268, App
128	30	1.6	10898	3	US-09-177-776-5	Sequence 5, Appl1	201	28	1.5	223	4	US-09-606-421B-268	Sequence 268, App
129	30	1.6	13953	4	US-09-738-884-3	Sequence 3, Appl1	202	28	1.5	227	3	US-08-522-813-2	Sequence 2, Appl1
130	30	1.6	13953	4	US-09-844-634-17	Sequence 17, Appl1	203	28	1.5	239	4	US-09-621-976-13876	Sequence 13876, A
131	30	1.6	15602	4	US-07-506-871-15	Sequence 15, Appl1	204	28	1.5	240	4	US-09-621-976-14890	Sequence 14890, A
132	30	1.6	17367	1	US-09-087-465-3	Sequence 3, Appl1	205	28	1.5	257	2	US-08-849-701-4	Sequence 4, Appl1
133	30	1.6	19796	3	US-09-740-035-3	Sequence 3, Appl1	206	28	1.5	273	4	US-09-621-976-11959	Sequence 11959, A
134	30	1.6	20284	4	US-09-526-193A-21	Sequence 21, Appl1	207	28	1.5	278	4	US-09-621-976-11694	Sequence 11694, A
135	30	1.6	21721	4	US-09-269-939A-41	Sequence 41, Appl1	208	28	1.5	280	4	US-09-621-976-11605	Sequence 11605, A
136	30	1.6	22976	4	US-09-269-939A-19	Sequence 19, Appl1	209	28	1.5	281	4	US-09-621-976-12443	Sequence 12443, A
137	30	1.6	23187	4	US-09-499-522-1	Sequence 1, Appl1	210	28	1.5	281	4	US-09-621-976-11615	Sequence 16115, A
138	30	1.6	32042	4	US-09-245-281-44	Sequence 44, Appl1	211	28	1.5	282	1	US-08-133-629-8	Sequence 8, Appl1
139	30	1.6	32042	4	US-09-340-620A-63	Sequence 63, Appl1	212	28	1.5	283	4	US-08-579-445-56	Sequence 26, Appl
140	30	1.6	36159	4	US-09-301-665-3	Sequence 3, Appl1	213	28	1.5	283	4	US-09-621-976-11769	Sequence 11769, A
141	30	1.6	36741	3	US-09-820-004-3	Sequence 3, Appl1	214	28	1.5	293	4	US-09-621-976-12408	Sequence 12408, A
142	30	1.6	40090	4	US-09-146-053-6	Sequence 6, Appl1	215	28	1.5	295	4	US-09-621-976-13065	Sequence 13065, A
143	30	1.6	44848	4	US-09-435-739-42	Sequence 42, Appl1	216	28	1.5	296	4	US-09-621-976-12310	Sequence 12310, A
144	30	1.6	45546	4	US-09-491-356C-1	Sequence 1, Appl1	217	28	1.5	297	4	US-09-621-976-11534	Sequence 11534, A
145	30	1.6	55298	4	US-09-813-133A-3	Sequence 3, Appl1	218	28	1.5	300	4	US-09-621-976-16139	Sequence 16139, A
146	30	1.6	55827	4	US-09-813-133A-3	Sequence 3, Appl1	219	28	1.5	301	4	US-09-621-976-11951	Sequence 11951, A
147	30	1.6	59065	4	US-09-813-817-3	Sequence 3, Appl1	220	28	1.5	302	4	US-09-621-976-8545	Sequence 8545, App
148	30	1.6	59065	4	US-09-813-817-3	Sequence 3, Appl1	221	28	1.5	302	4	US-09-621-976-11755	Sequence 11755, A
149	30	1.6	59065	4	US-09-978-197-3	Sequence 3, Appl1	222	28	1.5	303	4	US-09-621-976-11837	Sequence 11837, A
150	30	1.6	59065	4	US-09-978-197-3	Sequence 3, Appl1	223	28	1.5	304	4	US-09-621-976-12113	Sequence 12113, A
151	30	1.6	63006	4	US-09-780-172-18	Sequence 18, Appl1	224	28	1.5	304	4	US-09-621-976-16133	Sequence 16133, A
152	30	1.6	74962	4	US-09-685-853A-3	Sequence 3, Appl1	225	28	1.5	306	4	US-09-621-976-16133	Sequence 16133, A
153	30	1.6	75395	4	US-09-984-890-3	Sequence 3, Appl1	226	28	1.5	307	4	US-09-621-976-17841	Sequence 17841, App
154	30	1.6	84495	4	US-09-797-906-3	Sequence 3, Appl1	227	28	1.5	310	4	US-09-621-976-16133	Sequence 16133, A
155	30	1.6	90541	4	US-09-759-359A-3	Sequence 3, Appl1	228	28	1.5	310	4	US-09-621-976-16133	Sequence 16133, A
156	30	1.6	98844	4	US-09-791-211-10	Sequence 10, Appl1	229	28	1.5	310	4	US-09-621-976-16133	Sequence 16133, A
157	30	1.6	99500	4	US-09-798-096-10	Sequence 10, Appl1	230	28	1.5	311	4	US-09-621-976-12207	Sequence 12207, A
158	30	1.6	11282	4	US-09-754-250-3	Sequence 3, Appl1	231	28	1.5	312	4	US-09-621-976-11835	Sequence 11835, A
159	30	1.6	11282	4	US-09-741-150-3	Sequence 3, Appl1	232	28	1.5	313	4	US-09-621-976-11971	Sequence 11971, A
160	30	1.6	112132	4	US-10-160-187-3	Sequence 3, Appl1	233	28	1.5	313	4	US-09-621-976-12055	Sequence 12055, A
161	30	1.6	116592	4	US-09-818-512-3	Sequence 3, Appl1	234	28	1.5	313	4	US-09-621-976-12236	Sequence 12236, A
162	30	1.6	116592	4	US-09-818-512-3	Sequence 3, Appl1	235	28	1.5	313	4	US-09-621-976-13588	Sequence 13588, A
163	30	1.6	118067	4	US-09-497-855A-32	Sequence 32, Appl1	236	28	1.5	314	4	US-09-621-976-11896	Sequence 11896, A
164	30	1.6	152331	3	US-09-128-155-16	Sequence 16, Appl1	237	28	1.5	316	4	US-09-621-976-11542	Sequence 11542, A
165	30	1.6	168575	3	US-09-426-290-1	Sequence 1, Appl1	238	28	1.5	319	4	US-09-621-976-11125	Sequence 11125, A
166	30	1.6	176373	3	US-09-128-155-17	Sequence 17, Appl1	239	28	1.5	322	4	US-09-621-976-16131	Sequence 16131, A
167	30	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl1	240	28	1.5	323	4	US-09-621-976-16141	Sequence 16141, A
168	30	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl1	241	28	1.5	327	4	US-09-621-976-12141	Sequence 12141, A
169	30	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl1	242	28	1.5	341	4	US-09-621-976-11535	Sequence 11535, A
170	30	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl1	243	28	1.5	341	4	US-09-621-976-11535	Sequence 11535, A
171	30	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl1	244	28	1.5	347	4	US-09-621-976-11597	Sequence 11597, A
172	30	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl1	245	28	1.5	347	4	US-09-621-976-11600	Sequence 11600, A
173	30	1.6	319608	4	US-09-539-333D-1	Sequence 1, Appl1	246	28	1.5	347	4	US-09-621-976-16136	Sequence 16136, A

247	28	1.5	348	4	US-09-621-976-13340	Sequence 13340, A	330	28	1.5	1110	4	US-09-511-625B-43	Sequence 43, Appl
248	28	1.5	351	4	US-09-621-976-16440	Sequence 16340, A	321	28	1.5	1249	4	US-09-461-325-128	Sequence 128, App
249	28	1.5	355	4	US-09-621-976-13319	Sequence 13319, A	322	28	1.5	1248	4	US-10-012-542-128	Sequence 128, App
250	28	1.5	358	4	US-09-621-976-11727	Sequence 11727, A	323	28	1.5	1260	4	US-09-461-325-93	Sequence 93, Appl
251	28	1.5	361	4	US-09-621-976-11659	Sequence 11659, A	324	28	1.5	1260	4	US-10-012-542-93	Sequence 93, Appl
252	28	1.5	361	4	US-09-621-976-11695	Sequence 11695, A	325	28	1.5	1300	2	US-08-474-020A-13	Sequence 13, Appl
253	28	1.5	361	4	US-09-621-976-12227	Sequence 12227, A	326	28	1.5	1542	2	US-09-008-271A-13	Sequence 10, Appl
254	28	1.5	361	4	US-09-621-976-13543	Sequence 13543, A	327	28	1.5	1554	1	US-08-370-975B-10	Sequence 17, Appl
255	28	1.5	364	4	US-09-621-976-11742	Sequence 11742, A	328	28	1.5	1595	4	US-09-461-325-17	Sequence 17, Appl
256	28	1.5	370	4	US-09-621-976-13313	Sequence 13313, A	329	28	1.5	1595	4	US-10-012-542-17	Sequence 17, Appl
257	28	1.5	370	4	US-09-621-976-13486	Sequence 13486, A	330	28	1.5	1701	3	US-09-078-294-9	Sequence 9, Appl
258	28	1.5	371	4	US-09-621-976-11828	Sequence 11828, A	331	28	1.5	1827	3	US-08-737-571A-3	Sequence 3, Appl
259	28	1.5	371	4	US-09-621-976-11983	Sequence 11983, A	332	28	1.5	1827	5	PCT-US95-0585A-3	Sequence 3, Appl
260	28	1.5	371	4	US-09-621-976-12170	Sequence 12170, A	333	28	1.5	1838	2	US-09-227-357-32	Sequence 3, Appl
261	28	1.5	371	4	US-09-621-976-12176	Sequence 12176, A	334	28	1.5	1947	2	US-08-989-925-2	Sequence 2, Appl
262	28	1.5	371	4	US-09-621-976-12666	Sequence 12666, A	335	28	1.5	1988	2	US-08-257-963B-11	Sequence 11, Appl
263	28	1.5	372	4	US-09-621-976-12089	Sequence 12089, A	336	28	1.5	1988	4	US-08-367-841A-4	Sequence 11, Appl
264	28	1.5	372	4	US-09-621-976-12192	Sequence 12192, A	337	28	1.5	1988	5	PCT-US95-0720A-11	Sequence 11, Appl
265	28	1.5	373	4	US-09-621-976-12883	Sequence 12883, A	338	28	1.5	2560	4	US-08-786-256C-29	Sequence 29, Appl
266	28	1.5	373	4	US-09-621-976-12147	Sequence 12147, A	339	28	1.5	2630	3	US-08-669-286-6	Sequence 6, Appl
267	28	1.5	378	4	US-09-621-976-9207	Sequence 9207, A	340	28	1.5	2630	3	US-09-469-253-6	Sequence 6, Appl
268	28	1.5	396	4	US-09-621-976-10717	Sequence 10717, A	341	28	1.5	2630	3	US-09-642-146-6	Sequence 6, Appl
269	28	1.5	404	4	US-09-621-976-8285	Sequence 8285, A	342	28	1.5	2755	4	US-09-023-655-118	Sequence 11, Appl
270	28	1.5	407	4	US-09-621-976-18088	Sequence 18088, A	343	28	1.5	2784	1	US-08-471-454-1	Sequence 1, Appl
271	28	1.5	409	4	US-09-621-976-10551	Sequence 10551, A	344	28	1.5	2784	2	US-08-466-974-1	Sequence 1, Appl
272	28	1.5	413	4	US-09-621-976-12629	Sequence 12629, A	345	28	1.5	2784	2	US-08-471-453-1	Sequence 1, Appl
273	28	1.5	413	4	US-09-621-976-12730	Sequence 12730, A	346	28	1.5	3441	4	US-09-026-033-17	Sequence 17, Appl
274	28	1.5	416	4	US-09-702-705-469	Sequence 469, App	347	28	1.5	3512	4	US-09-691-538A-9	Sequence 9, Appl
275	28	1.5	416	4	US-09-736-457-459	Sequence 469, App	348	28	1.5	3607	2	US-08-629-001A-8	Sequence 8, Appl
276	28	1.5	416	4	US-09-614-124B-469	Sequence 469, App	349	28	1.5	3607	3	US-08-642-274D-8	Sequence 8, Appl
277	28	1.5	416	4	US-09-614-124B-469	Sequence 469, App	350	28	1.5	3607	3	US-08-952-127-8	Sequence 8, Appl
278	28	1.5	416	4	US-09-589-184-469	Sequence 469, App	351	28	1.5	3607	3	US-08-352-014C-8	Sequence 8, Appl
279	28	1.5	419	4	US-09-621-976-2249	Sequence 2249, A	352	28	1.5	3609	3	US-09-705-299-11	Sequence 11, Appl
280	28	1.5	419	4	US-09-621-976-19331	Sequence 19331, A	353	28	1.5	3667	4	US-09-347-114A-81	Sequence 81, Appl
281	28	1.5	420	4	US-09-621-976-11423	Sequence 11423, A	354	28	1.5	4080	2	US-08-710-249-3	Sequence 3, Appl
282	28	1.5	421	4	US-09-621-976-15040	Sequence 15040, A	355	28	1.5	4080	4	US-09-220-157A-3	Sequence 3, Appl
283	28	1.5	422	4	US-09-621-976-8237	Sequence 8237, A	356	28	1.5	4129	2	US-08-370-319C-12	Sequence 12, Appl
284	28	1.5	424	4	US-09-621-976-12991	Sequence 12991, A	357	28	1.5	4183	3	US-09-224-834-12	Sequence 12, Appl
285	28	1.5	447	4	US-09-621-976-17692	Sequence 17692, A	358	28	1.5	4183	3	US-09-460-145-1	Sequence 1, Appl
286	28	1.5	452	4	US-09-621-976-3451	Sequence 3451, A	359	28	1.5	4193	4	US-09-885-547-1	Sequence 1, Appl
287	28	1.5	452	4	US-09-621-976-9111	Sequence 9111, A	360	28	1.5	4192	4	US-09-122-126B-1	Sequence 1, Appl
288	28	1.5	454	4	US-09-621-976-9423	Sequence 9423, A	361	28	1.5	4321	4	US-09-634-286A-6	Sequence 6, Appl
289	28	1.5	458	4	US-09-621-976-12606	Sequence 12606, A	362	28	1.5	4335	3	US-09-058-489-19	Sequence 19, Appl
290	28	1.5	460	4	US-09-621-976-8118	Sequence 8118, A	363	28	1.5	4335	3	US-08-974-549A-6	Sequence 6, Appl
291	28	1.5	463	4	US-09-621-976-15534	Sequence 15534, A	364	28	1.5	4335	3	US-08-721-456-6	Sequence 6, Appl
292	28	1.5	465	4	US-09-621-976-3677	Sequence 3677, A	365	28	1.5	4335	3	US-09-023-655-1482	Sequence 1482, Ap
293	28	1.5	467	4	US-09-621-976-3278	Sequence 3278, A	366	28	1.5	4517	4	US-09-470-881-7	Sequence 7, Appl
294	28	1.5	476	4	US-09-621-976-3281	Sequence 3281, A	367	28	1.5	4517	5	PCT-US93-06251-83	Sequence 83, Appl
295	28	1.5	484	4	US-09-621-976-3281	Sequence 3281, A	368	28	1.5	4531	4	US-09-620-312D-893	Sequence 15, Appl
296	28	1.5	484	4	US-09-621-976-3281	Sequence 3281, A	369	28	1.5	4736	4	US-09-526-193A-15	Sequence 9, Appl
297	28	1.5	484	4	US-09-621-976-14625	Sequence 14625, A	370	28	1.5	4736	3	US-08-884-324-9	Sequence 3, Appl
298	28	1.5	485	4	US-09-621-976-13249	Sequence 13249, A	371	28	1.5	5035	2	US-08-616-392C-3	Sequence 3, Appl
299	28	1.5	485	4	US-09-621-976-11770	Sequence 11770, A	372	28	1.5	5262	4	US-08-520-373D-5	Sequence 5, Appl
300	28	1.5	495	4	US-09-621-976-14126	Sequence 14126, A	373	28	1.5	5984	4	US-09-703-872-2	Sequence 2, Appl
301	28	1.5	503	4	US-09-621-976-14126	Sequence 14126, A	374	28	1.5	6330	4	US-09-880-427-2	Sequence 2, Appl
302	28	1.5	511	4	US-09-621-976-17595	Sequence 17595, A	375	28	1.5	6330	4	US-09-306-538B-2	Sequence 2, Appl
303	28	1.5	511	4	US-09-621-976-13954	Sequence 13954, A	376	28	1.5	6769	3	US-09-480-784-40	Sequence 20, Appl
304	28	1.5	526	4	US-08-579-445-24	Sequence 3687, Ap	377	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
305	28	1.5	532	4	US-09-621-976-3687	Sequence 18218, A	378	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
306	28	1.5	555	4	US-09-621-976-18218	Sequence 15057, Ap	379	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
307	28	1.5	559	4	US-09-621-976-15057	Sequence 11500, A	380	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
308	28	1.5	577	4	US-09-621-976-11500	Sequence 37, Appl	381	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
309	28	1.5	654	4	US-09-288-143-37	Sequence 43, Appl	382	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
310	28	1.5	656	4	US-08-896-164-43	Sequence 37, Appl	383	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
311	28	1.5	852	3	US-09-078-294-18	Sequence 18, Appl	384	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
312	28	1.5	1000	3	US-09-018-584A-32	Sequence 32, Appl	385	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
313	28	1.5	1001	4	US-09-641-538-518	Sequence 518, App	386	28	1.5	7130	3	PCT-US95-10202-20	Sequence 20, Appl
314	28	1.5	1001	4	US-09-671-317-238	Sequence 238, App	387	28	1.5	7130	3	PCT-US95-10202-20	Sequence 20, Appl
315	28	1.5	1001	4	US-09-671-317-239	Sequence 239, App	388	28	1.5	7130	3	US-09-056-105-21	Sequence 1, Appl
316	28	1.5	1001	4	US-09-671-317-259	Sequence 259, App	389	28	1.5	7620	1	US-07-767-135-1	Sequence 1, Appl
317	28	1.5	1001	4	US-09-671-317-259	Sequence 259, App	390	28	1.5	7620	1	US-07-841-652-1	Sequence 1, Appl
318	28	1.5	1001	4	US-09-671-317-260	Sequence 260, App	391	28	1.5	7676	1	US-08-451-777A-7	Sequence 7, Appl
319	28	1.5	1094	4	US-09-205-258-42	Sequence 42, Appl	392	28	1.5	7676	2	US-08-998-208-7	Sequence 7, Appl

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
DB 37 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 73

RESULT 6

US-09-621-976-9200
; Sequence 9200, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9200
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9200

Query Match 2.0%; Score 37; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
DB 398 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 434

RESULT 7

US-09-621-976-14241
; Sequence 14241, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14241
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14241

Query Match 2.0%; Score 37; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
DB 342 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 378

RESULT 8

US-09-685-166A-881
; Sequence 881, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-881

Query Match 2.0%; Score 37; DB 4; Length 2455;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
DB 866 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 902

RESULT 9

US-09-685-166A-882
; Sequence 882, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 882
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-882

Query Match 2.0%; Score 37; DB 4; Length 2455;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 866 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 902

RESULT 10
US-09-050-159-129/c
; Sequence 129, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
; APPLICANT: No. 6197505berg, Ielf T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; FILE OF INVENTION: COMPOSITIONS FOR USE THEREOF
; FILE REFERENCE: 1248/1D042
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; EARLIER FILING DATE: 1987-04-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 5590
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Angiotensin I converting enzyme, 5' region
US-09-050-159-129

Query Match 2.0%; Score 37; DB 3; Length 5590;
Best Local Similarity 100.0%; Pred. No. 6,4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 2051 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 2015

RESULT 11
US-09-616-289-51/c
; Sequence 51, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 22255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-51

Query Match 2.0%; Score 37; DB 4; Length 22255;
Best Local Similarity 100.0%; Pred. No. 6e-07;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 7780 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 7744

RESULT 12
US-09-820-924-3
; Sequence 3, Application US/09820924
; Patent No. 655351
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: C1001213
; CURRENT APPLICATION NUMBER: US/09/820,924
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 39982
; TYPE: DNA
; ORGANISM: Human
US-09-820-924-3

Query Match 2.0%; Score 37; DB 4; Length 39982;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 3375 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 3411

RESULT 13
US-09-916-204-3/c
; Sequence 3, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 48763
; TYPE: DNA
; ORGANISM: Human
US-09-916-204-3

Query Match 2.0%; Score 37; DB 4; Length 48763;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 24147 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 24111

RESULT 14
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C

APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMING, GREGORY
APPLICANT: QIAN, PENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 2.0%; Score 37; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 1284 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1248

RESULT 15
US-08-658-136-1/c
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDER, GREGORY M
APPLICANT: BURR, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMING, GREGORY
APPLICANT: QIAN, PENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 2.0%; Score 37; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 1284 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1248

RESULT 16
US-09-873-404-3/c
Sequence 3, Application US/09873404
Patent No. 6500656
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO01212-CIP
CURRENT APPLICATION NUMBER: US/09/873,404
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63588
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(63588)
OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

Query Match 2.0%; Score 37; DB 4; Length 63588;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 52181 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 52145

RESULT 17
US-09-685-853A-3/c
Sequence 3, Application US/09685853A
Patent No. 6479270
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00871
CURRENT APPLICATION NUMBER: US/09/685,853A

```

CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/182,194
PRIOR FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 74962
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(74962)
OTHER INFORMATION: n = A,T,C or G
US-09-685-853A-3

Query Match      2.0%; Score 37; DB 4; Length 74962;
Best Local Similarity 100.0%; Pred.No.5.6e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 1561
Db      53008 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 52972

RESULT 18
US-09-345-892-1/c
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G

FEATURE:
NAME/KEY: allele
LOCATION: 92117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID32
FEATURE:
```

```

NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele

```

```

LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

```

```

Query Match      2.0%; Score 37; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db      54253 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 54217

```

```

RESULT 19
US-09-804-471A-3/C
Sequence 3, Application US/09804471A
Patent No. 6479269
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(174493)
OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

```

```

Query Match      2.0%; Score 37; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db      23036 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 23000

```

```

RESULT 20
US-10-238-709-3/C
Sequence 3, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(174493)
OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

```

Query Match 2.0%; Score 37; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 23036 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 23000

RESULT 21

US-09-702-705-583/c
; Sequence 583, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 67 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 32

RESULT 22

US-09-736-457-583/c
; Sequence 583, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 67 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 32

RESULT 23

US-09-614-124B-583/c
; Sequence 583, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 67 CAGGCACAGTGGCTCACACCTGTATCCGACACTT 32

RESULT 24

US-09-671-325-583/c
; Sequence 583, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-583

Query Match 1.9%; Score 36; DB 4; Length 481;

Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 67 CAGGACAGTGGCTCACACCTGTATCCGACACTT 32

RESULT 25
US-09-589-184-583/c
; Sequence 583, Application US/09589.184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF LUNG CANCER
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-583

Query Match 1.9%; Score 36; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2e-06; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 1526 CAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 67 CAGGACAGTGGCTCACACCTGTATCCGACACTT 32

RESULT 26
US-09-621-976-12021
; Sequence 12021, Application US/09621.976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12021
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12021

Query Match 1.8%; Score 34; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 27 GGACAGTGGCTCACACCTGTATCCGACACTT 60

RESULT 27

US-09-621-976-12333
; Sequence 12333, Application US/09621.976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12333
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12333

Query Match 1.8%; Score 34; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 27 GGACAGTGGCTCACACCTGTATCCGACACTT 60

RESULT 28
US-09-621-976-11582
; Sequence 11582, Application US/09621.976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 11582
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-11582

Query Match 1.8%; Score 34; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 27 GGACAGTGGCTCACACCTGTATCCGACACTT 60

RESULT 29
US-09-621-976-11620
; Sequence 11620, Application US/09621.976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 11620
; LENGTH: 322

TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-11620

Query Match 1.8%; Score 34; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 27 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 60

RESULT 30
US-09-621-976-2482
Sequence 2482, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621.976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 2482

LENGTH: 479

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 103..390

US-09-621-976-2482

Query Match 1.8%; Score 34; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 434 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 467

RESULT 31
US-09-621-976-18845
Sequence 18845, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621.976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 18845

LENGTH: 494

TYPE: DNA

ORGANISM: Homo sapiens

Query Match 1.8%; Score 34; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 163 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 196

RESULT 32

US-09-621-976-14555
Sequence 14555, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621.976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 14555

LENGTH: 498

TYPE: DNA

ORGANISM: Homo sapiens

US-09-621-976-14555

Query Match 1.8%; Score 34; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 113 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 146

RESULT 33

US-09-621-976-14219
Sequence 14219, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621.976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 14219

LENGTH: 503

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 248..

OTHER INFORMATION: n=a, g, c o r t

US-09-621-976-14219

Query Match 1.8%; Score 34; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 427 GGACAGTGGCTCACACCTGTAAATCCAGCACTT 460

RESULT 34

US-09-811-825A-10/c
Sequence 10, Application US/09811825A
Patent No. 6638738
GENERAL INFORMATION:

APPLICANT: KODER, Stephan et al

TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

TITLE OF INVENTION: THEROF
FILE REFERENCE: CLO01170


```

; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-10

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      282 GGCACAGTGGCTCACACCTGTATCCAGCACTT 249

RESULT 35
US-09-811-825A-11/c
; Sequence 11, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-11

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      265 GGCACAGTGGCTCACACCTGTATCCAGCACTT 232

RESULT 36
US-09-811-825A-12/c
; Sequence 12, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-12

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
```

```

DB      247 GGCACAGTGGCTCACACCTGTATCCAGCACTT 214

RESULT 37
US-09-811-825A-13/c
; Sequence 13, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-13

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      58 GGCACAGTGGCTCACACCTGTATCCAGCACTT 25

RESULT 38
US-09-443-184-35
; Sequence 35, Application US/09443184A
; Patent No. 6372431
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mary Jane
; APPLICANT: Zweigert, Gary
; APPLICANT: Kaser, Matthew R.
; APPLICANT: Panzer, Scott
; APPLICANT: Seilhammer, Jeffrey J.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah
; APPLICANT: Azimzai, Valida
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
; FILE REFERENCE: PC-0007 US
; CURRENT APPLICATION NUMBER: US/09/443,184A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6372431 2742442CB1
US-09-443-184-35

Query Match          1.8%; Score 34; DB 4; Length 1762;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      1480 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1513

RESULT 39
US-08-687-080-68/c
```

```
Sequence 68, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 6623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3' END OF INTRON 5 OF RAD50 GENOMIC
US-08-687-080-68

Query Match
Best Local Similarity 1.8%; Score 34; DB 2; Length 6623;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 3054 GGCACAGTGGCTCACACCTGTATCCAGCACTT 3021

RESULT 40
US-08-976-594-683
Sequence 683, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 683
LENGTH: 7050
TYPE: DNA
```

```
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 003303.2
US-09-976-594-683

Query Match
Best Local Similarity 1.8%; Score 34; DB 4; Length 7050;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 3056 GGCACAGTGGCTCACACCTGTATCCAGCACTT 3089

RESULT 41
US-09-022-461-1/c
Sequence 1, Application US/09022461
Patent No. 5964371
GENERAL INFORMATION:
APPLICANT: HENDERSON, Daniel R.
APPLICANT: SCHUR, Eric R.
APPLICANT: LAMPARSKI, Henry G.
APPLICANT: YU, De Chao
TITLE OF INVENTION: PROSTATE CANCER DRUG SCRE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,461
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/906,192
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12047 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-022-461-1

Query Match
Best Local Similarity 1.8%; Score 34; DB 2; Length 12047;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 4277 GGCACAGTGGCTCACACCTGTATCCAGCACTT 4244

RESULT 42
US-09-033-556-3/c
```

```
; Sequence 3, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-033-556-3
;
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGACAGTGGCTCACCTGTATCCCGACACTT 1561
; DB 4277 GGACAGTGGCTCACCTGTATCCCGACACTT 4244
;
; RESULT 43
; US-09-474-699-11/C
; Sequence 11, Application US/09474699
; Patent No. 6495130
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
; TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022001300
; CURRENT APPLICATION NUMBER: US/09/474,699
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/114,262
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
; US-09-474-699-11
;
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGACAGTGGCTCACCTGTATCCCGACACTT 1561
; DB 4277 GGACAGTGGCTCACCTGTATCCCGACACTT 4244
;
; RESULT 44
; US-09-151-376-3/C
; Sequence 3, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-151-376-3
;
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGACAGTGGCTCACCTGTATCCCGACACTT 1561
; DB 4277 GGACAGTGGCTCACCTGTATCCCGACACTT 4244
;
; RESULT 45
; US-09-345-217-3
; Sequence 3, Application US/09345217
; Patent No. 6268142
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: COX, ANGELA
; APPLICANT: CAMP, NICOLA J.
; APPLICANT: DIGIOVINE, FRANCESCO S.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
; FILE REFERENCE: MSA-010.02
; CURRENT APPLICATION NUMBER: US/09/345,217
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: PCT/GB98/01481
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 9711040.7
; EARLIER FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12565
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-345-217-3
;
; Query Match 1.8%; Score 34; DB 3; Length 12565;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 1234 GGACAGTGGCTCACACCTGTATCCAGCACTT 1267

RESULT 46
 US-08-975-080-35
 Sequence 35, Application US/08975080
 Patent No. 6245523
 GENERAL INFORMATION:

APPLICANT: Altieri, Dario C.
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 CELLULAR APOPTOSIS, AND ITS MODULATION
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,080
 FILING DATE: 20-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,288
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14796 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-975-080-35

Query Match 1.8%; Score 34; DB 3; Length 14796;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 47
 US-09-630-706-10
 Sequence 10, Application US/09630706
 Patent No. 6277640
 GENERAL INFORMATION:

APPLICANT: C. Frank Bennett
 APPLICANT: Lex M. Cowart
 TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
 FILE REFERENCE: RTS-0053
 CURRENT APPLICATION NUMBER: US/09/630,706
 CURRENT FILING DATE: 2000-08-01
 NUMBER OF SEQ ID NOS: 94
 SEQ ID NO 10
 LENGTH: 14796
 TYPE: DNA
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: CDS
 LOCATION: (2811)...(2921)
 NAME/KEY: CDS
 LOCATION: (3174)...(3283)
 NAME/KEY: CDS
 LOCATION: (5158)...(5275)
 NAME/KEY: CDS
 LOCATION: (11955)...(12044)
 US-09-630-706-10

Query Match 1.8%; Score 34; DB 3; Length 14796;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 48
 US-09-496-694B-3
 Sequence 3, Application US/09496694B
 Patent No. 635194
 GENERAL INFORMATION:

APPLICANT: C. Frank Bennett
 APPLICANT: Elizabeth J. Ackermann
 APPLICANT: Eric E. Swartz
 APPLICANT: Lex M. Cowart
 TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
 FILE REFERENCE: ISPH-0439
 CURRENT APPLICATION NUMBER: US/09/496,694B
 CURRENT FILING DATE: 2000-02-02
 PRIOR APPLICATION NUMBER: 09/286,407
 PRIOR FILING DATE: 1999-04-05
 PRIOR APPLICATION NUMBER: 09/163,162
 PRIOR FILING DATE: 1998-09-29
 NUMBER OF SEQ ID NOS: 245
 SEQ ID NO 3
 LENGTH: 14796
 TYPE: DNA
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: CDS
 LOCATION: (2811)...(2921)
 NAME/KEY: CDS
 LOCATION: (3174)...(3283)
 NAME/KEY: CDS
 LOCATION: (5158)...(5275)
 NAME/KEY: CDS
 LOCATION: (11955)...(12044)
 US-09-496-694B-3

Query Match 1.8%; Score 34; DB 4; Length 14796;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 49
 US-09-146-053-7
 Sequence 7, Application US/09146053A
 Patent No. 6399349
 GENERAL INFORMATION:

APPLICANT: Ryan, James W.
 APPLICANT: Sprinkle, Terry Joe Curtis
 APPLICANT: Venema, Richard C.
 TITLE OF INVENTION: Human Antipeptidase P Gene
 FILE REFERENCE: MCG103
 CURRENT APPLICATION NUMBER: US/09/146,053A

CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 16595
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-7

Query Match 1.8%; Score 34; DB 4; Length 16595;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCGACACTT 1561
DB 4600 GGCAAGTGGCTCACACCTGTATCCGACACTT 4633

RESULT 50
US-09-657-346A-17
Sequence 17, Application US/09657346A
Patent No. 6503754
GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0135
CURRENT APPLICATION NUMBER: US/09/657,346A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 17
LENGTH: 18000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2144)...(2155)
NAME/KEY: CDS
LOCATION: (18247)...(18457)
NAME/KEY: CDS
LOCATION: (12772)...(12911)
NAME/KEY: CDS
LOCATION: (14031)...(14243)
NAME/KEY: CDS
LOCATION: (16669)...(16680)
US-09-657-346A-17

Query Match 1.8%; Score 34; DB 4; Length 18000;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCGACACTT 1561
DB 11539 GGCAAGTGGCTCACACCTGTATCCGACACTT 11572

RESULT 51
US-09-811-825A-3/c
Sequence 3, Application US/09811825A
Patent No. 6638738
GENERAL INFORMATION:
APPLICANT: Kodet, Stephen et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
FILE REFERENCE: C1001170
CURRENT APPLICATION NUMBER: US/09/811,825A
CURRENT FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 18554
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-811-825A-3

Query Match 1.8%; Score 34; DB 4; Length 18554;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCGACACTT 1561
DB 3050 GGCAAGTGGCTCACACCTGTATCCGACACTT 3017

RESULT 52
US-09-780-049-18/c
Sequence 18, Application US/09780049
Patent No. 6465250
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0134
CURRENT APPLICATION NUMBER: US/09/780,049
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 40000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-780-049-18

Query Match 1.8%; Score 34; DB 4; Length 40000;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCGACACTT 1561
DB 7811 GGCAAGTGGCTCACACCTGTATCCGACACTT 7778

RESULT 53
US-08-781-891-79
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-Bi
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4500
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-781-891-79
Query Match 1.8%; Score 34; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 41134 GGCAAGTGGCTCACACCTGTATCCAGCACTT 41167

RESULT 54

US-09-618-166-79
Sequence 79, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

Query Match 1.8%; Score 34; DB 4; Length 87350;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 41134 GGCAAGTGGCTCACACCTGTATCCAGCACTT 41167

RESULT 55

US-09-791-211-3
Sequence 3, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 87543

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12742
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29370
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29422
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29979
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29980
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29981
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30136
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30140
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31205
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31206
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31592
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33160
OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 34066
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34072
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 36816
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 39020
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42164
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42459
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52786
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 61290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure

LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION: unknown
US-09-791-211-3

Query Match 1.8%; Score 34; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 41327 GGCACAGTGGCTCACACCTGTATCCGACACTT 41360

RESULT 56
US-09-918-686-1/C
Sequence 1, Application US/09918686
Patent No. 64/5739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Prohl, Sean
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 92139
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 1.8%; Score 34; DB 4; Length 92139;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 70462 GGCACAGTGGCTCACACCTGTATCCGACACTT 70429

RESULT 57
US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6393373
GENERAL INFORMATION:
APPLICANT: Bouguetelret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10

FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
Query Match 1.8%; Score 34; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 141662 GGACAGTGGCTCACACCTGTATCCAGCACTT 141695
RESULT 58
US-09-621-976-11747
Sequence 11747, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11747
LENGTH: 565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-11747
Query Match 1.8%; Score 33; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1529 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 297 GGACAGTGGCTCACACCTGTATCCAGCACTT 329
RESULT 59
US-09-318-448-30
Sequence 30, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 3464
TYPE: DNA
ORGANISM: Homo sapiens
US-09-318-448-30
Query Match 1.8%; Score 33; DB 3; Length 3464;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGC 1557
DB 1578 CCAGGCACAGTGGCTCACACCTGTATCCAGC 1610
RESULT 60
US-08-781-891-79/c
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-Bn
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Scheilenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620cendury Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match 1.8%; Score 33; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTTAGG 1564
DB 44558 CAGTGGCTCACACCTGTATCCGACACTTAGG 44526

RESULT 61

US-09-618-166-79/c
Sequence 79, Application US/09618166

PATENT No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui

Yoshioka, Junko
Mulligan, John T.
Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 240052,419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

Query Match 1.8%; Score 33; DB 4; Length 87350;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTTAGG 1564
DB 44558 CAGTGGCTCACACCTGTATCCGACACTTAGG 44526

RESULT 62
US-09-791-211-3/c
Sequence 3, Application US/09791211

PATENT No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 87543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12742
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29370
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29422
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29979
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29980
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29981
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30136
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30140
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31205
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31206
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31592
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33160
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34066
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34072
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 36816

OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 39020
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42164
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42459
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52786
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION:
US-09-791-211-3

Query Match 1.8%; Score 33; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACCTGTATCCGACACTAGG 1564
DB 44751 CAGTGGCTCACCTGTATCCGACACTTAGG 44719

RESULT 63
US-09-798-096-10
Sequence 10, Application US/09798096
Patent No. 639378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Query Match 1.8%; Score 33; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1529 GCACAGTGGCTCACCTGTATCCGACACTT 1561
DB 82455 GCACAGTGGCTCACCTGTATCCGACACTT 82487

RESULT 64
US-09-621-976-1934/c
Sequence 1934, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Maline Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1934
LENGTH: 530
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..291
NAME/KEY: sig_peptide
LOCATION: 1..159
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 3.90000009536743
OTHER INFORMATION: seq SYLSTLHVSLVSLV/IG
US-09-621-976-1934

Query Match 1.7%; Score 32; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches	32;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1530	CACAGTGGCTCACACCTGTAATCCAGCACTT	1561						
Db	454	CACAGTGGCTCACACCTGTAATCCAGCACTT	423						

```

US-08-323-443B-1/c
; Sequence 1, Application US/08923443B
; Patent No. 5654170
;
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LINDER, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: DACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
;
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
US-08-323-443B-1
;
Query Match 1.7%; Score 32; DB 1; Length 31571
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels
;
1530 CACAGTGGCTCACACCTGTAAATCCAGACTT 1561
|||||
683 CACAGTGGCTCACACCTGTAAATCCAGACTT 652
;
RESULT 66
US-09-741-150-3
; Sequence 3, Application US/09741150
; Patent No. 6436689
;
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al

```

```

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00968
; CURRENT APPLICATION NUMBER: US/09/741,150
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112132
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

```

	Query Match	Similarity	1.7%; Score 32;	DB 4;	Length 1213;
	Best Local	Similarity	100.0%;	Pred. No. 8.6e-05;	
	Matches	32;	Conservative	0;	Mismatches 0;
				Indels	0;
				Gaps	0;
QY	1550	CACAGTGGCTCACACCTGTATATCCACACACTT	1561		
Db	8296	CACAGTGGCTCACACCTGTATATCCACGACTT	8327		

```

RESULT 67
US-10-160-187-3
/ Sequence 3, Application US/10160187
/ Patent No. 6620607
/ GENERAL INFORMATION:
/ APPLICANT: GUEGLER, Karl et al.
/ TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: CLO00968DIV
/ CURRENT APPLICATION NUMBER: US/10/160.187
/ CURRENT FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/252,410
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: 09/741,150
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 112132
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1) ..(112132)
/ OTHER INFORMATION: n = A,T,C or G
US-10-160-187-3

```

```

; CLONE: PKD1 GENOMIC
US-08-323-443B-1
Query Match      1.7%; Score 32; DB 1; Length 31571;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1530 CACAGTGCGCTCACACTGTATATCCGAGCACTT 1561
        |||||
DB       683 CACAGTGCGTCACACTGTATATCCGAGCACTT 652

RESULT 66
US-09-741-150-3
; Sequence 3, Application US/09741150
; Patent No. 6436689
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al

; CLONE: PKD1 GENOMIC
US-08-323-443B-1
Query Match      1.7%; Score 32; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1530 CACAGTGCGCTCACACTGTATATCCGAGCACTT 1561
        |||||
DB       8296 CACAGTGCGCTCACACTGTATATCCGAGCACTT 8327

RESULT 68
US-09-621-976-14833
; Sequence 14833, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
```

```
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14833
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-14833

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 405;
Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCA 1558
DB 175 GGCACAGTGGCTCACACCTGTATCCAGCA 205

RESULT 69
US-09-621-976-1688
Sequence 1688, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1688
LENGTH: 456
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 75..242
NAME/KEY: sig peptide
LOCATION: 75..113
OTHER INFORMATION: von Heijne matrix
OTHER INFORMATION: score 5.0999990463257
OTHER INFORMATION: seq MSLYLLCXKXLA/XV
US-09-621-976-1688

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 456;
Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCA 1558
DB 183 GGCACAGTGGCTCACACCTGTATCCAGCA 213

RESULT 70
US-09-621-976-3286
Sequence 3286, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3286
LENGTH: 526
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 83..250
US-09-621-976-3286

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 526;
Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 ACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 283 ACAGTGGCTCACACCTGTATCCAGCACTT 313

RESULT 71
US-09-691-861A-19/C
Sequence 19, Application US/09691861A
Patent No. 6482935
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEROOF
FILE REFERENCE: C1000892
CURRENT APPLICATION NUMBER: US/09/691.861A
CURRENT FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 601
TYPE: DNA
ORGANISM: Homo sapiens
US-09-691-861A-19

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 601;
Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 ACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 156 ACAGTGGCTCACACCTGTATCCAGCACTT 126

RESULT 72
US-09-659-791A-10/C
Sequence 10, Application US/09659791A
Patent No. 6383808
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659.791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 8133
TYPE: DNA
ORGANISM: Homo sapiens
US-09-659-791A-10

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 8133;
Pred. No. 0.00027;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGACAGTGGCTCACACCTGTATCCAG 1556
DB 3065 CAGGACAGTGGCTCACACCTGTATCCAG 3035

RESULT 73
```

```
US-09-691-861A-3/C
; Sequence 3, Application US/09691861A
; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-3

Query Match      1.7%; Score 31; DB 4; Length 9862;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1531 ACAGTGCTCACACCTGTATCCGACACTT 1561
DB      4478 ACAGTGCTCACACCTGTATCCGACACTT 4448

RESULT 74
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
```

```
LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195342)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223581)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(236651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11

Query Match      1.7%; Score 31; DB 4; Length 392000;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1531 ACAGTGCTCACACCTGTATCCGACACTT 1561
DB      34332 ACAGTGCTCACACCTGTATCCGACACTT 34362

RESULT 75
US-09-643-597-265
; Sequence 265, Application US/09643597
```

```
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 265
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(271)
OTHER INFORMATION: n = A,T,C or G
US-09-643-597-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      149 CAGTGGCTCACACCTGTATCCAGCACTT 178

RESULT 76
US-09-480-884A-265
Sequence 265, Application US/09480884A
Patent No. 6482597
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 265
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(271)
OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 77
US-09-542-615A-265
Sequence 265, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 265
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(271)
OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB      149 CAGTGGCTCACACCTGTATCCAGCACTT 178

RESULT 78
US-09-606-421B-265
Sequence 265, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 265
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(271)
OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1532	CAGTGGCTCACACCTGTATCCGACACTT	1561
Db	149	CAGTGGCTCACACCTGTATCCGACACTT	178

```

RESULT 79
US-09-621-976-13274
/ Sequence 13274, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Estns and Encoded Human Proteins
/ FILE REFERENCE: GENSET_054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2005-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 13274
/ LENGTH: 1322
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-621-976-13274

```

Query Match	1.6%;	Score 30;	DB 4;	Length 322;
Best Local Similarity	100.0%;	Pred. No. 0.00087;		
Matches 30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Dy 1532 CAGTGGCTCACACCTGTATCCGACTT 1561
Db 47 CAGTGGCTCACACCTGTATCCGACTT 76

```

RESULT 80
US-09-621-976-14200
/ Sequence 14200, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Robert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins
/ FILE REFERENCE: GENSET_054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2006-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 14200
/ LENGTH: 390
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-621-976-14200

```

```
Query Match      1.6%; Score 30; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Qy	1532	CAGTGGCTACACCTGTAACTCCAGCACTT	1561
Db	135	CAGTGGCTACACCTGTAACTCCAGCACTT	164

RESULT 81
 US-09-621-976-18294
 : Sequence 18294, Application US/09621976
 : Patent No. 6638063
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Dumas Milne Edwards, J.B.
 : APPLICANT: Ubbert, S.
 : APPLICANT: Giordano, J.Y.
 : TITLE OF INVENTION: ESTs and Encoded Human Proteins

```

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
;

```

```

Query Match      1.6%; Score 30; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

```

QY      1532 CAGTGGCTCACACCTGTATCCCGACACTT 1561
          |||||
Db      114  CAGTGGCTCACACCTGTATCCCGACACTT 143

```

```

RESULT 82
US-09-621-976-9263
; Sequence 9263, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Robert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCE: GENSET_054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9263
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9263

```

```

Query March Similarity      1.6%; score 30; DB 4; length 466;
Best Local Similarity      100.0%; Pred. No. 0.00045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1532 CAGTGGCTCACACCTGTAATCCAGCACTT 1561
Db 332 CAGTGGCTCACACCTGTAATCCAGCACTT 361

```

RESULT 83
US-09-621-976-219/c
Sequence 219, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Coblert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Ests and Encoded Human Proteins
FILE REFERENCE: GENSET-054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 219
LENGTH: 468
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 187..468
NAME/KEY: sig_peptide
LOCATION: 187..255
OTHER INFORMATION: Von Heijne matrix

```


OTHER INFORMATION: score 4.6999980926514
; OTHER INFORMATION: seq LKLTSSDLPASA/SQ
US-09-621-976-219

Query Match 1.6%; Score 30; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 290 CAGTGGCTCACACCTGTATCCGACACTT 261

RESULT 84

US-09-621-976-218/c
; Sequence 218, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 218
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..468
; NAME/KEY: sig_peptide
; LOCATION: 187..255
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.6999980926514
; OTHER INFORMATION: seq LKLTSSDLPASA/SQ
US-09-621-976-218

Query Match 1.6%; Score 30; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 290 CAGTGGCTCACACCTGTATCCGACACTT 261

RESULT 85

US-09-621-976-14057
; Sequence 14057, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14057
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14057

Query Match 1.6%; Score 30; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 274 CAGTGGCTCACACCTGTATCCGACACTT 303

RESULT 86

US-09-621-976-17711
; Sequence 17711, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17711
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17711

Query Match 1.6%; Score 30; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 407 CAGTGGCTCACACCTGTATCCGACACTT 436

RESULT 87

US-09-621-976-17517
; Sequence 17517, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17517
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17517

Query Match 1.6%; Score 30; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 334 CAGTGGCTCACACCTGTATCCGACACTT 363

RESULT 88

US-09-621-976-16439
; Sequence 16439, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16439
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 449
OTHER INFORMATION: n=a, g, c o r t
US-09-621-976-16439

Query Match 1.6%; Score 30; DB 4; Length 505;
Best Local Similarity 100.0%; Pred.No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCC 1554
DB 476 CCAGGACAGTGGCTCACACCTGTATCCC 505

RESULT 89
US-09-621-976-10635
Sequence 10635, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10635
LENGTH: 514
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-10635

Query Match 1.6%; Score 30; DB 4; Length 514;
Best Local Similarity 100.0%; Pred.No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCCAGCACTT 1561
DB 241 CAGTGGCTCACACCTGTATCCCAGCACTT 270

RESULT 90
US-09-621-976-3654
Sequence 3654, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3654
LENGTH: 595
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: 324..554
US-09-621-976-3654

Query Match 1.6%; Score 30; DB 4; Length 595;
Best Local Similarity 100.0%; Pred.No. 0.00084;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCCAGCACTT 1561
DB 158 CAGTGGCTCACACCTGTATCCCAGCACTT 187

RESULT 91
US-09-227-357-62
Sequence 62, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227.357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051.926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052.793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052.803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052.732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052.733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052.795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051.928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055.949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055.953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055.950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055.947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055.964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056.360

```

; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-227-357-62

Query Match          1.6%; Score 30; DB 4; Length 998;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
Db      699 CAGTGGCTCACACCTGTATCCGACACTT 728

RESULT 92
US-09-671-317-274
; Sequence 274 Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Amick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 274
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-603-191 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 502..520
; OTHER INFORMATION: 12-603-191.misl, complement
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-603-191.mis2, potential
; NAME/KEY: primer_bind
; LOCATION: 668..688
; OTHER INFORMATION: upstream amplification primer, complement
; NAME/KEY: primer_bind
; LOCATION: 191
```

```

; LOCATION: 240..260
; OTHER INFORMATION: downstream amplification primer
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-603-191 potential probe
; NAME/KEY: misc_feature
; LOCATION: 339
; OTHER INFORMATION: n=a, g, c o r t
; US-09-671-317-274

Query Match          1.6%; Score 30; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
Db      742 CAGTGGCTCACACCTGTATCCGACACTT 771

RESULT 93
US-09-539-333D-37
; Sequence 37 Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 37
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..719
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 720..1118
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1119..1154
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1131..1136
; FEATURE:
; NAME/KEY: allele
; LOCATION: 191
```

```
OTHER INFORMATION: 8-121-187 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 313
OTHER INFORMATION: 8-122-271 : deletion of CAAA
FEATURE:
NAME/KEY: allele
LOCATION: 314
OTHER INFORMATION: 8-122-272 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 368
OTHER INFORMATION: 8-122-326 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 390
OTHER INFORMATION: 8-123-55 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 814
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 821
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 822
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 838
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 897
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 908
OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-37
```

```
Query Match 1.6%; Score 30; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561

Db 526 CAGTGGCTCACACCTGTATCCGACACTT 555

```
RESULT 94
US-09-178-115-110
; Sequence 110, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorek, Jaromir
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
```

```
EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 110
; LENGTH: 1247
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1247)
US-09-178-115-110
```

```
Query Match 1.6%; Score 30; DB 3; Length 1247;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561

Db 845 CAGTGGCTCACACCTGTATCCGACACTT 874

```
RESULT 95
US-09-177-776-110
; Sequence 110, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorek, Jaromir
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
```

```

; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 110
; LENGTH: 1247
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1247)
US-09-177-776-110

Query Match
Best Local Similarity 1.6%; Score 30; DB 3; Length 1247;
Matches 30; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 845 CAGTGGCTCACACCTGTATCCAGCACTT 874

RESULT 96
US-09-247-155-138
; Sequence 138, Application US/09247.155A
; Patent No 631282
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duchet, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247.155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074.121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081.563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096.116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099.273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 138
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 50..637
; FEATURE:
; NAME/KEY: sig.peptide
; LOCATION: 50..151
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.90000009536743
; OTHER INFORMATION: seq LGAAALALALANT/DV
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 1277..1289
US-09-247-155-138

Query Match
Best Local Similarity 1.6%; Score 30; DB 4; Length 1289;
Matches 30; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 1009 CAGTGGCTCACACCTGTATCCAGCACTT 1038

RESULT 97
US-09-539-333D-36
; Sequence 36, Application US/09539333D
; Patent No. 6476208

; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marra
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539.333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126.903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131.971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132.065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143.928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145.915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146.453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146.452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162.286
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416.384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 36
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..899
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 900..1265
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1266..1301
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1277..1282
; FEATURE:
; NAME/KEY: allele
; LOCATION: 191
; OTHER INFORMATION: 8-121-187 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 313
; OTHER INFORMATION: 8-122-271 : deletion of CAA
; FEATURE:
; NAME/KEY: allele
; LOCATION: 314
; OTHER INFORMATION: 8-122-272 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 368
; OTHER INFORMATION: 8-122-126 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 390
; OTHER INFORMATION: 8-123-55 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 806
; OTHER INFORMATION: 8-127-28 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
```

LOCATION: 897
OTHER INFORMATION: 8-127-119 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 937
OTHER INFORMATION: 8-127-159 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 961
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 968
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 969
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 985
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1044
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1055
OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-36

Query Match 1.6%; Score 30; DB 4; Length 1301;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCAGCTGTATCCGACGACTT 1561
DB 526 CAGTGGCTCAGCTGTATCCGACGACTT 555

RESULT 98
US-09-539-333D-40
Sequence 40; Application US/09539333D
Patent No. 6476208
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marra
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Bastoux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384

PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
SEQ ID NO 40
LENGTH: 1386
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..984
FEATURE:
NAME/KEY: CDS
LOCATION: 985..1350
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1351..1386
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1362..1367
FEATURE:
NAME/KEY: allele
LOCATION: 191
OTHER INFORMATION: 8-121-187 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 398
OTHER INFORMATION: 8-122-271 : deletion of CAAA
FEATURE:
NAME/KEY: allele
LOCATION: 399
OTHER INFORMATION: 8-122-272 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 453
OTHER INFORMATION: 8-122-326 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 475
OTHER INFORMATION: 8-123-55 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 891
OTHER INFORMATION: 8-127-28 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 982
OTHER INFORMATION: 8-127-119 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1022
OTHER INFORMATION: 8-127-159 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1046
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 1053
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1054
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 1070
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1129
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele

```
LOCATION: 1140
; OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-40

Query Match
Best Local Similarity 1.6%; Score 30; DB 4; Length 1386;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGACACTT 1561
DB 611 CAGTGGCTCACACCTGTATCCAGACACTT 640

RESULT 99
US-09-620-312D-743
; Sequence 743, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillingshast
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 743
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(1714)
US-09-620-312D-743

Query Match
Best Local Similarity 1.6%; Score 30; DB 4; Length 2091;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGACACTT 1561
DB 1753 CAGTGGCTCACACCTGTATCCAGACACTT 1782

RESULT 100
US-08-381-691-17/C
; Sequence 17, Application US/08381691
; Patent No. 5852224
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Alpha-1ac Albumin Gene Constructs
; NUMBER OF SEQUENCES: 17
; COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION FOR SEQ ID NO: 17;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-381-691-17

Query Match
Best Local Similarity 1.6%; Score 30; DB 2; Length 2119;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCC 1554
DB 1321 CCAGGCACAGTGGCTCACACCTGTATCCC 1292
```

Search completed: April 17, 2004, 19:03:34
Job time : 207 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:11 / Search time 7206 Seconds

(without alignments)
11121.464 Million cell updates/sec

Title: US-10-063-523-21

Sequence: 1 ctagagcgccgctgcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 10

Total number of hits satisfying chosen parameters: 3719961

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

GenBank: 1: gb_ba: 2: gb_htg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: gb_wa: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htg_mus: 34: em_htg_pln: 35: em_htg_rtd: 36: em_htg_mam: 37: em_htg_vit: 38: em_sy: 39: em_htgo_hum: 40: em_htgo_mus: 41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	ID	Description
1	1849	100.0	1849	AR252489	AR252489 Sequence
2	1849	100.0	1849	AX092290	AX092290 Sequence
3	1849	100.0	1849	AX376066	AX376066 Sequence
4	1849	100.0	1849	AX403270	AX403270 Sequence
5	1849	100.0	1849	AY585876	AY585876 Homo sapi
6	1775	96.0	2649	BC039573	BC039573 Homo sapi
7	1546	83.6	2663	AX879640	AX879640 Sequence
8	1546	83.6	2663	BD157945	BD157945 Primer fo
9	1546	83.6	2663	AK022704	AK022704 Homo sapi
10	1483	80.2	2719	AX880746	AX880746 Sequence
11	1483	80.2	2719	BD158566	BD158566 Primer fo
12	1483	80.2	2719	AK023676	AK023676 Homo sapi
13	916	49.5	180430	AC096768	AC096768 Homo sapi
14	815	44.1	1896	AX881436	AX881436 Sequence
15	815	44.1	1896	BD158031	BD158031 Primer fo
16	815	44.1	1896	AK021582	AK021582 Homo sapi
17	549	29.7	736	AX867484	AX867484 Sequence
18	549	29.7	736	BD147546	BD147546 Primer fo
19	454	24.6	480	AR412420	AR412420 Sequence
20	454	24.6	480	BD107973	BD107973 EST and e
21	360	19.5	440	BD076179	BD076179 5' EST of
22	314	17.0	668	AX870066	AX870066 Sequence
23	314	17.0	668	BD150128	BD150128 Primer fo
24	275	14.9	645	AX870976	AX870976 Sequence
25	275	14.9	645	BD151038	BD151038 Primer fo
26	172	9.3	1744	BC016905	BC016905 Homo sapi
27	140	7.6	403	AX071613	AX071613 Sequence
28	134	7.2	220818	AC124242	AC124242 Homo sapi
29	121	6.5	346	G30051	G30051 human SRS S
30	91	4.9	153472	AB020868	AB020868 Homo sapi
31	91	4.9	168921	AP006203	AP006203 Homo sapi
32	91	4.9	177888	AP006208	AP006208 Homo sapi
33	79	4.3	163111	AC080014	AC080014 Homo sapi
34	79	4.3	192819	AC012280	AC012280 Homo sapi
35	73	3.9	521	G22972	G22972 human SRS W
36	73	3.9	92134	AC018406	AC018406 Homo sapi
37	51	2.8	70659	AX199349	AX199349 Sequence
38	49	2.7	70659	AC124267	AC124267 Homo sapi
39	44	2.4	9630	AF220172	AF220172 Homo sapi
40	43	2.3	140241	AC079355	AC079355 Homo sapi
41	43	2.3	156131	AC146373	AC146373 Pan trogl
42	43	2.3	192281	AC130708	AC130708 Homo sapi
43	43	2.3	211395	AC137779	AC137779 Homo sapi
44	42	2.3	45415	AC091321	AC091321 Homo sapi
45	42	2.3	83585	AL060475	AL060475 Human DNA
46	42	2.3	98935	AC025435	AC025435 Homo sapi
47	42	2.3	98935	AC008671	AC008671 Homo sapi
48	42	2.3	133581	AC129623	AC129623 Homo sapi
49	42	2.3	147812	AC062025	AC062025 Homo sapi
50	42	2.3	155735	AC007583	AC007583 Homo sapi
51	42	2.3	164498	AC020898	AC020898 Homo sapi
52	42	2.3	172917	AC140973	AC140973 Papio ham
53	42	2.3	182834	AC027523	AC027523 Homo sapi
54	42	2.3	183397	AC146301	AC146301 Callithr
55	42	2.3	192065	AC146469	AC146469 Pan trogl
56	42	2.3	208039	AC011774	AC011774 Homo sapi
57	42	2.3	224010	AP001848	AP001848 Homo sapi
58	41	2.2	39687	AL391690	AL391690 Human DNA
59	41	2.2	94508	AC004086	AC004086 Homo sapi
60	41	2.2	104081	HS026307	HS026307 Human DNA
61	41	2.2	110580	AP000446	AP000446 Homo sapi
62	41	2.2	157504	AC008086	AC008086 Homo sapi
63	41	2.2	161251	AC147284	AC147284 Pan trogl
64	41	2.2	162771	AC027121	AC027121 Homo sapi
65	41	2.2	163157	AC012567	AC012567 Homo sapi

Pred. No. is the number of results predicted by chance to have a

66	41	2.2	166338	9	AC026165	Homo sapi	139	39	2.1	117751	9	AC020913	AC020913 Homo sapi
67	41	2.2	184032	9	AC073353	Homo sapi	140	39	2.1	118035	9	AC092676	AC092676 Homo sapi
68	41	2.2	208881	2	AC074171	Homo sapi	141	39	2.1	118338	9	AC010463	AC010463 Homo sapi
69	41	2.2	226572	2	AL354652	Homo sapi	142	39	2.1	123146	9	AC011736	AC011736 Homo sapi
70	40	2.2	37170	9	HSEI2919	Human DNA	143	39	2.1	128133	9	AL138787	AL138787 Human DNA
71	40	2.2	39400	2	AC135786	Homo sapi	144	39	2.1	128240	9	AL138826	AL138826 Homo sapi
72	40	2.2	55100	2	AC036154	Homo sapi	145	39	2.1	132290	9	AL627402	AL627402 Homo sapi
73	40	2.2	59903	2	AC015782	Homo sapi	146	39	2.1	132875	9	AC112907	AC112907 Homo sapi
74	40	2.2	64706	2	AC136358	Homo sapi	147	39	2.1	135423	9	AC093636	AC093636 Homo sapi
75	40	2.2	77879	2	AC027403	Homo sapi	148	39	2.1	144021	2	AC092628	AC092628 Homo sapi
76	40	2.2	91516	9	AL731577	Human DNA	149	39	2.1	144491	2	AL161458	AL161458 Homo sapi
77	40	2.2	101158	9	AC092624	Homo sapi	150	39	2.1	146832	2	AC074285	AC074285 Homo sapi
78	40	2.2	109138	9	AC104084	Homo sapi	151	39	2.1	150813	9	AC118758	AC118758 Homo sapi
79	40	2.2	109864	9	AL451052	Human DNA	152	39	2.1	150813	9	AL136220	AL136220 Homo sapi
80	40	2.2	110000	2	AC009801	Homo sapi	153	39	2.1	155084	9	AC055845	AC055845 Homo sapi
81	40	2.2	116236	9	AL354877	Human DNA	154	39	2.1	155304	2	AC141591	AC141591 Homo sapi
82	40	2.2	118831	9	HSJ98911	Human DNA	155	39	2.1	157989	2	AC019061	AC019061 Homo sapi
83	40	2.2	126525	9	HSJ107719	Human DNA	156	39	2.1	158052	2	AC010200	AC010200 Homo sapi
84	40	2.2	134403	9	HS436M11	Human DNA	157	39	2.1	158149	9	AC012000	AC012000 Homo sapi
85	40	2.2	138539	2	AC137504	Homo sapi	158	39	2.1	158548	9	AC013440	AC013440 Homo sapi
86	40	2.2	142000	2	AC141241	Homo sapi	159	39	2.1	158981	2	AC016242	AC016242 Homo sapi
87	40	2.2	146466	9	AL353637	Human DNA	160	39	2.1	159134	9	AC093004	AC093004 Homo sapi
88	40	2.2	147184	2	AC135778	Homo sapi	161	39	2.1	159681	2	AC084192	AC084192 Homo sapi
89	40	2.2	148548	2	AC093011	Homo sapi	162	39	2.1	160653	2	AC141071	AC141071 Homo sapi
90	40	2.2	148624	2	AC084815	Homo sapi	163	39	2.1	162151	9	AC008364	AC008364 Homo sapi
91	40	2.2	152709	2	AC114799	Homo sapi	164	39	2.1	162594	9	AC142541	AC142541 Homo sapi
92	40	2.2	152829	2	AC013533	Homo sapi	165	39	2.1	162751	2	AC026876	AC026876 Homo sapi
93	40	2.2	152964	2	AC092726	Homo sapi	166	39	2.1	163535	2	AC125392	AC125392 Homo sapi
94	40	2.2	158849	2	AC021454	Homo sapi	167	39	2.1	163616	9	AC095038	AC095038 Homo sapi
95	40	2.2	160169	2	AC051664	Homo sapi	168	39	2.1	163666	9	AL135927	AL135927 Homo sapi
96	40	2.2	160210	9	AL138815	Human DNA	169	39	2.1	164179	9	AC007227	AC007227 Homo sapi
97	40	2.2	160855	9	AC109925	Homo sapi	170	39	2.1	164179	9	AC127533	AC127533 Homo sapi
98	40	2.2	160984	2	AC082181	Homo sapi	171	39	2.1	165791	9	AC099552	AC099552 Homo sapi
99	40	2.2	163915	2	AC087451	Homo sapi	172	39	2.1	165791	9	AC146118	AC146118 Homo sapi
100	40	2.2	166485	9	AC123900	Homo sapi	173	39	2.1	166181	2	AC079919	AC079919 Homo sapi
101	40	2.2	166867	9	AP003733	Homo sapi	174	39	2.1	168311	2	AC018963	AC018963 Homo sapi
102	40	2.2	168714	2	AC138876	Homo sapi	175	39	2.1	168311	2	AP002338	AP002338 Homo sapi
103	40	2.2	174809	2	AC092122	Homo sapi	176	39	2.1	168637	2	AC023506	AC023506 Homo sapi
104	40	2.2	176578	2	AC040895	Homo sapi	177	39	2.1	169065	9	AC006064	AC006064 Homo sapi
105	40	2.2	178770	2	AP002793	Homo sapi	178	39	2.1	172571	9	CNS0771V	CNS0771V Homo sapi
106	40	2.2	181140	2	AC0040167	Homo sapi	179	39	2.1	173025	2	AC009863	AC009863 Homo sapi
107	40	2.2	181823	2	CNS07ECY	Human chr	180	39	2.1	173550	2	AC146189	AC146189 Homo sapi
108	40	2.2	181987	9	AL391827	Human DNA	181	39	2.1	175771	2	AC0912149	AC0912149 Homo sapi
109	40	2.2	183430	9	AC012412	Human sapi	182	39	2.1	176155	2	AC093106	AC093106 Homo sapi
110	40	2.2	183514	2	AC147317	Par trogl	183	39	2.1	177806	9	AC072044	AC072044 Homo sapi
111	40	2.2	186338	2	AC010540	Homo sapi	184	39	2.1	178453	2	AC021848	AC021848 Homo sapi
112	40	2.2	188455	2	AC016590	Homo sapi	185	39	2.1	178453	2	AC021848	AC021848 Homo sapi
113	40	2.2	188823	2	AC138475	Homo sapi	186	39	2.1	181663	2	AC068982	AC068982 Homo sapi
114	40	2.2	202661	2	AC091984	Homo sapi	187	39	2.1	181663	2	AC123506	AC123506 Homo sapi
115	40	2.2	207040	2	AC143870	Macaca mu	188	39	2.1	183493	2	AC021163	AC021163 Homo sapi
116	40	2.2	216571	2	HS147924	Human chrom	189	39	2.1	186322	2	AC080124	AC080124 Homo sapi
117	40	2.2	222330	9	AC022146	Homo sapi	190	39	2.1	187681	2	AC009146	AC009146 Homo sapi
118	40	2.2	226699	9	AC136285	Homo sapi	191	39	2.1	188249	2	AC026495	AC026495 Homo sapi
119	40	2.2	235286	2	AC009050	Homo sapi	192	39	2.1	188605	9	AC143324	AC143324 Homo sapi
120	40	2.2	264051	2	AC019731	Homo sapi	193	39	2.1	189155	2	AC126503	AC126503 Homo sapi
121	39	2.1	15473	9	AC117431	Homo sapi	194	39	2.1	189363	9	CNS07EBK	CNS07EBK Homo sapi
122	39	2.1	17301	9	AY248697	Homo sapi	195	39	2.1	189410	2	AC009883	AC009883 Homo sapi
123	39	2.1	29388	9	AP000549	Homo sapi	196	39	2.1	189476	2	AC142534	AC142534 Homo sapi
124	39	2.1	35878	9	AP0018342	Homo sapi	197	39	2.1	191823	9	AC092169	AC092169 Homo sapi
125	39	2.1	36532	9	AC118942	Homo sapi	198	39	2.1	192927	9	AC092169	AC092169 Homo sapi
126	39	2.1	51473	9	AL591419	Human DNA	199	39	2.1	193159	9	AC006946	AC006946 Homo sapi
127	39	2.1	53423	9	AL591419	Human DNA	200	39	2.1	193159	9	AC026512	AC026512 Homo sapi
128	39	2.1	57075	9	AL590093	Human DNA	201	39	2.1	193159	9	AC143322	AC143322 Homo sapi
129	39	2.1	62485	9	AL590093	Human DNA	202	39	2.1	196465	2	AC141449	AC141449 Homo sapi
130	39	2.1	64136	2	AC103730	Homo sapi	203	39	2.1	196857	2	CNS081DW	CNS081DW Homo sapi
131	39	2.1	70300	2	AC084074	Homo sapi	204	39	2.1	198714	9	AC134678	AC134678 Homo sapi
132	39	2.1	71639	9	AL162539	Human DNA	205	39	2.1	200389	2	AC004676	AC004676 Homo sapi
133	39	2.1	91026	9	AL162539	Human DNA	206	39	2.1	201175	9	AC091628	AC091628 Homo sapi
134	39	2.1	93835	9	AL162539	Human DNA	207	39	2.1	201397	2	AC073924	AC073924 Homo sapi
135	39	2.1	101319	9	AL162539	Human DNA	208	39	2.1	201470	2	AC145311	AC145311 Homo sapi
136	39	2.1	108822	9	AC112164	Homo sapi	209	39	2.1	203928	9	AC022483	AC022483 Homo sapi
137	39	2.1	110822	9	AC008683	Homo sapi	210	39	2.1	206156	2	AC004387	AC004387 Homo sapi
138	39	2.1	114127	9	AC008683	Homo sapi	211	39	2.1	206156	2	AC004387	AC004387 Homo sapi

C 212	39	2.1	209317	9	AL672032	285	37	2.0	473	9	AF323485	AF323485 Erythroce
C 213	39	2.1	210957	2	AL392218	C 286	37	2.0	461	9	AF005578S6	AF022208 Homo sapi
C 214	39	2.1	220349	2	AC136438	C 287	37	2.0	552	6	AB875154	AF022208 Homo sapi
C 215	39	2.1	228156	9	AC022150	C 288	37	2.0	552	6	BD155216	BD155216 Primer to
C 216	39	2.1	257365	2	AC141450	C 289	37	2.0	568	6	AB872380	AB872380 Sequence
C 217	38	2.1	346	11	HS003504	C 290	37	2.0	568	6	BD152442	BD152442 Primer to
C 218	38	2.1	4834	9	AC126473	C 291	37	2.0	593	6	AX3867734	AX3867734 Sequence
C 219	38	2.1	49875	9	ALC06491	C 292	37	2.0	622	6	AX389779	AX389779 Sequence
C 220	38	2.1	61313	2	AC087172	C 293	37	2.0	624	9	HSYDACS	AF151096 Homo sapi
C 221	38	2.1	70422	9	AP001961	C 294	37	2.0	663	6	AX866839	AX866839 Primer to
C 222	38	2.1	76000	9	AC092793	C 295	37	2.0	663	6	BD146901	BD146901 Primer to
C 223	38	2.1	80992	9	AP005137	C 296	37	2.0	666	9	HUMY003C01	AB057067 Homo sapi
C 224	38	2.1	82412	2	AC040940	C 297	37	2.0	719	9	AB053110	AB053110 Homo sapi
C 225	38	2.1	90015	9	AL513264	C 298	37	2.0	814	9	HSMB02726	AL359610 Homo sapi
C 226	38	2.1	108716	9	HS101A4	C 299	37	2.0	853	6	AX541120	AX541120 Sequence
C 227	38	2.1	110192	9	AC004070	C 300	37	2.0	1404	9	EC007731	BC007731 Homo sapi
C 228	38	2.1	114875	9	AC090281	C 301	37	2.0	1545	9	EC041924	BC041924 Homo sapi
C 229	38	2.1	121017	9	AC087388	C 302	37	2.0	1739	9	AK026047	AK026047 Homo sapi
C 230	38	2.1	121623	9	AC002412	C 303	37	2.0	1781	9	AK130909	AK130909 Homo sapi
C 231	38	2.1	131903	9	HS360E18	C 304	37	2.0	1801	6	AX882099	AX882099 Sequence
C 232	38	2.1	134010	9	AL353579	C 305	37	2.0	1801	9	BD159519	BD159519 Primer to
C 233	38	2.1	138416	9	AC105218	C 306	37	2.0	1801	9	AK022374	AK022374 Homo sapi
C 234	38	2.1	139843	2	AL158145	C 307	37	2.0	1840	9	AC046415	BC046415 Homo sapi
C 235	38	2.1	148045	9	AC021860	C 308	37	2.0	1868	9	AK03807	AK03807 Homo sapi
C 236	38	2.1	155001	2	AC013827	C 309	37	2.0	1871	9	HSINB2	Y10697 H. sapiens I
C 237	38	2.1	155682	9	AP003384	C 310	37	2.0	1906	9	BC022542	BC022542 Homo sapi
C 238	38	2.1	156712	2	AC044874	C 311	37	2.0	2022	9	AK097122	AK097122 Homo sapi
C 239	38	2.1	158792	2	AC044874	C 312	37	2.0	2073	6	AB083310	AB083310 Macaca fa
C 240	38	2.1	163542	2	AC129071	C 313	37	2.0	2354	6	AX882122	AX882122 Sequence
C 241	38	2.1	163542	2	AC024612	C 314	37	2.0	2354	6	BD158540	BD158540 Primer to
C 242	38	2.1	166620	2	AC024612	C 315	37	2.0	2361	9	AK022409	AK022409 Homo sapi
C 243	38	2.1	166651	2	AC008049	C 316	37	2.0	2361	9	AK051568	AK051568 Homo sapi
C 244	38	2.1	168665	9	AC007783	C 317	37	2.0	2455	6	AR405832	AR405832 Sequence
C 245	38	2.1	169303	9	AL354808	C 318	37	2.0	2455	6	AR405833	AR405833 Sequence
C 246	38	2.1	170000	2	AC004394	C 319	37	2.0	2455	6	AX201108	AX201108 Sequence
C 247	38	2.1	173608	9	AC107993	C 320	37	2.0	2455	6	AX201109	AX201109 Sequence
C 248	38	2.1	173767	9	AC022007	C 321	37	2.0	2455	6	AX267907	AX267907 Sequence
C 249	38	2.1	174347	9	AC008066	C 322	37	2.0	2455	6	AX267908	AX267908 Sequence
C 250	38	2.1	174537	2	AC022917	C 323	37	2.0	2476	9	AK097927	AK097927 Homo sapi
C 251	38	2.1	186561	9	AC093159	C 324	37	2.0	2483	6	AX714417	AX714417 Sequence
C 252	38	2.1	186739	9	AC093159	C 325	37	2.0	2483	6	AK056719	AK056719 Homo sapi
C 253	38	2.1	187421	9	AL590453	C 326	37	2.0	2568	6	AX880796	AX880796 Sequence
C 254	38	2.1	188679	2	AC023121	C 327	37	2.0	2568	6	BD158596	BD158596 Primer to
C 255	38	2.1	190000	2	AC004580	C 328	37	2.0	2568	9	AK027850	AK027850 Homo sapi
C 256	38	2.1	190701	9	AC022274	C 329	37	2.0	2586	9	AK130512	AK130512 Homo sapi
C 257	38	2.1	191318	2	AC020670	C 330	37	2.0	2649	9	AT428593	AT428593 Homo sapi
C 258	38	2.1	191937	2	AC026196	C 331	37	2.0	2915	9	AK025420	AK025420 Homo sapi
C 259	38	2.1	192688	9	AC100823	C 332	37	2.0	2947	6	BC000380	BC000380 Homo sapi
C 260	38	2.1	196272	2	AC026675	C 333	37	2.0	2949	6	AX877315	AX877315 Sequence
C 261	38	2.1	201854	9	AL590128	C 334	37	2.0	2949	6	AX877315	AX877315 Sequence
C 262	38	2.1	204394	9	AL590128	C 335	37	2.0	2971	9	BC041838	BC041838 Homo sapi
C 263	38	2.1	210515	9	AC097382	C 336	37	2.0	3021	9	HSMB02400	HSMB02400 Homo sapi
C 264	38	2.1	211345	9	AP002453	C 337	37	2.0	3049	6	AX880849	AX880849 Sequence
C 265	38	2.1	211509	9	CNS08C8D	C 338	37	2.0	3049	6	BD158629	BD158629 Primer to
C 266	38	2.1	216911	9	AC018809	C 339	37	2.0	3049	6	AX880849	AX880849 Sequence
C 267	38	2.1	218485	2	AC127470	C 340	37	2.0	3226	6	AX833599	AX833599 Sequence
C 268	38	2.1	270178	2	EX572623	C 341	37	2.0	3226	6	AX833599	AX833599 Sequence
C 269	37	2.0	287	9	AF323486	C 342	37	2.0	3298	9	AK122887	AK122887 Homo sapi
C 270	37	2.0	292	9	AF323486	C 343	37	2.0	3298	9	HSMB06835	HSMB06835 Homo sapi
C 271	37	2.0	314	6	AR422581	C 344	37	2.0	3700	9	AX834110	AX834110 Sequence
C 272	37	2.0	314	6	BD181813	C 345	37	2.0	3710	6	AX096631	AX096631 Homo sapi
C 273	37	2.0	323	6	AR421399	C 346	37	2.0	3710	6	HSACO0961	HSACO0961 Homo sapi
C 274	37	2.0	323	6	BD116952	C 347	37	2.0	3761	9	AX409498	AX409498 Sequence
C 275	37	2.0	330	6	AR422011	C 348	37	2.0	3779	6	HUMEC8D	LO7077 Human enyol
C 276	37	2.0	330	6	BD117564	C 349	37	2.0	3811	9	BC038948	BC038948 Homo sapi
C 277	37	2.0	335	6	AR421398	C 350	37	2.0	4188	9	AX596870	AX596870 Sequence
C 278	37	2.0	335	6	BD116951	C 351	37	2.0	4603	6	AX074132	AX074132 Homo sapi
C 279	37	2.0	400	11	G16950	C 352	37	2.0	4848	6	AX096870	AX096870 Sequence
C 280	37	2.0	446	6	AR417703	C 353	37	2.0	5549	6	AR137382	AR137382 Sequence
C 281	37	2.0	446	6	BD113256	C 354	37	2.0	5549	6	BD075534	BD075534 Methods f
C 282	37	2.0	464	6	AR422744	C 355	37	2.0	5590	6	BD075534	BD075534 Methods f
C 283	37	2.0	464	6	BD116297	C 356	37	2.0	5590	6	BD075534	BD075534 Methods f
C 284	37	2.0	464	6	BD116297	C 357	37	2.0	5590	6	BD075534	BD075534 Methods f

C 358	37	2.0	5590	9	HSACE5	X94359 H. sapiens g	431	37	2.0	37274	9	AC005272	AC005272 Homo sapi
C 359	37	2.0	6047	9	AX133016	X94359 H. sapiens g	432	37	2.0	37349	9	AC010524	AC010524 Homo sapi
C 360	37	2.0	6047	9	D86979	D86979 Homo sapien	433	37	2.0	37391	9	AC005779	AC005779 Homo sapi
C 361	37	2.0	6354	9	HSMB06750	EX640685 Homo sapi	434	37	2.0	37490	9	AC026356	AC026356 Homo sapi
C 362	37	2.0	6664	6	AX822167	AX822167 Sequence	435	37	2.0	37501	9	AC024104	AC024104 Homo sapi
C 363	37	2.0	6664	6	AX825807	AX825807 Sequence	436	37	2.0	37631	9	AC004030	AC004030 Homo sapi
C 364	37	2.0	6682	6	AX780186	AX780186 Sequence	437	37	2.0	38031	9	AC005764	AC005764 Homo sapi
C 365	37	2.0	6682	6	AX780187	AX780187 Sequence	438	37	2.0	38374	6	AX336192	AX336192 Sequence
C 366	37	2.0	8277	9	HSABE201	U76667 Homo sapien	439	37	2.0	38374	6	AX33652	AX33652 Sequence
C 367	37	2.0	8807	2	AC022123	AC022123 Homo sapi	440	37	2.0	38374	6	AX33652	AX33652 Sequence
C 368	37	2.0	8807	2	AL606523	AL606523 Homo sapi	441	37	2.0	38374	6	AX33652	AX33652 Sequence
C 369	37	2.0	9180	6	AX410815	AX410815 Homo sapi	442	37	2.0	38374	6	AX33652	AX33652 Sequence
C 370	37	2.0	9180	6	BD083442	BD083442 MEN1, the	443	37	2.0	38437	9	AC104094	AC104094 Homo sapi
C 371	37	2.0	9180	6	HSU93237	U93237 Human menin	444	37	2.0	38565	9	HS433G19	HS433G19 Homo sapi
C 372	37	2.0	9236	6	AX135853	AX135853 Sequence	445	37	2.0	38602	9	EX248133	EX248133 Homo sapi
C 373	37	2.0	9236	6	HS435231	AX252311 Homo sapi	446	37	2.0	38761	9	HSN13E1	HSN13E1 Homo sapi
C 374	37	2.0	9238	6	AX135854	AX135854 Sequence	447	37	2.0	38785	9	HS695020B	HS695020B Homo sapi
C 375	37	2.0	9238	6	HS4252312	AX252312 Homo sapi	448	37	2.0	38841	9	AC139076	AC139076 Homo sapi
C 376	37	2.0	9241	6	AX135852	AX135852 Sequence	449	37	2.0	38849	9	AC005346	AC005346 Homo sapi
C 377	37	2.0	9241	6	HS4252313	AX252313 Homo sapi	450	37	2.0	38891	9	AC010298	AC010298 Homo sapi
C 378	37	2.0	9391	9	AP000306	AP000306 Homo sapi	451	37	2.0	38981	9	AC110784	AC110784 Homo sapi
C 379	37	2.0	10091	9	HS4314901	AL15697 Homo sapi	452	37	2.0	39210	9	HSE118G4	HSE118G4 Homo sapi
C 380	37	2.0	12243	9	AL15697	AL15697 Homo sapi	453	37	2.0	39383	9	AC022149	AC022149 Homo sapi
C 381	37	2.0	13927	6	BD093712	BD093712 Homo sapi	454	37	2.0	39426	9	AC008983	AC008983 Homo sapi
C 382	37	2.0	14564	6	AP363482S1	AP363482 Homo sapi	455	37	2.0	39721	2	AC139772	AC139772 Homo sapi
C 383	37	2.0	15122	9	AB036993	AB036993 Homo sapi	456	37	2.0	39951	2	AC005602	AC005602 Homo sapi
C 384	37	2.0	16256	6	AX647079	AX647079 Sequence	457	37	2.0	39982	6	AR308846	AR308846 Homo sapi
C 385	37	2.0	16433	9	AP000294	AP000294 Homo sapi	458	37	2.0	40108	2	AC146476	AC146476 Homo sapi
C 386	37	2.0	16781	9	AL156422	AL156422 Homo sapi	459	37	2.0	40108	2	AC146476	AC146476 Homo sapi
C 387	37	2.0	17138	9	AP000310	AP000310 Homo sapi	460	37	2.0	40125	2	AC132818	AC132818 Homo sapi
C 388	37	2.0	17705	6	AC123576	AC123576 Homo sapi	461	37	2.0	40129	9	AF006501	AF006501 Homo sapi
C 389	37	2.0	19068	9	HS1206D7	Z67987 Homo sapi	462	37	2.0	40166	9	AL591670	AL591670 Homo sapi
C 390	37	2.0	19531	9	AC092622	AC092622 Homo sapi	463	37	2.0	40272	9	AC145343	AC145343 Homo sapi
C 391	37	2.0	19985	6	HUMPSAPA	M86181 Human prosa	464	37	2.0	40307	9	AC025153	AC025153 Homo sapi
C 392	37	2.0	22255	6	AR409342	AR409342 Sequence	465	37	2.0	40419	9	AC004653	AC004653 Homo sapi
C 393	37	2.0	22255	6	AX239608	AX239608 Sequence	466	37	2.0	40697	2	AC107874	AC107874 Homo sapi
C 394	37	2.0	23241	6	BD093729	BD093729 Homo sapi	467	37	2.0	40887	2	AC011526	AC011526 Homo sapi
C 395	37	2.0	23241	6	BD093730	BD093730 Homo sapi	468	37	2.0	41319	2	AC107932	AC107932 Homo sapi
C 396	37	2.0	23895	2	AC144837	AC144837 Homo sapi	469	37	2.0	41385	9	AC144836	AC144836 Homo sapi
C 397	37	2.0	24052	9	AC104522	AC104522 Homo sapi	470	37	2.0	41471	2	AC008996	AC008996 Homo sapi
C 398	37	2.0	24137	9	AL157368	AL157368 Homo sapi	471	37	2.0	41571	2	AC145660	AC145660 Homo sapi
C 399	37	2.0	24360	9	AL1590400	AL1590400 Homo sapi	472	37	2.0	41685	2	AC145992	AC145992 Homo sapi
C 400	37	2.0	25069	9	AL139252	AL139252 Homo sapi	473	37	2.0	41696	9	AC005932	AC005932 Homo sapi
C 401	37	2.0	25193	9	AF200923	AF200923 Homo sapi	474	37	2.0	41921	2	AC068358	AC068358 Homo sapi
C 402	37	2.0	25285	9	AC006997	AC006997 Homo sapi	475	37	2.0	42681	9	AC004560	AC004560 Homo sapi
C 403	37	2.0	25309	6	AX571860	AX571860 Sequence	476	37	2.0	42700	2	AC010383	AC010383 Homo sapi
C 404	37	2.0	25500	9	AC110754	AC110754 Homo sapi	477	37	2.0	42925	9	AL844165	AL844165 Homo sapi
C 405	37	2.0	25507	9	AC118943	AC118943 Homo sapi	478	37	2.0	42930	9	AF241732	AF241732 Homo sapi
C 406	37	2.0	25803	9	AC096510	AC096510 Homo sapi	479	37	2.0	43192	2	AC139090	AC139090 Homo sapi
C 407	37	2.0	26400	9	AC024585	AC024585 Homo sapi	480	37	2.0	43467	9	AC000086	AC000086 Homo sapi
C 408	37	2.0	26928	6	AX277527	AX277527 Sequence	481	37	2.0	43527	9	AC006293	AC006293 Homo sapi
C 409	37	2.0	26928	6	AX418091	AX418091 Sequence	482	37	2.0	43591	9	AC004236	AC004236 Homo sapi
C 410	37	2.0	27273	9	AL365206	AL365206 Homo sapi	483	37	2.0	43674	9	AC106040	AC106040 Homo sapi
C 411	37	2.0	27754	6	AX614798	AX614798 Sequence	484	37	2.0	44065	2	AC087281	AC087281 Homo sapi
C 412	37	2.0	28984	9	AB002059	AB002059 Homo sapi	485	37	2.0	44971	9	AC105251	AC105251 Homo sapi
C 413	37	2.0	29186	9	AL357560	AL357560 Homo sapi	486	37	2.0	44971	9	AF241731	AF241731 Homo sapi
C 414	37	2.0	29230	2	AC068219	AC068219 Homo sapi	487	37	2.0	45089	2	AC090156	AC090156 Homo sapi
C 415	37	2.0	30237	2	AC115096	AC115096 Homo sapi	488	37	2.0	45120	9	AC090163	AC090163 Homo sapi
C 416	37	2.0	30634	9	AL589725	AL589725 Homo sapi	489	37	2.0	45311	9	AC084398	AC084398 Homo sapi
C 417	37	2.0	32303	9	AL627108	AL627108 Homo sapi	490	37	2.0	45350	9	AC116908	AC116908 Homo sapi
C 418	37	2.0	32638	2	AC146707	AC146707 Homo sapi	491	37	2.0	45589	2	AC090823	AC090823 Homo sapi
C 419	37	2.0	33297	9	AF293358	AF293358 Homo sapi	492	37	2.0	45594	2	AC090823	AC090823 Homo sapi
C 420	37	2.0	33795	9	AC136977	AC136977 Homo sapi	493	37	2.0	45594	2	AC090823	AC090823 Homo sapi
C 421	37	2.0	34012	9	AL954743	AL954743 Homo sapi	494	37	2.0	45626	2	AT207045	AT207045 Homo sapi
C 422	37	2.0	34315	9	AC092306	AC092306 Homo sapi	495	37	2.0	45929	2	AC005757	AC005757 Homo sapi
C 423	37	2.0	35144	9	AC133542	AC133542 Homo sapi	496	37	2.0	46534	2	HS1057D18	HS1057D18 Homo sapi
C 424	37	2.0	36099	9	HSAB007973	HSAB007973 Homo sapi	497	37	2.0	46546	2	AC111161	AC111161 Homo sapi
C 425	37	2.0	36200	9	AC004792	AC004792 Homo sapi	498	37	2.0	46546	2	AC111161	AC111161 Homo sapi
C 426	37	2.0	36269	9	AT291060	AT291060 Homo sapi	499	37	2.0	46582	2	AC068325	AC068325 Homo sapi
C 428	37	2.0	36740	9	AC126120	AC126120 Homo sapi	500	37	2.0	47811	9	AC092161	AC092161 Homo sapi
C 429	37	2.0	36810	9	AC108014	AC108014 Homo sapi							
C 430	37	2.0	36810	9	AC125280	AC125280 Homo sapi							

ALIGNMENTS

RESULT 1
AR252489 1849 bp DNA linear PAT 20-DEC-2002
LOCUS AR252489
DEFINITION Sequence 157 from patent US 6478825.
ACCESSION AR252489
VERSION AR252489.1 GI:27300397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 157.12-NOV-2002;
FEATURES
Location/Qualifiers
source 1..1849
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGGGGGGGATGAGTGAAGGAGAGTACGTCGGCGCTGCTCGGGCTTTGCT 60
DB 1 CTGAGGGGGGGGATGAGTGAAGGAGAGTACGTCGGCGCTGCTCGGGCTTTGCT 60
QY 61 CGGCGACTGCTTTCAGACCTCAACGAGCTCGACACGGAAGTTTCTTTG 120
DB 61 CGGCGACTGCTTTCAGACCTCAACGAGCTCGACACGGAAGTTTCTTTG 120
QY 121 GGAAGTAAAGGAGAGCCCAAGACGATCTGATTCCTCAATGATGATGAAAT 180
DB 121 GGAAGTAAAGGAGAGCCCAAGACGATCTGATTCCTCAATGATGATGAAAT 180
QY 181 TGTTATACATGACATTCAGAAATATATTCATGCTTATGCTTTTATGCTTATA 240
DB 181 TGTTATACATGACATTCAGAAATATATTCATGCTTATGCTTTTATGCTTATA 240
QY 241 TTCTTACGCGAATGATGAGCAAGACCTGAAGAAATATATGCAATGTCAAAAA 300
DB 241 TTCTTACGCGAATGATGAGCAAGACCTGAAGAAATATATGCAATGTCAAAAA 300
QY 301 TGTGTAGGTGGTGAACAAATTCGCTGCTCATTCAGATCAGATGACGTTAGAGAG 360
DB 301 TGTGTAGGTGGTGAACAAATTCGCTGCTCATTCAGATCAGATGACGTTAGAGAG 360
QY 361 GGTGCTTCAAAAACCTTGAGAGCATTTTCAACCAAGACCTTGTCTGTAT 420
DB 361 GGTGCTTCAAAAACCTTGAGAGCATTTTCAACCAAGACCTTGTCTGTAT 420
QY 421 AAGACCAAGTATATACAGAAAGCTGCTACTCATTCAGCTGAAACATTTCTTATATA 480
DB 421 AAGACCAAGTATATACAGAAAGCTGCTACTCATTCAGCTGAAACATTTCTTATATA 480
QY 481 ACCTCAAAAAGGACTTTTCAAGGATACCTTTAGTGTGCTCAATCTGCGCATGCTGA 540
DB 481 ACCTCAAAAAGGACTTTTCAAGGATACCTTTAGTGTGCTCAATCTGCGCATGCTGA 540
QY 541 AGAAGCTGGTATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 AGAAGCTGGTATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 ACAACCTGGTATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ACAACCTGGTATATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 AATGAAATGATGCTTATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 AATGAAATGATGCTTATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 720

DB 661 AATGAAATGATGCTTATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 CAGTGAACAGCAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 CAGTGAACAGCAGTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 GAAAAGAGAGACACAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 GAAAAGAGAGACACAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GAGAGACATTTTCTTGTGAGGATTAAGGACCTTTTTCATTTCTGATTTCTTCA 900
DB 841 GAGAGACATTTTCTTGTGAGGATTAAGGACCTTTTTCATTTCTGATTTCTTCA 900
QY 901 TTTCATGCTTATGCTTTTAAAAATGACATGTTTCTTAAAAAGTGTGATCTAACCA 960
DB 901 TTTCATGCTTATGCTTTTAAAAATGACATGTTTCTTAAAAAGTGTGATCTAACCA 960
QY 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TAGTCAGCTAGTACACCAAAATCATTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1080
DB 1021 TAGTCAGCTAGTACACCAAAATCATTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1080
QY 1081 GCAATTCAGAGATCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 GCAATTCAGAGATCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TAGTATACCAAGATTAAGATCAAAATGAGGACCCAGAAACAGATGAGAAATGGA 1200
DB 1141 TAGTATACCAAGATTAAGATCAAAATGAGGACCCAGAAACAGATGAGAAATGGA 1200
QY 1201 AAGATGAGAGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 AAGATGAGAGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 CAAGAGATTTTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 CAAGAGATTTTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GTTGAAGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GTTGAAGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ACAATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 ACAATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 TTTCGAACCTTTTTCACCTTCACTTAAGTGTGAGGAGAGGCTTACAGACACACA 1500
DB 1441 TTTCGAACCTTTTTCACCTTCACTTAAGTGTGAGGAGAGGCTTACAGACACACA 1500
QY 1501 TTCTTGAATTTGAAAAGTGAACAGACAGAGCTGCTCAACCTTAAATCCAGACACT 1560
DB 1501 TTCTTGAATTTGAAAAGTGAACAGACAGAGCTGCTCAACCTTAAATCCAGACACT 1560
QY 1561 TAGGAGACAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 TAGGAGACAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GTATGAGACATGCTATTTAAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 GTATGAGACATGCTATTTAAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 AATATGAG 1740
DB 1681 AATATGAG 1740
QY 1741 ACTTTTGAAG 1800
DB 1741 ACTTTTGAAG 1800

RESULT 2
LOCUS AX092290 1849 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116318.
ACCESSION AX092290
VERSION AX092290.1 GI:13444459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Batton, D.L., Filvarsoff, E., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same
TITLE Patent: WO 0116318-A 21 08-MAR-2001; Genentech, Inc. (US)
JOURNAL Location/Qualifiers
FEATURES 1. 1849
SOURCE /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
 Query Match 100.0%; Score 1849; DB 6; Length 1849;
 Best Local Similarity 100.0%; Pired. No. 0;
 Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CTGAGGCGGCGGTGATGAGGAGGAGAGTACGTCGCGCGTCTCTCGGCGTTTGCT 60
 1 CTGAGGCGGCGGTGATGAGGAGGAGAGTACGTCGCGCGTCTCTCGGCGTTTGCT 60
 61 CGGCGCACTCGCTTCCAGACCTCAACACGGAATCGGACCGAAGGTTTCTCTG 120
 61 CGGCGCACTCGCTTCCAGACCTCAACACGGAATCGGACCGAAGGTTTCTCTG 120
 121 GGAAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGT 180
 121 GGAAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGT 180
 181 TGTATTAACAATGACATTCAGAAATATATTCATGCTATGAGTTTAACTTTTAA 240
 181 TGTATTAACAATGACATTCAGAAATATATTCATGCTATGAGTTTAACTTTTAA 240
 181 TGTATTAACAATGACATTCAGAAATATATTCATGCTATGAGTTTAACTTTTAA 240
 241 TTCTTCAGGCAAGTAAATGAGCAAGCACTGAGAAATATATTCATGCTATGAGTTTAA 300
 241 TTCTTCAGGCAAGTAAATGAGCAAGCACTGAGAAATATATTCATGCTATGAGTTTAA 300
 301 TGTGTAAGTGTGTAACAATTCGTCGTCATTCAGATCAGATCAGATCAGATCAGATC 360
 301 TGTGTAAGTGTGTAACAATTCGTCGTCATTCAGATCAGATCAGATCAGATCAGATC 360
 361 GCTGTTTACAAAACTTGCAGAGCATTTTCAACCAAGACCTTGTGTTTCTGCTATT 420
 361 GCTGTTTACAAAACTTGCAGAGCATTTTCAACCAAGACCTTGTGTTTCTGCTATT 420
 421 AACACCAAGTAAATTAACAAGAGTGTCTACTCATGAGTGAAGTGAAGTGAAGTGAAGT 480
 421 AACACCAAGTAAATTAACAAGAGTGTCTACTCATGAGTGAAGTGAAGTGAAGTGAAGT 480
 481 ACCTTAAGAGAGTCTTTTCAAGAGTCTTTAGTGTGTTGTTGTTGTTGTTGTTGTTGTT 540
 481 ACCTTAAGAGAGTCTTTTCAAGAGTCTTTAGTGTGTTGTTGTTGTTGTTGTTGTTGTT 540
 541 ACAACTGGGTTTAAACTGTATCAGTTTCTGTATGTCACTGTTTAAAGCCGAGAGT 600

541 ACAACTGGGTTTAAACTGTATCAGTTTCTGTATGTCACTGTTTAAAGCCGAGAGT 600
 601 ACAACACAGAGCTCTAAATTTTGAAGAAGATGATCTTAAAGAGGATACATTAAGT 660
 601 ACAACACAGAGCTCTAAATTTTGAAGAAGATGATCTTAAAGAGGATACATTAAGT 660
 661 AAATGAATGTATGCTTCAATTAACAAGAGTAAAGATTAAGATTAAGATTAAGATTAAG 720
 661 AAATGAATGTATGCTTCAATTAACAAGAGTAAAGATTAAGATTAAGATTAAGATTAAG 720
 721 CAGTGAACAAGCAGTGAATTAAGTAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 780
 721 CAGTGAACAAGCAGTGAATTAAGTAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 780
 781 GAAAAGAGAGAGACACAGATTCAGGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 781 GAAAAGAGAGAGACACAGATTCAGGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 841 GAGAGACATTTTCTTGTGAGGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 900
 841 GAGAGACATTTTCTTGTGAGGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 900
 901 TTCAATGTATGTCTTAAATAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 960
 901 TTCAATGTATGTCTTAAATAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 960
 961 CCATTCGATGATGATGACATTCGACCTTAATGATTAAGATTAAGATTAAGATTAAGATTA 1020
 961 CCATTCGATGATGATGACATTCGACCTTAATGATTAAGATTAAGATTAAGATTAAGATTA 1020
 1021 TAGTCACGCTAGTACACCAAAATCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080
 1021 TAGTCACGCTAGTACACCAAAATCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080
 1081 GCAATTAAGAGATTCGCTGTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140
 1081 GCAATTAAGAGATTCGCTGTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1140
 1141 TAGTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200
 1141 TAGTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200
 1201 AAAGATTAAGAGTGTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1260
 1201 AAAGATTAAGAGTGTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1260
 1261 CAAGAGATTTTATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320
 1261 CAAGAGATTTTATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320
 1321 GTTGAAGTCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1380
 1321 GTTGAAGTCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1380
 1381 AAGATTAAGTCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1440
 1381 AAGATTAAGTCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1440
 1441 TTTCGAACTTTTATTTTCACTTCACTTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1500
 1441 TTTCGAACTTTTATTTTCACTTCACTTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1500
 1501 TTCTTGAATTTGAGAAAGTGAAGACAGGACAGGACAGGACAGGACAGGACAGGACAGGAC 1560
 1501 TTCTTGAATTTGAGAAAGTGAAGACAGGACAGGACAGGACAGGACAGGACAGGACAGGAC 1560
 1561 TAGGAGAGCAAGTCAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1620
 1561 TAGGAGAGCAAGTCAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1620
 1621 GTATTGAGCAATGCTATTAATAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1680

Db 1621 GATATGAGACCATGTCTATTTAAAAATAAATGAAAAAGCAAGAAATGACCTTATTTTCA 1680
QY 1681 AATATGAAAAAGAAATTTATATGAAATTTATCTGAGTCATTTAAATTTCTCTTAAGTAT 1740
Db 1681 AATATGAAAAAGAAATTTATATGAAATTTATCTGAGTCATTTAAATTTCTCTTAAGTAT 1740
QY 1741 ACTTTTATGAAAGTACATTAATGAGTTCAGATGCAATTAATGCTGATATCATGCAAT 1800
Db 1741 ACTTTTATGAAAGTACATTAATGAGTTCAGATGCAATTAATGCTGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
Db 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849

RESULT 3
AX376066 1849 bp DNA linear PAT 01-MAR-2002
LOCUS AX376066
DEFINITION Sequence 133 from Patent WO0168848.
ACCESSION AX376066
VERSION AX376066.1 GI:19170425
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godwaski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 133 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source 1. 1849
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTGCGGCGTGTCTCTGCGGCTTTGTGCT 60
Db 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTGCGGCGTGTCTCTGCGGCTTTGTGCT 60
QY 61 CGGCGCATCTGCTTTCCAGCACTTCAACGAGACTTGGACAGGAGGTTTCTTTTGG 120
Db 61 CGGCGCATCTGCTTTCCAGCACTTCAACGAGACTTGGACAGGAGGTTTCTTTTGG 120
QY 121 GGAAGTAAAGGTGAAGCAAGACAGCTTCTGATTTCCCAATGAGATGTTGAGT 180
Db 121 GGAAGTAAAGGTGAAGCAAGACAGCTTCTGATTTCCCAATGAGATGTTGAGT 180
QY 181 TGTATTACAAATGACATTCAGAAATATATTCATGCTATACGCTTTTATGCTTTATTA 240
Db 181 TGTATTACAAATGACATTCAGAAATATATTCATGCTATACGCTTTTATGCTTTATTA 240
QY 241 TTCTTAGGCGAAGTAAATGAGCAAGCACTGAAAGAAATATATGCTTTTAAAGAA 300
Db 241 TTCTTAGGCGAAGTAAATGAGCAAGCACTGAAAGAAATATATGCTTTTAAAGAA 300
QY 301 TGTGTAGGTGTATCAAAATTCGTGTCATTCAGATCATGATGATGATTTAGAGAG 360
Db 301 TGTGTAGGTGTGTATCAAAATTCGTGTCATTCAGATCATGATGATGATTTAGAGAG 360
QY 361 GGTGCTTCAAAAATTTGAGAGAGATTTTCAAAACCAAGACTTTGTTTCTCTAT 420
Db 361 GGTGCTTCAAAAATTTGAGAGAGATTTTCAAAACCAAGACTTTGTTTCTCTAT 420

QY 421 AACACAGTATATATAACAGAAAGCTGCTACTCATCGACTGGAACTTCTTATATA 480
Db 421 AACACAGTATATATAACAGAAAGCTGCTACTCATCGACTGGAACTTCTTATATA 480
QY 481 ACCTCAAAAAGACTTTTCAAGGGTACCTTTTATGTTGGCCATCTGGGCACTGTCTGA 540
Db 481 ACCTCAAAAAGACTTTTCAAGGGTACCTTTTATGTTGGCCATCTGGGCACTGTCTGA 540
QY 541 ACACTGGTTATATAAATCTGATTCAGGTTCTGATGTCATGCTGTTTATGCGCAGAGT 600
Db 541 ACACTGGTTATATAAATCTGATTCAGGTTCTGATGTCATGCTGTTTATGCGCAGAGT 600
QY 601 ACAACACACAGCTCTAAATTTTGAAGAATGATCCTTAAAGAGGTACATTAAT 660
Db 601 ACAACACACAGCTCTAAATTTTGAAGAATGATCCTTAAAGAGGTACATTAAT 660
QY 661 AATGAATGTATGCTTATTAACAAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720
Db 661 AATGAATGTATGCTTATTAACAAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAAGCATATTAACCTAGTAAAGATGTAACAAGATTTAAACGAGAAATTTGA 780
Db 721 CAGTGAACAAGCATATTAACCTAGTAAAGATGTAACAAGATTTAAACGAGAAATTTGA 780
QY 781 GAAAAGAGAGAGACAGATTCAGGACAGAGAGAGAAAGATCCAAAAGACCTCTCA 840
Db 781 GAAAAGAGAGAGACAGATTCAGGACAGAGAGAGAAAGATCCAAAAGACCTCTCA 840
QY 841 GGAAGACATTTTCTTTGTGAGGCAATTCAGGACCTTTTCCAAATTTCTGAATTTCTCA 900
Db 841 GGAAGACATTTTCTTTGTGAGGCAATTCAGGACCTTTTCCAAATTTCTGAATTTCTCA 900
QY 901 TTCAATGCTATGCTTTTAAATTAAGATGATGCTTTTAAAGAGTGTACTAGAACCA 960
Db 901 TTCAATGCTATGCTTTTAAATTAAGATGATGCTTTTAAAGAGTGTACTAGAACCA 960
QY 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 TAGTCCAGCTATGATACCAATTCATTAAGCATTAAGCCTTTAGCTTATATGACGATG 1080
Db 1021 TAGTCCAGCTATGATACCAATTCATTAAGCATTAAGCCTTTAGCTTATATGACGATG 1080
QY 1081 GCAATTCAGAGATCTGCTGTTGATGATACAGAGCAAGCAAGATCTTAACCAATTA 1140
Db 1081 GCAATTCAGAGATCTGCTGTTGATGATACAGAGCAAGCAAGATCTTAACCAATTA 1140
QY 1141 TAGTATGATACCAAGATTAAGCATTCATTAAGCATTAAGCCTTTAGCTTATATGACGATG 1200
Db 1141 TAGTATGATACCAAGATTAAGCATTCATTAAGCATTAAGCCTTTAGCTTATATGACGATG 1200
QY 1201 AAAGATGAAGGTTTGTGATATTCACGCTCTCTCACTTTTGAATCCCTTTAACTTGA 1260
Db 1201 AAAGATGAAGGTTTGTGATATTCACGCTCTCTCACTTTTGAATCCCTTTAACTTGA 1260
QY 1261 CAAGGATTTTATTTATTTGGTGAATGGAAGCAACATTTCTATTTTACTAT 1320
Db 1261 CAAGGATTTTATTTATTTGGTGAATGGAAGCAACATTTCTATTTTACTAT 1320
QY 1321 GTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 ACAGATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 ACAGATATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 TTTCCTCAAACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1500
Db 1441 TTTCCTCAAACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1500
QY 1501 TTCTTTGAATGGAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1560

D	b		1501	TTCCTTAGAATTGGAAAAAGTGAACAAGGCACAGTGCGCTCACACTGTTATCCAGCACT	1560
Q	y		1561	TAGGAAAGAACAAGTACAGASGATTTGATTGAAGCTAAGAGCTTAAGAACCGAGCCTGGGCCAAC	1620
D	b		1561	TAGGAAAGAACAAGTACAGASGATTTGATTGAAGCTAAGAGCTTAAGAACCGAGCCTGGGCCAAC	1620
Q	y		1621	GTAATGAGACCATGTCTATTAAAATAAATGGAAAAAGCAGAAATAGCCTTATTTTTCCA	1680
D	b		1621	GTAATGAGACCATGTCTATTAAAATAAATGGAAAAAGCAGAAATAGCCTTATTTTTCCA	1680
Q	y		1681	AATATGGAAGAAATTTTATGAAATAATTTATCGAGCATTAATAATTCCTCCTAATGAT	1740
D	b		1681	AATATGGAAGAAATTTTATGAAATAATTTATCGAGCATTAATAATTCCTCCTAATGAT	1740
Q	y		1741	ACTTTTATGAGATCATTTATGGCTAGAGITGCCAGATPAATAATGCTGANTATCATGCAAT	1800
D	b		1741	ACTTTTATGAGATCATTTATGGCTAGAGITGCCAGATPAATAATGCTGANTATCATGCAAT	1800
Q	y		1801	AAATTGCAAACATCATCTAAATTATTAATAAAAAAAAAAAAAAAAAAAAAAA	1849
D	b		1801	AAATTGCAAACATCATCTAAATTATTAATAAAAAAAAAAAAAAAAAAAAAAA	1849
R	E	S	RESULT 4 LOCUS AX403270 1849 bp DNA linear PAT 14-JUN-2002		
A	C	I	DEFINITION Sequence 157 from Patent WO0073454.		
V	E	N	ACCESSION AX403270 GI:21436843		
K	E	M	VERSION AX403270.1 GI:21436843		
O	R	G	KEYWORDS Homo sapiens (human)		
S	O		Homo sapiens		
R	E	F	ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
R	E	F	REFERENCE 1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnyovers,L., Eaton,D., Ferreira,N., Gerber,H., Gertzelman,M., Goddard,A., Godowski,P., Grimaldi,C.U., Gueney,A.L., Kijavlin,I., Napier,W.A., Fan,J., Pacini,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,B., Wood,W.I. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0073454-A 157 07-DEC-2000;		
J	O	L	JOURNAL Genentech Inc. (US) Location/Qualifiers source l..1849 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
O	R	I	ORIGIN		
C	H	E	Query Match 100.0%; Score 1849; DB 6; Length 1849; Best Local Similarity 100.0%; Pred. No. C; Mismatches 0; Indels 0; Gaps 0; Matches 1849; Conservative 0;		
Q	y		1 CTGAGCGCGCGGTAGCATGAGAGGGGAGAGTACGTGGCGGTCTCTCGGCGTTGTGCT	60	
D	b		1 CTGAGCGCGCGGTAGCATGAGAGGGGAGAGTACGTGGCGGTCTCTCGGCGTTGTGCT	60	
Q	y		61 CGGCGACCTCGGTTCCAGCACTCAACACGSACTCGSACACGSAAAGSTTTCTCTGSG	120	
D	b		61 CGGCGACCTCGGTTCCAGCACTCAACACGSACTCGSACACGSAAAGSTTTCTCTGSG	120	
Q	y		121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATCCCAGATGATGTTGAGT	180	
D	b		121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATCCCAGATGATGTTGAGT	180	
Q	y		181 TGTTTATCAATTGACATTCAGAAATATATATTCATGCTATCAAGGTTTATAGCTTTATA	240	
D	b		181 TGTTTATCAATTGACATTCAGAAATATATATTCATGCTATCAAGGTTTATAGCTTTATA	240	
Y	y		241 TTCTTCAGCGCAAGTAATAGCAAGCACTGAGAGAAATATATCAAAAGTCAAAAAGA	300	

Db	241	TTCTTCAGGCGCAAGTAATATGACAGACATGAAAGAAATATATATCAAAATGTCACAAAANA	300
Qy	301	TTGGTAGGTGTGACAAATTCGCGTGCAATTAGATCAGATCATGACGTTTAGAGAG	360
Db	301	TTGGTAGGTGTGACAAATTCGCGTGCAATTAGATCAGATCATGACGTTTAGAGAG	360
Qy	361	GCTGCTTCAAAAACTTGCAGAGCATTTTCAACCAAGACTTGTTTTCTGCTAT	420
Db	361	GCTGCTTCAAAAACTTGCAGAGCATTTTCAACCAAGACTTGTTTTCTGCTAT	420
Qy	421	AACACCAATTAATTAACAGAAAGCTGTCTATCTATCGACCTGGAACTTCTTATATA	480
Db	421	AACACCAATTAATTAACAGAAAGCTGTCTATCTATCGACCTGGAACTTCTTATATA	480
Qy	481	ACCTCAAAAAGACTTTTTCACAGGGTACTTTAGTGTTGCCAATCTGGGCAATGCTCGA	540
Db	481	ACCTCAAAAAGACTTTTTCACAGGGTACTTTAGTGTTGCCAATCTGGGCAATGCTCGA	540
Qy	541	ACAACCTGGGTTATATAAATCTGATCAGGTTCCGTATGTCACATGTTTAGCCGACAGT	600
Db	541	ACAACCTGGGTTATATAAATCTGATCAGGTTCCGTATGTCACATGTTTAGCCGACAGT	600
Qy	601	ACAAAACAACAGCTCTAAATTTTGTGAAGAAATGATCCTTAAAGAGGTATCAATAGT	660
Db	601	ACAAAACAACAGCTCTAAATTTTGTGAAGAAATGATCCTTAAAGAGGTATCAATAGT	660
Qy	661	AAATAAATATGATGCTTCATTACACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA	720
Db	661	AAATAAATATGATGCTTCATTACACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA	720
Qy	721	CAGTGAACACAGATGATTAACCTAGTAAAGATGTAAACAGATTAAACAGAAATTGA	780
Db	721	CAGTGAACACAGATGATTAACCTAGTAAAGATGTAAACAGATTAAACAGAAATTGA	780
Qy	781	GAAAAGAGAGAGACAGATTCAGGACAGAAAGAAAGAAATCTCAAAAAGACCTTCA	840
Db	781	GAAAAGAGAGAGACAGATTCAGGACAGAAAGAAAGAAATCTCAAAAAGACCTTCA	840
Qy	841	GGAGAACATTTTCTTTGTCAAGGATTAACGACCTTTTCCAAATCTGAATTTCTTCA	900
Db	841	GGAGAACATTTTCTTTGTCAAGGATTAACGACCTTTTCCAAATCTGAATTTCTTCA	900
Qy	901	TTTCAGTGTATATGCTTTTAAAAAATAGACATGTTTTCTAAAGATAGCTGTAACTACACCA	960
Db	901	TTTCAGTGTATATGCTTTTAAAAAATAGACATGTTTTCTAAAGATAGCTGTAACTACACCA	960
Qy	961	CCATCTCGATGTATGATACAAATCTGACCTTAAATGTATGAACACATGCAATTCGAAAGC	1020
Db	961	CCATCTCGATGTATGATACAAATCTGACCTTAAATGTATGAACACATGCAATTCGAAAGC	1020
Qy	1021	TAGTCACAGTAGTACACCAAAATCATTAAGCATTAAGCCTTGAATGATGACAGATG	1080
Db	1021	TAGTCACAGTAGTACACCAAAATCATTAAGCATTAAGCCTTGAATGATGACAGATG	1080
Qy	1081	GCAATTCAGAGATTTGCGTTGTATGATACACAGACAAACATCTAAAGCAAAATCTG	1140
Db	1081	GCAATTCAGAGATTTGCGTTGTATGATACACAGACAAACATCTAAAGCAAAATCTG	1140
Qy	1141	TAGTAGTAAACCAAGTAAAGCATCCAAATAGACAGCCGAAACAGATGAAGAAATTGA	1200
Db	1141	TAGTAGTAAACCAAGTAAAGCATCCAAATAGACAGCCGAAACAGATGAAGAAATTGA	1200
Qy	1201	AAAAGATGAAGGTTTGGTGAATATTCACGCTGCCCACTTTTGAATCCTTTAAACCTTA	1260
Db	1201	AAAAGATGAAGGTTTGGTGAATATTCACGCTGCCCACTTTTGAATCCTTTAAACCTTA	1260
Qy	1261	CAAGAGATTTTTTATTTGGCTATGAGGTTAAAGCCAAACATTTCTATTTGTTTAACTAT	1320
Db	1261	CAAGAGATTTTTTATTTGGCTATGAGGTTAAAGCCAAACATTTCTATTTGTTTAACTAT	1320
Qy	1321	GTTTAGCTACTGACGTAAATTCATTTGTTTAACTATGTTCACTGTTTGACGATATAC	1380

Db 1321 GTGAGCTACTGTCAGTAAGTTCATTTGTTTACTAGTTCACCTGTTTGCAGTAATAC 1380

QY 1381 ACGAATTAATCTTAAGCAATTAATCTTCAAGTAATCTTTTCAACATCAATGCTTTTA 1440

Db 1381 ACGAATTAATCTTAAGCAATTAATCTTCAAGTAATCTTTTCAACATCAATGCTTTTA 1440

QY 1441 TTTCACAACTTTTTCACCTTTCACTAAGTTGTTGAGGGAGGCTTACACAGACACA 1500

Db 1441 TTTCACAACTTTTTCACCTTTCACTAAGTTGTTGAGGGAGGCTTACACAGACACA 1500

QY 1501 TTCTTTAGAAATGGAAAAAGTGAGACGACCAAGTGGCTCAACCTGTATATCCAGCACT 1560

Db 1501 TTCTTTAGAAATGGAAAAAGTGAGACGACCAAGTGGCTCAACCTGTATATCCAGCACT 1560

QY 1561 TAGGGAAGCAAGTCAAGAGATTTGATGAGCTAGAGTTAGACGACGCTGGGCAAC 1620

Db 1561 TAGGGAAGCAAGTCAAGAGATTTGATGAGCTAGAGTTAGACGACGCTGGGCAAC 1620

QY 1621 GTATTGAGACCATGCTCTATTAAAAAATGAAAAAGCAAGTAAGCTTATTTTCA 1680

Db 1621 GTATTGAGACCATGCTCTATTAAAAAATGAAAAAGCAAGTAAGCTTATTTTCA 1680

QY 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTAT 1740

Db 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTAT 1740

QY 1741 ACTTTTATGAAATGATATGAGCTAGAGTTGACAGATTAATGCTGATATCATGCAAT 1800

Db 1741 ACTTTTATGAAATGATATGAGCTAGAGTTGACAGATTAATGCTGATATCATGCAAT 1800

QY 1801 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTAT 1849

Db 1801 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTAT 1849

RESULT 5
AY358576 1849 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DNA56410 EMBL496 (UNQ496) mRNA, complete cds.
DEFINITION AY358576
ACCESSION AY358576.1 GI:37182273
VERSION FLI CDNA.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1849)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chow,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hase,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimovskii,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,V.,
Schonfeld,J., Sehnaghi,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagstad,A., Vanden,R., Watanabe,C., Wleand,D., Woods,K.,
Xie,M.H., Yaneura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secretd Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secretd and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 1849)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
Source
1. .1849
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA56410"
1. .1849
gene

CDS
/locus_tag="UNQ496"
17..1246
/locus_tag="UNQ496"
/note="PRO1013"
/codon_start=1
/product="EGES496"
/protein_id="AA088939.1"
/db_xref="GI:37182274"
/translation="MESESATVLSRVGALAFQHLNDSPDEGLGKLVKGVKAKNS
ITSDMDVEVVTIDLOKIPCTQLFSPFNSSGEVNEQLKILSVKRVKGVKTF
RRSDQIMTRERLRLKLEHNSNDLVFLTPSTLTSCTHRLHSLVYRQKL
FHRYPFLVANKSEQLGKTVSGSCSTSPSAVQHSRFEEDSLKLVKHEM
VASLOELKILCKKVEDSEQAVRLVYDVRLEIKERGAQIOAKARENIOKDE
NIFLCALRTFFPSEFLSHSCMSLKRVHYSKSCNVNHLIDVDVNTLWVHTDIE
ASPSATFOILKHALDLDDEWQKRSRLDTPQKRSKANTSSNODKASWSSPETDE
EIEEMKFGSYSSPT"

ORIGIN
Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CTGAGGGGGGGGTAGCATGAGAGGGGGAGATAGTGGCGCGGTGCTCGGGCTTTGGCT 60
1 CTGAGGGGGGGGTAGCATGAGAGGGGGAGATAGTGGCGCGGTGCTCGGGCTTTGGCT 60
61 CGGCGCACTGGCTTTCCAGACACTCAACAGGACTCGGACACGGAAGTTTCTTCTGG 120
61 CGGCGCACTGGCTTTCCAGACACTCAACAGGACTCGGACACGGAAGTTTCTTCTGG 120
QY 121 GGAAGTAAAGGTGAAGCAAGCAAGCAATTCATGATCCCAATGGATGATGAGT 180
Db 121 GGAAGTAAAGGTGAAGCAAGCAAGCAATTCATGATCCCAATGGATGATGAGT 180
QY 181 TGTATTATACATGACATTCAGAAATATATTCATGCTATACGCTTTTATATTA 240
Db 181 TGTATTATACATGACATTCAGAAATATATTCATGCTATACGCTTTTATATTA 240
QY 241 TTCTTCAGGGCAAGTAATATGACAGCACTGGAAGAAATTTATCAATGTCAAAAAGA 300
Db 241 TTCTTCAGGGCAAGTAATATGACAGCACTGGAAGAAATTTATCAATGTCAAAAAGA 300
QY 241 TTCTTCAGGGCAAGTAATATGACAGCACTGGAAGAAATTTATCAATGTCAAAAAGA 300
Db 241 TTCTTCAGGGCAAGTAATATGACAGCACTGGAAGAAATTTATCAATGTCAAAAAGA 300
QY 301 TGTGTAGTGTGATCAATTCGCTCGTCAATTCAGATCAATGATGATGATGATGATGAT 360
Db 301 TGTGTAGTGTGATCAATTCGCTCGTCAATTCAGATCAATGATGATGATGATGATGAT 360
QY 361 GCTGCTTCAAAAAGCTTGGAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
Db 361 GCTGCTTCAAAAAGCTTGGAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
QY 361 GCTGCTTCAAAAAGCTTGGAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
Db 361 GCTGCTTCAAAAAGCTTGGAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
QY 421 AAGCAGAGTATATACAGAAAGCTCTCACTGATGATGATGATGATGATGATGATGAT 480
Db 421 AAGCAGAGTATATACAGAAAGCTCTCACTGATGATGATGATGATGATGATGATGAT 480
QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACTTTAGTGGTCCCATCTGGGCAATGCTGGA 540
Db 481 ACCTCAAAAAGACTTTTTCACAGGGTACTTTAGTGGTCCCATCTGGGCAATGCTGGA 540
QY 541 ACAACCTGGTTATTAACCTGATACAGGTTCTGATATCCATGATGATGATGATGATGAT 600
Db 541 ACAACCTGGTTATTAACCTGATACAGGTTCTGATATCCATGATGATGATGATGATGAT 600
QY 601 ACAACCAACAGCTCTAATTTTTCAGAGAGATGATCTTTAAGAGGATCAATTAAGAT 660
Db 601 ACAACCAACAGCTCTAATTTTTCAGAGAGATGATCTTTAAGAGGATCAATTAAGAT 660
QY 661 AATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 AATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 CAGTGAACAAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 CAGTGAACAAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

QY	781	GAAGAGAGAGAGACACAGATTCCAGGAGACAGAGAGAAACAACATCCAAAAAGCCCTCA	840
Db	781	GAAGAGAGAGAGACACAGATTCCAGGAGACAGAGAGAAAGAATCCAAAAAGCCCTCA	840
QY	841	GGAGACAATTTTTCTTTGTCAAGGATTAAGGACCTTTTTCCAAATTCGTATTTCTTCA	900
Db	841	GGAGACAATTTTTCTTTGTCAAGGATTAAGGACCTTTTTCCAAATTCGTATTTCTTCA	900
QY	901	TTCAATGCTTATGCTTTTAAAAAATAACATGTGTTCTAAAAAGTGCCTGACTACACA	960
Db	901	TTCAATGCTTATGCTTTTAAAAAATAACATGTGTTCTAAAAAGTGCCTGACTACACA	960
QY	961	CCATCTCGATGTAGTAGCAATCTGACCTTAATGTGTAAACACACTGACATTTCTGAAGC	1020
Db	961	CCATCTCGATGTAGTAGCAATCTGACCTTAATGTGTAAACACACTGACATTTCTGAAGC	1020
QY	1021	TAGTCCAGCTAGTACACCAACCAATCATTAAGCATTAAGCCTTAGACTTAGTGCACATG	1080
Db	1021	TAGTCCAGCTAGTACACCAACCAATCATTAAGCATTAAGCCTTAGACTTAGTGCACATG	1080
QY	1081	GCAATTCAGAAGATCTGGTGTGTAGATACACAAGACAAAGCATCTTAAGCAATACTGG	1140
Db	1081	GCAATTCAGAAGATCTGGTGTGTAGATACACAAGACAAAGCATCTTAAGCAATACTGG	1140
QY	1141	TAGTAGTAAACAATTAAGAGATCCAAATAGAGAGCCAGAAACAATAGAGAAATGGA	1200
Db	1141	TAGTAGTAAACAATTAAGAGATCCAAATAGAGAGCCAGAAACAATAGAGAAATGGA	1200
QY	1201	AAAGATGAAGGGTTTTGGTGAATATTTCAAGGTCTTCATTTTGATTCCTTTTAACCTTA	1260
Db	1201	AAAGATGAAGGGTTTTGGTGAATATTTCAAGGTCTTCATTTTGATTCCTTTTAACCTTA	1260
QY	1261	CAAGAGATTTTTTTATTTGAGCTAGTGGGTAAAGCCAAACATTTCTATTTGTTTTTACTAT	1320
Db	1261	CAAGAGATTTTTTTATTTGAGCTAGTGGGTAAAGCCAAACATTTCTATTTGTTTTTACTAT	1320
QY	1321	GTTTAGCTACTGTCAGTAAGTTCAATTTGTTTTTACTATGTTCACCTGTTTGCAATATAC	1380
Db	1321	GTTTAGCTACTGTCAGTAAGTTCAATTTGTTTTTACTATGTTCACCTGTTTGCAATATAC	1380
QY	1381	ACAGATAAAGCTTTAGTGCATTTACTCTCCACAAGTACTTTTCAACAACATCAGATGCTTTTA	1440
Db	1381	ACAGATAAAGCTTTAGTGCATTTACTCTCCACAAGTACTTTTCAACAACATCAGATGCTTTTA	1440
QY	1441	TTTCCAAACCTTTTTTTCACCTTTCACTAAGATTTGTGAGGGGAAAGGCTTACACAGACA	1500
Db	1441	TTTCCAAACCTTTTTTTCACCTTTCACTAAGATTTGTGAGGGGAAAGGCTTACACAGACA	1500
QY	1501	TTCTTTTGAATTTGAAAAAGTAGAGACAGAGGCTCACACCTGTAATCCAGAGACT	1560
Db	1501	TTCTTTTGAATTTGAAAAAGTAGAGACAGAGGCTCACACCTGTAATCCAGAGACT	1560
QY	1561	TAGGGAGACAAAGTCAAGAGATGATTGAAGCTTAGAGATTAAGACCAAGCTGTGGCAAC	1620
Db	1561	TAGGGAGACAAAGTCAAGAGATGATTGAAGCTTAGAGATTAAGACCAAGCTGTGGCAAC	1620
QY	1621	GTAATTGAGACCATGTCTATTAATAAATAATGAAGAAAGCAAGATAGCCTTATTTTCAA	1680
Db	1621	GTAATTGAGACCATGTCTATTAATAAATAATGAAGAAAGCAAGATAGCCTTATTTTCAA	1680
QY	1681	AATATGAAAAAATTTATATGAAAAATTTATCTGAGCATTAATAATCTCTCTTAAGGAT	1740
Db	1681	AATATGAAAAAATTTATATGAAAAATTTATCTGAGCATTAATAATCTCTCTTAAGGAT	1740
QY	1741	ACTTTTTAGAGTCACTTATGTGCTAGAGTTGCCAGATTAATATGCTGAGATTCATGCAAT	1800
Db	1741	ACTTTTTAGAGTCACTTATGTGCTAGAGTTGCCAGATTAATATGCTGAGATTCATGCAAT	1800
QY	1801	AAATTTGCAAAACATCATCTAAATTTTAAAAAAGAAAAAAGAAAAAAGAAAAA	1849
Db	1801	AAATTTGCAAAACATCATCTAAATTTTAAAAAAGAAAAAAGAAAAAAGAAAAA	1849

RESULT 6
 BC039573
 LOCUS
 DEFINITION
 BC039573
 ACCESSION
 BC039573
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 JOURNAL
 REMARK
 COMMENT
 gene

2649 bp mRNA linear PRI 07-OCT-2003
 Homo sapiens hypothetical protein FLJ13614, mRNA (cDNA clone
 MGC:48664 IMAGE:6045433), complete cds.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2649)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stepien, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,
 Scheet, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carrinci, P., Prange, C., Raha, S.S., Loughran, N.A., Peters, G.J.,
 Abramson, R.D., Miliani, S.J., Boeck, S.A., McKernan, P.J.,
 McKernan, K.U., Malek, J.A., Gnatatne, P.H., Richards, S.,
 Woley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,
 Viallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Yadan, A.C., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y.,
 Boiford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Buterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalls, D.E.,
 Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A. full-length
 generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2 (bases 1 to 2649)
 Strausberg, R.
 Direct Submission
 Submitted (01-NOV-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgaps-remail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbioology.org>
 contact: amadarsystemsbiology.org
 Amp Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 84 Row: 1
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 20589960
 Location/Qualifiers
 1..2649
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:48664 IMAGE:6045433"
 /cissue_type="Testis, embryonal carcinoma"
 /cissue_lib="NIH_MGC_92"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
 1..2649
 /gene="FTL13614"

/note="synonyms: FLJ1520, FLJ12642"
/db_xref="LocustID:84142"
340..1242
/codon_start=1
/product="FLJ1614 protein"
/protein_id="AAH39573.1"
/db_xref="GI:24660390"
/db_xref="LocustID:84142"

translation="MTFERLHKNLOEHFNSQDVFLLTPSIITSCSTRLEHSL
YPOKGLFRVPLVVALNLMSEQLGYKIVSGSMSTGSRVQTHSKFPEEDSLKE
YKINEMVASLOELKSLCKYVEDSBOADVLDKLVNRYKREIERKRGALQAAERK
IOKDPEMTFLCOALRTFEPNSELHSCVMSLKRNHVSKSSQNTVYHHLDVYDNLTKY
EHRTDPEASPASTPQIIKKKALDLDKRWQFKSRLLDIDYDKRSKADTSSNQDKASKK
SSPEDEIERKKGFEIYSRSPF"

ORIGIN

Query Match 96.0%; Score 1775; DB 9; Length 2649;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1825; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGGGGGGAGCATGAGGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCTCGGC 64
DB 1 GGGGGGGGAGCATGAGGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCTCGGC 60
QY 65 GCACTGCTTTCCAGCACCCTCAACACGAGCTCGGACACGGAAGTTTCTTCTGGGGAA 124
DB 61 GCACTGCTTTCCAGCACCCTCAACACGAGCTCGGACACGGAAGTTTCTTCTGGGGAA 120
QY 125 GTTAAAGGTGAAGCCAAAGAACAGCATTTACTGATTTCCCAATGAGATGTTGAAGTTGT 184
DB 121 GTTAAAGGTGAAGCCAAAGAACAGCATTTACTGATTTCCCAATGAGATGTTGAAGTTGT 180
QY 185 TTATCAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATATCT 244
DB 181 TTATCAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATATCT 240
QY 245 TCAGGGGAAGTAATAGGACACATCGAAGAAATATATCAATGTCAAAAAGATGTG 304
DB 241 TCAGGGGAAGTAATAGGACACATCGAAGAAATATATCAATGTCAAAAAGATGTG 300
QY 305 GTTAGGTGTACAAATTCGCTGTCTATTCAGATCAGATCAGATCAGATCAGATCAGATCAG 364
DB 301 GTTAGGTGTACAAATTCGCTGTCTATTCAGATCAGATCAGATCAGATCAGATCAGATCAG 360
QY 365 CTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTTCTGCTATTAACA 424
DB 361 CTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTTCTGCTATTAACA 420
QY 425 CCAAGTATATTAACAGAAAGCTGCTTACTCATCGACTGGAAACATTCTTATATTAACCT 484
DB 421 CCAAGTATATTAACAGAAAGCTGCTTACTCATCGACTGGAAACATTCTTATATTAACCT 480
QY 485 CAAAAGAGCTTTTCAAGGGTACCTTAGTGTGTCACATCTGGGACATGCTGAACA 544
DB 481 CAAAAGAGCTTTTCAAGGGTACCTTAGTGTGTCACATCTGGGACATGCTGAACA 540
QY 545 CTGGGTATTAACCTGTATCAGGTTCTGTATGTCACCTGTTTACCGGACAGTACA 604
DB 541 CTGGGTATTAACCTGTATCAGGTTCTGTATGTCACCTGTTTACCGGACAGTACA 600
QY 605 AACACAGCTTAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGTAAT 664
DB 601 AACACAGCTTAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGTAAT 660
QY 665 GAAATGTATGCTTCAATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 724
DB 661 GAAATGTATGCTTCAATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 720
QY 725 GAAACAGAGCTGATTAACCTAGTAAAGATGTAACAGATTAACAGATTAACAGATTAAGAA 784
DB 721 GAAACAGAGCTGATTAACCTAGTAAAGATGTAACAGATTAACAGATTAACAGATTAAGAA 780
QY 785 AGGAGAGAGACAGATTCAGCAGCAGCAAGAGAGAAAGATCAAAAAGACCTCAGAG 844

DB 781 AGGAGAGAGACAGATTCAGCAGCAGCAAGAGAGAAAGATCAAAAAGACCTCAGAG 840
QY 845 AACATTTTCTTGTGAGGATTAACGACCTTTTTCCTCAATCTGAATTTCTTCAATCA 904
DB 841 AACATTTTCTTGTGAGGATTAACGACCTTTTTCCTCAATCTGAATTTCTTCAATCA 900
QY 905 TGTGTATGCTTTAAAAAATAGACATGTTCTTAAAGAGCTGTAACTAACACACCAT 964
DB 901 TGTGTATGCTTTAAAAAATAGACATGTTCTTAAAGAGCTGTAACTAACACACCAT 960
QY 965 CTCATGTAGTAAACATCTGACCTTAATGCTTAAACACCTGACATTTCTGAGCTAGT 1024
DB 961 CTCATGTAGTAAACATCTGACCTTAATGCTTAAACACCTGACATTTCTGAGCTAGT 1020
QY 1025 CCAAGTATGACACCAACAAATCAATTAAGCATTAAGACCTTATAGCTTATAGTACAA 1084
DB 1021 CCAAGTATGACACCAACAAATCAATTAAGCATTAAGACCTTATAGCTTATAGTACAA 1080
QY 1085 TTCAAGCATCTCGGTGTTTATGATACACAGACAAAGATCTTAAAGCAATCTGTAGT 1144
DB 1081 TTCAAGCATCTCGGTGTTTATGATACACAGACAAAGATCTTAAAGCATCTGTAGT 1140
QY 1145 AGTAACCAAGATTAAGGATCCAAATAGAGCAGCCAGAAACAGATGAGAAATGAAAG 1204
DB 1141 AGTAACCAAGATTAAGGATCCAAATAGAGCAGCCAGAAACAGATGAGAAATGAAAG 1200
QY 1205 ATGAGGCTTTGGTGAAATATTCACGCTCTCTACATTTTGAATCTTTTAACTTACAA 1264
DB 1201 ATGAGGCTTTGGTGAAATATTCACGCTCTCTACATTTTGAATCTTTTAACTTACAA 1260
QY 1265 GAGATTTTATTTTGTGCTAGTGGTAAAGCCAAACATTTCTATGTTTATCATAGTTG 1324
DB 1261 GAGATTTTATTTTGTGCTAGTGGTAAAGCCAAACATTTCTATGTTTATCATAGTTG 1320
QY 1325 AGCTACTGACATGATGATCAATTTGTTTATCTATGTTTACCTGTTGACATTAACA 1384
DB 1321 AGCTACTGACATGATGATCAATTTGTTTATCTATGTTTACCTGTTGACATTAACA 1380
QY 1385 ATACCTGTAGTGAATTACTTCAACAAAGTCTTTTCAACATCAGATGCTTTTATTC 1444
DB 1381 ATACCTGTAGTGAATTACTTCAACAAAGTCTTTTCAACATCAGATGCTTTTATTC 1440
QY 1445 CAAACCTTTTTCACCTTCACTAAGTTGTTAGGGGAAGCTTACACAGACATCTT 1504
DB 1441 CAAACCTTTTTCACCTTCACTAAGTTGTTAGGGGAAGCTTACACAGACATCTT 1500
QY 1505 TTGAATTTGAAGAGTGAAGCAGGACAGTGGCTCACCTGTATTTCCAGACATTAAG 1564
DB 1501 TTGAATTTGAAGAGTGAAGCAGGACAGTGGCTCACCTGTATTTCCAGACATTAAG 1560
QY 1565 GAAACAGTCAAGAGATTAATGAAGCTTAGAGATTGAACAGCAGCTGGGCAACGTAT 1624
DB 1561 GAAACAGTCAAGAGATTAATGAAGCTTAGAGATTGAACAGCAGCTGGGCAACGTAT 1620
QY 1625 TGAGACCATGCTATTAATAAATTAATAAGAAAGAAATGCTTATTTCAAAATA 1684
DB 1621 TGAGACCATGCTATTAATAAATTAATAAGAAAGAAATGCTTATTTCAAAATA 1680
QY 1685 TGAGAAAGAAATTAATAAATTAATAAGTATCTAGTCAATTAATAATCTCTTAAGTATCT 1744
DB 1681 TGAGAAAGAAATTAATAAATTAATAAGTATCTAGTCAATTAATAATCTCTTAAGTATCT 1740
QY 1745 TTTTGAAGATCATTAATGCTTAAGTTCACAGATTAATAAGCTGTGATATCATGCAATTAAT 1804
DB 1741 TTTTGAAGATCATTAATGCTTAAGTTCACAGATTAATAAGCTGTGATATCATGCAATTAAT 1800
QY 1805 TTGCAAAACATCATTAATTTTAA 1830
DB 1801 TTGCAAAACATCATTAATTTTAA 1826

RESULT 7

AX879640
 LOCUS AX879640 2663 bp DNA linear PAT 17-DEC-2003
 DEFINITION Sequence 14545 from Patent EP1074617.
 ACCESSION AX879640
 VERSION AX879640.1 GI:40034376
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., and Otsuki, T.
 TITLE Primers for synthesizing full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 14545 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES
 source
 1. 2663
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 379..1281
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAE90598.1"
 /db_xref="GI:40034376"
 /translation="MTFRRLHKQLQEHFSNODLVFLPLPSITTESCTHREHSL
 VKRQGLFHRVPLVAVNIGMSHOLGKTVGSCMSTGSRVAVQTSKPEPDSIKS
 VKIKINMYASLOEELKSKICKEDSEQANDKLYKDVNLEKRIEERAOQOAAERKX
 IKQDPEKFLICQALNTFENSEFLHSCWMLKRNHVESKSNVHHLVDVNDLTVW
 EHTDIPKASPASTPOLIKRKLIDLDNRQFKSRLLDQDKSKADTSSNODKSKRM
 SSPEDEEIEKKMGFEYERSPTF"
 ORIGIN
 Query Match 83.6%; Score 1546; DB 6; Length 2663;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1816; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 541 ACAACCTGGTTATTAACCTGTATCAGGTCCTGTATGTCACCTGGTTTACCCGACAGT 600
 DB 576 ACAACCTGGTTATTAACCTGTATCAGGTCCTGTATGTCACCTGGTTTACCCGACAGT 635
 QY 601 ACAACCAACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGATCATTAAGAT 660
 DB 636 ACAACCAACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGATCATTAAGAT 695
 QY 661 AAATGAATGTATGCTTCATTACAGAAGATTAAGAATTAATGCAAAAAAGTGAAGA 720
 DB 696 AAATGAATGTATGCTTCATTACAGAAGATTAAGAATTAATGCAAAAAAGTGAAGA 755
 QY 721 CAGTGAACAAGCAAGTGTATTAATAGTAAAGATGTAACAGTTAAACGAGAAATGA 780
 DB 756 CAGTGAACAAGCAAGTGTATTAATAGTAAAGATGTAACAGTTAAACGAGAAATGA 815
 QY 781 GAAAAGAGAGAGACACAGATTGAGCAGACAGAGAGAGAGAGAGATCCAAAAGACCTCA 840
 DB 816 GAAAAGAGAGAGACACAGATTGAGCAGACAGAGAGAGAGAGATCCAAAAGACCTCA 875
 QY 841 GAGAAATTTTCTTTGACAGCATTAAGACCTTTTCCAAATTCGAATTTCTCA 900
 DB 876 GAGAAATTTTCTTTGACAGCATTAAGACCTTTTCCAAATTCGAATTTCTCA 935
 QY 901 TTCAATGTATGTCTTTAAATAATAGACATGTTTCTAAAGAGTGTAACTACAACA 960
 DB 936 TTCAATGTATGTCTTTAAATAATAGACATGTTTCTAAAGAGTGTAACTACAACA 995
 QY 961 CCATCTGATGTATGATACAACTGACCTTAATAGTAAACACAGACATTCCTGAAGC 1020
 DB 996 CCATCTGATGTATGATACAACTGACCTTAATAGTAAACACAGACATTCCTGAAGC 1055
 QY 1021 TAGTCCAGTAGTACACCAAAATCATTAAGCATTAAGCCTTGAATAGATGACAGATG 1080
 DB 1056 TAGTCCAGTAGTACACCAAAATCATTAAGCATTAAGCCTTGAATAGATGACAGATG 1115
 QY 1081 GCAATTTCAAGATCTCGGTTGTTAGATACACAAGACAAACGATCTTAAGCAATCTCG 1140
 DB 1116 GCAATTTCAAGATCTCGGTTGTTAGATACACAAGACAAACGATCTTAAGCAATCTCG 1175
 QY 1141 TAGTAGTAACCAAGATTAAGCATCAAAATAGACAGCCAGAAACAGATGAAGAAATGA 1200
 DB 1176 TAGTAGTAACCAAGATTAAGCATCAAAATAGACAGCCAGAAACAGATGAAGAAATGA 1235
 QY 1201 AAGATGAAGGTTTGTGAATATTCAGGTCCTCAATTTTGAATCCTTTAACTTA 1260
 DB 1236 AAGATGAAGGTTTGTGAATATTCAGGTCCTCAATTTTGAATCCTTTAACTTA 1295
 QY 1261 CAAGAGATTTTATTTGAGTGAATGAAGCCAAACATTTCTATTTTACTAT 1320
 DB 1296 CAAGAGATTTTATTTGAGTGAATGAAGCCAAACATTTCTATTTTACTAT 1355
 QY 1321 GTTAGCTACTTGCAGTAAGTCAATTTGTTTATCTATGTTCACTGTTTGCAGTAATAC 1380
 DB 1356 GTTAGCTACTTGCAGTAAGTCAATTTGTTTATCTATGTTCACTGTTTGCAGTAATAC 1415
 QY 1381 ACAGATTAAGTGTAGTCAATTTTCAACAAGATCTTTTCAACATCAGATGCTTTTA 1440
 DB 1416 ACAGATTAAGTGTAGTCAATTTTCAACAAGATCTTTTCAACATCAGATGCTTTTA 1475
 QY 1441 TTTCAAAACCTTTTTCACCTTCACTAAGTTGTTGAAGGGAAGGCTTACACAGACACA 1500
 DB 1476 TTTCAAAACCTTTTTCACCTTCACTAAGTTGTTGAAGGGAAGGCTTACACACA 1534
 QY 1501 TTCTTTGAATTTGAAAAGTGAACACAGGACAGTGTCTACACCTGTAATCCAGAGACT 1560
 DB 1535 TTCTTTGAATTTGAAAAGTGAACACAGGACAGTGTCTACACCTGTAATCCAGAGACT 1594
 QY 1561 TAGGAAAGACAAAGTCAAGAGATTAAGTGAAGCTTAAGAGATTAAGACCAAGCTGGGCAAC 1620
 DB 1595 TAGGAAAGACAAAGTCAAGAGATTAAGTGAAGCTTAAGAGATTAAGACCAAGCTGGGCAAC 1654

QY 1621 GATTAGACATCTCTATTAAAAATGAAAAAGAAAGATAGCTTATTTTCA 1680
 Db 1655 GATTAGACATCTCTATTAAAAATGAAAAAGAAAGATAGCTTATTTTCA 1714
 QY 1681 AATATGAAAGAAATTTATATGAAAAATTTATCTGACTCATTAATTTCCCTTAAGTAT 1740
 Db 1715 AATATGAAAGAAATTTATATGAAAAATTTATCTGACTCATTAATTTCCCTTAAGTAT 1774
 QY 1741 ACTTTTATGAAAGTATATGCTTAGAGTGGCAGATATAATGCTGATATCATGCAAT 1800
 Db 1775 ACTTTTATGAAAGTATATGCTTAGAGTGGCAGATATAATGCTGATATCATGCAAT 1834
 QY 1801 AATTTGCAAAAACATCATCT 1820
 Db 1835 AATTTGCAAAAACATCATCT 1854

RESULT 8
 BD157945 2663 bp DNA linear PAT 17-JAN-2003
 LOCUS Primer for synthesizing full-length cDNA and use thereof.
 DEFINITION
 ACCESSION BD157945.1 GI:27863703
 VERSION JP 2002191363-A/12788.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 2663)
 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002191363-A 12788 09-JUL-2002;
 JOURNAL HELIX RESEARCH INSTITUTE
 COMMENT OS Homo sapiens (human)
 FN JP 2002191363-A/12788
 PD 09-JUL-2002
 PE 28-JUL-2000 JP 200280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, XAORU PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,
 PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 FEATURES Location/Qualifiers
 FT CDS (379)..(1278).
 source Location/Qualifiers
 1.2663
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 83.6%; Score 1546; DB 6; Length 2663;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1816; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CTGAGCGCGCGTAGCATGAGAGGAGAGTACGTGCGCGTGTCTCTCGGCTTTGTGCT 60
 Db 36 CTGAGCGCGCGTAGCATGAGAGGAGAGTACGTGCGCGTGTCTCTCGGCTTTGTGCT 95
 QY 61 CGGCGCACTGCTTTCCAGCACTCAACAGCACTGGACAGGAAAGTTTCTTCTTG 120
 Db 96 CGGCGCACTGCTTTCCAGCACTCAACAGCACTGGACAGGAAAGTTTCTTCTTG 155
 QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATCCCAATGATGATGGAAGT 180
 Db 156 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATCCCAATGATGATGGAAGT 215
 QY 181 TGTATATACATTTGACATTCAGAAATATATTCATCTCATTCAGCTTTTATATA 240

Db 216 TGTATATACATTTGACATTCAGAAATATATTCATCTCATTCAGCTTTTATATA 275
 QY 241 TTCTTCAGCGGAAGTAAATAGCAGACATGAGAAATATTTATCAATGTCAAAAAGAA 300
 Db 276 TTCTTCAGCGGAAGTAAATAGCAGACATGAGAAATATTTATCAATGTCAAAAAGAA 335
 QY 301 TGTGCTAGTGTGGTAAATTCGCTGCTATTCAGATCAATCAATGACGTTTAGAGAG 360
 Db 336 TGTGCTAGTGTGGTAAATTCGCTGCTATTCAGATCAATCAATGACGTTTAGAGAG 395
 QY 361 GCTGCTCACAAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTCGCAATT 420
 Db 396 GCTGCTCACAAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTCGCAATT 455
 QY 421 AACACCAAGTAAATTAACAGAAAGCTGCTTACTCATGACAGCAATTCCTTAATAA 480
 Db 456 AACACCAAGTAAATTAACAGAAAGCTGCTTACTCATGACAGCAATTCCTTAATAA 515
 QY 481 ACCTCAAAAGACTTTTGAACAGGGTACCTTTAGAGTGGCCAAATCGGGCAATGCTGA 540
 Db 516 ACCTCAAAAGACTTTTGAACAGGGTACCTTTAGAGTGGCCAAATCGGGCAATGCTGA 575
 QY 541 ACAACTGGATTATATAAATCTGATCAGGTTCTGTATGCTGCTTTTAGCCGACAGT 600
 Db 576 ACAACTGGATTATATAAATCTGATCAGGTTCTGTATGCTGCTTTTAGCCGACAGT 635
 QY 601 ACAACACACAGCTCTAAATTTTGAAGAAGTGAATCCTTTAAGAGGTACATAGAT 660
 Db 636 ACAACACACAGCTCTAAATTTTGAAGAAGTGAATCCTTTAAGAGGTACATAGAT 695
 QY 661 AATGAATGTATGCTTCATTACAGAGATTTAAAGATATATGCAAAAAGTGAAGA 720
 Db 696 AATGAATGTATGCTTCATTACAGAGATTTAAAGATATATGCAAAAAGTGAAGA 755
 QY 721 CAGTGAACAGCACTATATAAATCTGATTAAGATGTAAACAGATTAACAGAAATTTGA 780
 Db 756 CAGTGAACAGCACTATATAAATCTGATTAAGATGTAAACAGATTAACAGAAATTTGA 815
 QY 781 GAAAGAGAGAGAGCAGATTCAGCAGACAGAGAGAGAAACATCCAAAAGACCTCA 840
 Db 816 GAAAGAGAGAGAGCAGATTCAGCAGACAGAGAGAGAAACATCCAAAAGACCTCA 875
 QY 841 GGAGAACATTTTCTTTGTGACGATTTAGGACCTTTTCCAAATCTGAATTTCTTCA 900
 Db 876 GGAGAACATTTTCTTTGTGACGATTTAGGACCTTTTCCAAATCTGAATTTCTTCA 935
 QY 901 TTCAATGTTATGCTTTTAAATAAATAGACATGTTTCTTAAAGTATGCTATCAACCA 960
 Db 936 TTCAATGTTATGCTTTTAAATAAATAGACATGTTTCTTAAAGTATGCTATCAACCA 995
 QY 961 CCATCTGATGTATGATACCAATCTGACCTTAATGTGTAACAACATGACTTCTGAAGC 1020
 Db 996 CCATCTGATGTATGATACCAATCTGACCTTAATGTGTAACAACATGACTTCTGAAGC 1055
 QY 1021 TAGTCCAGCTAGTACACCACAAAATCATTAAAGCATTAAGCCTTAGCTTAGATGACAGATG 1080
 Db 1056 TAGTCCAGCTAGTACACCACAAAATCATTAAAGCATTAAGCCTTAGCTTAGATGACAGATG 1115
 QY 1081 GCAATTCAGAGATCTCGGTTGTATGATACACAAGAACAAAGATCTTAAACAGATCTCG 1140
 Db 1116 GCAATTCAGAGATCTCGGTTGTATGATACACAAGAACAAAGATCTTAAACAGATCTCG 1175
 QY 1141 TAGTAGTACCAAGATTAAGATCAAAATGAGAGAGCCAGAAACAGATGAAGAAATTTGA 1200
 Db 1176 TAGTAGTACCAAGATTAAGATCAAAATGAGAGAGCCAGAAACAGATGAAGAAATTTGA 1235
 QY 1201 AAGAGTAAAGGTTTGTGTAATATTCAGGCTCTCTCAATTTTGAATCTTTTAACTTAA 1260
 Db 1236 AAGAGTAAAGGTTTGTGTAATATTCAGGCTCTCTCAATTTTGAATCTTTTAACTTAA 1295
 QY 1261 CAAGAGATTTTATTTGCTGATGGGTAAAGCCAAATTCATTTGTTTACTAT 1320

Db 1296 CAAGGAGATTTTATTTGGCTGATGGGTAAGCAACATTTCATTTGTTTACAT 1355
QY 1321 GTTGAAGCTACTGCACTAGTCAATTTGTTTACTATGTTCACTGTTTGGCAATAC 1380
Db 1356 GTTGAAGCTACTGCACTAGTCAATTTGTTTACTATGTTCACTGTTTGGCAATAC 1415
QY 1381 ACAGATACTCTAGTCACTAGTCAATTTGTTTACTATGTTCACTGTTTGGCAATAC 1440
Db 1416 ACAGATACTCTAGTCACTAGTCAATTTGTTTACTATGTTCACTGTTTGGCAATAC 1475
QY 1441 TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGCTTTACACACAC 1500
Db 1476 TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGCTTTACACAC 1534
QY 1501 TTTCTTGAATTTGAAAAGTGAACGACGACGACGACGACGACGACGACGACGACGAC 1560
Db 1535 TTTCTTGAATTTGAAAAGTGAACGACGACGACGACGACGACGACGACGACGACGAC 1594
QY 1561 TAGGGAAGACAGTCAAGGAGATTGTAAGCTAGAGTTAGACACAGCTTGGGCAAC 1620
Db 1595 TAGGGAAGACAGTCAAGGAGATTGTAAGCTAGAGTTAGACACAGCTTGGGCAAC 1654
QY 1621 GTATTGAGACCACTCTATTAATAAATGGAAGCAAGATAGCCTTAATTTTCA 1680
Db 1655 GTATTGAGACCACTCTATTAATAAATGGAAGCAAGATAGCCTTAATTTTCA 1714
QY 1681 AATATGGAAGAATTTATATGAAAATTTATCTAGTCACTTAATTTCTTAAGTAT 1740
Db 1715 AATATGGAAGAATTTATATGAAAATTTATCTAGTCACTTAATTTCTTAAGTAT 1774
QY 1741 ACTTTTATAGTCACTTTATGCTAGAGTTGCGCAATTAATGCTGATATCAGCAAT 1800
Db 1775 ACTTTTATAGTCACTTTATGCTAGAGTTGCGCAATTAATGCTGATATCAGCAAT 1834
QY 1801 AAATTGCAAAACATCATCT 1820
Db 1835 AAATTGCAAAACATCATCT 1854

RESULT 9
AK022704 2663 bp mRNA linear PRI 01-AUG-2002
LOCUS Homo sapiens cDNA FLJ12642 fls, clone NT2RM4001965.
DEFINITION AK022704.1 GI:10434253
ACCESSION AK022704.1 GI:10434253
VERSION Oligo capping, fls (full insert sequence).
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Iisogi,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Mogatasuma,M., Hosokita,T., Kaku,Y., Kodaira,H., Komodo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Oho,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Makamatsu,A.,
Nakamura,Y., Nagahara,K., Masuno,Y., Ninomiya,K. and Iwayanagi,T.
MDO human cDNA sequencing project
TITLE Unpublished
JOURNAL 2 (bases 1 to 2663)
REFERENCE Iisogi,T. and Otsuki,T.
AUTHORS Direct Submission
TITLE Submitted (23-AUG-2000) Takao Iisogi, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
E-mail:genomics@hri.co.jp. Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT MEMO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology, cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
SOURCE
Location/Qualifiers
1..2663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4001965"
/cell_line="NT2"
/cell_type="keratinocarcinoma"
/clone_1bp="NT2RM4"
/note="Cloning vector: pME18SFL3-mRNA from uninduced NT2
neutonal precursor cells."
379..1281
/note="unamed protein product"
/codon_start=1
/protein_id="BAB14189.1"
/db_xref="GI:10434254"
/translation="MPFERLLHKNLOEHPNSODLVLLTPSITTESCSTRLEHSL
YKPKGLFHRVPLVAVNTGMSBOLGYKTVSGMSTGFSRAVOTHSKPEEDSLKE
VHKINERTASLOELKISICKVEDSDQANDKLYKDYNRALREIEXRGAQLOAREK
IQKDPENITFLCALRTFFPNSFFLSGVSLKRVYSKSCYNHHLVDVDTLTV
EHHDIPASPASTPQIIKHKTYLDLDRWQFKSRLLDTDKRSKADTGSNDKASKM
SPSETEIEIKMGFEYSRSPTF"

ORIGIN
Query Match 83.6%; Score 1546; DB 9; Length 2663;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 CTGAGGCGGCGGTGATGATGAGGGGAGAGTACGTCGCGGCTGCTCGGCGTTTGTCT 60
Db 36 CTGAGGCGGCGGTGATGATGAGGGGAGAGTACGTCGCGGCTGCTCGGCGTTTGTCT 95
QY 61 CGGCGCACTCGCTTTCCAGCACTTCCAGCACTCGGAGCACTCGGAGAGTTTCTCTGG 120
Db 96 CGGCGCACTCGCTTTCCAGCACTTCCAGCACTCGGAGCACTCGGAGAGTTTCTCTGG 155
QY 121 GGAAGTAAAGGTGAAGCAAGAAACAGCACTTCTGATTTCCCAATGATGATGATGAT 180
Db 156 GGAAGTAAAGGTGAAGCAAGAAACAGCACTTCTGATTTCCCAATGATGATGATGAT 215
QY 181 TGTATTATCAATTGATGATTTCAAAATATATTCATGCTATCAGCTTTTATGCTTTTAA 240
Db 216 TGTATTATCAATTGATGATTTCAAAATATATTCATGCTATCAGCTTTTATGCTTTTAA 275
QY 241 TTTCTTCAAGCGAATTAATGAGCAAGCACTGAGAAATATTTATCAATGTCAGAAAGAA 300
Db 276 TTTCTTCAAGCGAATTAATGAGCAAGCACTGAGAAATATTTATCAATGTCAGAAAGAA 335
QY 301 TGTGTAGTGTGATCAAAATTCGCTGCTATTCAGATCAATCATGACGTTTAAAGAGAG 360
Db 336 TGTGTAGTGTGATCAAAATTCGCTGCTATTCAGATCAATCATGACGTTTAAAGAGAG 395
QY 361 GGTGCTTCAAAAACCTTGACAGAGCACTTTTCAACCAAGACCTGTTTCTGCTATT 420
Db 396 GGTGCTTCAAAAACCTTGACAGAGCACTTTTCAACCAAGACCTGTTTCTGCTATT 455
QY 421 AACACCAAGTATTAATACAGAAAGCTGCTACTCATGATGACTGAAACATTTCTTATATA 480
Db 456 AACACCAAGTATTAATACAGAAAGCTGCTACTCATGATGACTGAAACATTTCTTATATA 515
QY 481 ACCCTGAAAAGACCTTTTCAAGGAGCTTTAGTGTGCTTCCCAATCTGGACATGCTGA 540
Db 516 ACCCTGAAAAGACCTTTTCAAGGAGCTTTAGTGTGCTTCCCAATCTGGACATGCTGA 575
QY 541 ACAACTGAGTTATTAACCTGATACGTTCTGATGCTCACTGTTTACCGAGCAGT 600
Db 576 ACAACTGAGTTATTAACCTGATACGTTCTGATGCTCACTGTTTACCGAGCAGT 635
QY 601 ACAACCAACAGCTTAATTTTGAAGAAGATGATCCTTAAGAAGATACATAGAT 660
Db 636 ACAACCAACAGCTTAATTTTGAAGAAGATGATCCTTAAGAAGATACATAGAT 695
QY 661 AATGAAATGATGCTTCAATTAACAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720

```

Db      696 AATGAAATGTAAGCTTCATTAACAGAGATTTAAAGATTAATGCAAAAAAGTGGAGA 755
Qy      721 CAGTAAACAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 780
Db      756 CAGTGAACAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 815
Qy      781 GAAAGAGAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 840
Db      816 GAAAGAGAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 875
Qy      841 GGAGAACATTTTCTTTGTCAGGACATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 900
Db      876 GGAGAACATTTTCTTTGTCAGGACATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 935
Qy      901 TTGATGTTATGCTTTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 960
Db      936 TTGATGTTATGCTTTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 995
Qy      961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db      996 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1055
Qy      1021 TAATCAAGCTAGTACACCAATATCTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1080
Db      1056 TAATCAAGCTAGTACACCAATATCTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1115
Qy      1081 GCATTCAGAGATCTCGGTTGTTAGATACACAGACAAACGATCTAAAGCAATCTGAG 1140
Db      1116 GCATTCAGAGATCTCGGTTGTTAGATACACAGACAAACGATCTAAAGCAATCTGAG 1175
Qy      1141 TAGTAGTAACCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200
Db      1176 TAGTAGTAACCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1235
Qy      1201 AAGATGAAGAGGTTTGGTGAATTAATCAAGGCTCTGATCAATTTGATCTTTAACTTA 1260
Db      1236 AAGATGAAGAGGTTTGGTGAATTAATCAAGGCTCTGATCAATTTGATCTTTAACTTA 1295
Qy      1261 CAAAGAGATTTTATTTGGCTGATGGTAAAGCCAAACATTTGATTTTAACTTA 1320
Db      1296 CAAAGAGATTTTATTTGGCTGATGGTAAAGCCAAACATTTGATTTTAACTTA 1355
Qy      1321 GTTAGAGTACTGCAAGTAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1380
Db      1356 GTTAGAGTACTGCAAGTAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1415
Qy      1381 ACAGATTAAGCTTTAGTATTAATCAACAAAGTACTTTTCAACATGATGATGCTTTTA 1440
Db      1416 ACAGATTAAGCTTTAGTATTAATCAACAAAGTACTTTTCAACATGATGATGCTTTTA 1475
Qy      1441 TTTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCT 1500
Db      1476 TTTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCT 1534
Qy      1501 TTTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCT 1560
Db      1535 TTTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCT 1594
Qy      1561 TAGGGAAGACAGTCAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1620
Db      1595 TAGGGAAGACAGTCAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1654
Qy      1621 GATTTGAGACATGCTATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAA 1680
Db      1655 GATTTGAGACATGCTATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAA 1714
Qy      1681 AATATGGAAGAAATTTATATGAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1740
Db      1715 AATATGGAAGAAATTTATATGAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1774
Qy      1741 ACTTTTAAAGATTAATGCTAGATTTGCAAGTAAATGCTGATATCATCAAT 1800

```

```

Db      1775 ACTTTTAAAGATTAATGCTAGATTTGCCAGATTAATAAGCTGATATCATCAAT 1834
Qy      1801 AATTTGCAAAAATCATCT 1820
Db      1835 AATTTGCAAAAATCATCT 1854

RESULT 10
AX880746
LOCUS      AX880746      2719 bp      DNA      linear      PAT 17-DEC-2003
DEFINITION Sequence 15651 from Patent EPI074617.
ACCESSION  AX880746
VERSION     AX880746.1 GI:40035482
KEYWORDS
SOURCE
  Homo sapiens (human)
  Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
  Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
  1 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,T.,
    Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., and Otsuki,T.
    Primers for synthesising full-length cDNA and their use
    Patent: BP 1074617-A 15651 07-FEB-2001;
    Research Association for Biotechnology (JRP)
FEATURES
    source
        1..2719
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="unnamed protein product"
    CDS
        293..1195
            /codon_start=1
            /protein_id="CA891067.1"
            /db_xref="GI:40035483"
            /translation="MPFRRLHKNLOEHFSDNOLVELLTPSIIITSCSTHRLHSL
            YKPOKGFHRLVPLVAVLNGMSQGLGYTVSGS CMSTGFSAVCHSSKFEEDGSLKE
            VHKINEMVSLIOELKSLCKKVEDSEAVKLVMDVRLKREIKREKRN
            IORPOENILCOALRPFPSERFSLCWSLKRRHYSKSCVYNHHLIDVDNLLVY
            EHTIDFPAASPASTQIIKKKALDIDDMQFKRRLDIDOKRSLADGSSNODKASAK
            SSPETDEIEIKMGFGYSRSPY"

ORIGIN
Query Match      80.2%; Score 1483; DB 6; Length 2719;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

297 AGAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 356
246 AGAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
357 AGAGGCTGCTCACAAAACCTTGACAGAGCATTTTTCACCAACCAAGACCTTGTTCCTGC 416
306 AGAGGCTGCTCACAAAACCTTGACAGAGCATTTTTCACCAACCAAGACCTTGTTCCTGC 365
417 TATTAAACCAAGATTAATAACAGAAAGCTGCTACTCATGCACTGGAACATTCCTTAT 476
366 TATTAAACCAAGATTAATAACAGAAAGCTGCTACTCATGCACTGGAACATTCCTTAT 425
477 AATAACCTCAAAAAGGACTTTTTCACAGGGATCTTAAAGTGTGCAATCTGGGCAATGT 536
426 AATAACCTCAAAAAGGACTTTTTCACAGGGATCTTAAAGTGTGCAATCTGGGCAATGT 485
537 CTGAACCACTGGGTTATTAACCTGATACGTTCTGTATGTCATCTGGTTTTCGCGAG 596
486 CTGAACCACTGGGTTATTAACCTGATACGTTCTGTATGTCATCTGGTTTTCGCGAG 545
597 CAGTCAAAACAACAAGCTTAATTTTTCAGAAAGATGATCTCTTAAAGAGGTACATA 656
546 CAGTCAAAACAACAAGCTTAATTTTTCAGAAAGATGATCTCTTAAAGAGGTACATA 605
657 AGATTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 716
606 AGATTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665

```

QY 717 AGACAGTGAACAAGCAGTATGATACTAGTAAGGATGTAAACAGATTAAAAACGAGAA 776
 DB 666 AAGCAGTGAACAAGCAGTATGATACTAGTAAGGATGTAAACAGATTAAAAACGAGAA 725
 QY 777 TTGAGAAAAGAGAGAGAGCAGAGATTGAGCAGCAAGAGAGAAACATCCAAAAGACC 836
 DB 726 TTGAGAAAAGAGAGAGAGCAGAGATTGAGCAGCAAGAGAGAAACATCCAAAAGACC 785
 QY 837 CTGAGAGAAACATTTTCTTTTCTGAGGACTTACGACCTTTTCCAAATTCGATTTTC 896
 DB 786 CTGAGAGAAACATTTTCTTTTCTGAGGACTTACGACCTTTTCCAAATTCGATTTTC 845
 QY 897 TTCAATCATGTGTATGTCTTTTAAAAATGACATGTTTCTAAAAGTAGCTGTAACTACA 956
 DB 846 TTCAATCATGTGTATGTCTTTTAAAAATGACATGTTTCTAAAAGTAGCTGTAACTACA 905
 QY 957 ACCACCATCTCGATGTGTAGTGAACAATCTGACCTTAATGTGAGAAACACATGACATCTCG 1016
 DB 906 ACCACCATCTCGATGTGTAGTGAACAATCTGACCTTAATGTGAGAAACACATGACATCTCG 965
 QY 1017 AAGCTAGTCCAGCTAGTACACCAAAATCATTAAGCACTTAAAGCCTTAACTAGATACA 1076
 DB 966 AAGCTAGTCCAGCTAGTACACCAAAATCATTAAGCACTTAAAGCCTTAACTAGATACA 1025
 QY 1077 GATGCGAATTCAGAGATCTCGGTGTGTATGATACAGAGCAAAAGCATCTTAAAGCAATA 1136
 DB 1026 GATGCGAATTCAGAGATCTCGGTGTGTATGATACAGAGCAAAAGCATCTTAAAGCAATA 1085
 QY 1137 CTGCTAGTATGAAACCAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAA 1196
 DB 1086 CTGCTAGTATGAAACCAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAA 1145
 QY 1197 TTGAAAAGAGAGAGGTTTGTGTGAATATCAAGCTCTCTCAATTTGATCCTTTTAAAC 1256
 DB 1146 TTGAAAAGAGAGAGGTTTGTGTGAATATCAAGCTCTCTCAATTTGATCCTTTTAAAC 1205
 QY 1257 CTTCAGAGAGATTTTATTTTGGCTGATGGGTAAGGCAAAACATTTCTATTTTAA 1316
 DB 1206 CTTCAGAGAGATTTTATTTTGGCTGATGGGTAAGGCAAAACATTTCTATTTTAA 1265
 QY 1317 CTATGTGAGTACTTGCAGTAAGTCAATTTGTTTCTATGTTTCTACCTGTTTGAGTA 1376
 DB 1266 CTATGTGAGTACTTGCAGTAAGTCAATTTGTTTCTATGTTTCTACCTGTTTGAGTA 1325
 QY 1377 ATACAGAGATTAATCTTAGTACTTACTTCAAAATGATCTTTTCAACATCAGATGCT 1436
 DB 1326 ATACAGAGATTAATCTTAGTACTTACTTCAAAATGATCTTTTCAACATCAGATGCT 1385
 QY 1437 TTTATTTCCAAACCTTTTTCACCTTCACTAAAGTTGTGAGGGAAGGCTTACACAGA 1496
 DB 1386 TTTATTTCCAAACCTTTTTCACCTTCACTAAAGTTGTGAGGGAAGGCTTACACAGA 1445
 QY 1497 CACATCTTTTGAATTTGAAAAGTGAAGCAGGCAAGTGGCTCAACCTGTATCCGAG 1556
 DB 1446 CACATCTTTTGAATTTGAAAAGTGAAGCAGGCAAGTGGCTCAACCTGTATCCGAG 1505
 QY 1557 CACTTAAAGAGACAACTCAAGAGATGATTAAGCTTAAAGAGTTAGAGACCAAGCTGGG 1616
 DB 1506 CACTTAAAGAGACAACTCAAGAGATGATTAAGCTTAAAGAGTTAGAGACCAAGCTGGG 1565
 QY 1617 CAAGGTATGAGACCACTGTATTAATAAAATTAATAAGGAAAGAAATAGGCTTATTT 1676
 DB 1566 CAAGGTATGAGACCACTGTATTAATAAAATTAATAAGGAAAGAAATAGGCTTATTT 1625
 QY 1677 TCAAAATATGAGAAAGAAATTTATATGAAAATTTATCTGAGTCACTTAAATTTCTCTTAAG 1736
 DB 1626 TCAAAATATGAGAAAGAAATTTATATGAAAATTTATCTGAGTCACTTAAATTTCTCTTAAG 1685
 QY 1737 TGATACCTTTTAAAGATGATTAAGTGTAGTGTGCAATGATTAAGTGTATCATG 1796
 DB 1686 TGATACCTTTTAAAGATGATTAAGTGTAGTGTGCAATGATTAAGTGTATCATG 1745

QY 1797 CAATTAATTTGCAAAAACATCATCTTAAATTTAA 1830
 DB 1746 CAATTAATTTGCAAAAACATCATCTTAAATTTAA 1779
 RESULT 11
 BD158566
 LOCUS
 DEFINITION
 Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION
 BD158566
 VERSION
 JP 2002191363-A/13409
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2719)
 Ota, T., Isegaki, T., Nishikawa, T., Hayaishi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 Primer for synthesizing full-length cDNA and use thereof
 JOURNAL
 Patent. JP 2002191363-A 13409 09-JUL-2002;
 HELIX RESEARCH INSTITUTE
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002191363-A/13409
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISEGAKI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
 10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 Location/Qualifiers
 (293)..(1192).
 FT CDS
 1..2719
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 80.2%; Score 1483; DB 6; Length 2719;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1533; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 297 AGAATGTGTGATGTTGTGATCAAAATTCGCTCATTCAGATCAGATCATGAGCTTTAGAG 356
 DB 246 AGAATGTGTGATGTTGTGATCAAAATTCGCTCATTCAGATCAGATCATGAGCTTTAGAG 305
 QY 357 AGAGGCTCTTACAAAACCTTGCAAGAGCAATTTTCAACCAAGACCTTGTGTTTCTGCG 416
 DB 306 AGAGGCTCTTACAAAACCTTGCAAGAGCAATTTTCAACCAAGACCTTGTGTTTCTGCG 365
 QY 417 TATTAACACCAAGTATTAACAGAAAGCTGCTACATCATGCACTGGAACATTCCTAT 476
 DB 366 TATTAACACCAAGTATTAACAGAAAGCTGCTACATCATGCACTGGAACATTCCTAT 425
 QY 477 ATTAACCTCAAAAAGAGCTTTTCAAGGATACCTTTTAGTGTGCTTGCATTCGGGCAATG 536
 DB 426 ATTAACCTCAAAAAGAGCTTTTCAAGGATACCTTTTAGTGTGCTTGCATTCGGGCAATG 485
 QY 537 CTGAACCACTGGGTATTAACAGTATGAGTTCCTGATGTCACCTGTTTGAAGCCGAG 596
 DB 486 CTGAACCACTGGGTATTAACAGTATGAGTTCCTGATGTCACCTGTTTGAAGCCGAG 545
 QY 597 CAGTACAAACACACAGCTCTAAATTTTGAAGAGATGATCTCTTAAAGAGGTACATA 656
 DB 546 CAGTACAAACACACAGCTCTAAATTTTGAAGAGATGATCTCTTAAAGAGGTACATA 605
 QY 657 AGATTAAGAAATGATATCTTCATTAAGAGAGGATTAAGAGATATATGCAAAAAGTGG 716


```

Db      606 AGATTAAATTAATGTAATGCTTCAATTCAGAGGAAATTTAAAGCTTTATGCAAAAAAGTGG 665
Qy      717 AAGACGTGACACAGACAGTAGATTAACCTAGTAAGAGTGTAAACAGATTAAACAGAGAA 776
Db      666 AAGACAGTGAACAGACAGTAGATTAACCTAGTAAGAGTGTAAACAGATTAAACAGAGAA 725
Qy      777 TTGAGAAAAGGAGAGAGACAGATTCCAGGAGCAAGAGAGAGAAACATCCAAAAAGACC 836
Db      726 TTGAGAAAAGGAGAGAGACAGATTCCAGGAGCAAGAGAGAGAAACATCCAAAAAGACC 785
Qy      837 CTCAGAGAAACATTTTCTTTCTTGTCCAGGCAATTAACGACCTTTTCCAAATTCGAATTC 896
Db      786 CTCAGAGAAACATTTTCTTTCTTGTCCAGGCAATTAACGACCTTTTCCAAATTCGAATTC 845
Qy      897 TTCATTGATGTGTATGTCTTTAAAAAATAGACATGTTTCTTAAAGTAGCTGTACTACA 956
Db      846 TTCATTGATGTGTATGTCTTTAAAAAATAGACATGTTTCTTAAAGTAGCTGTACTACA 905
Qy      957 ACCACCATCTCATGTAGTAGACAAATCTGACCTTAATGGTAGAGACACATGCTTCCTG 1016
Db      906 ACCACCATCTCATGTAGTAGAGCAATCTGACCTTAATGGTAGAGACACATGCTTCCTG 965
Qy      1017 AAGCTAGTCCAGTGTACTACCAACAAATCATTAAGCATTAAGCCTTAAGACTTAGTACA 1076
Db      966 AAGCTAGTCCAGTGTACTACCAACAAATCATTAAGCATTAAGCCTTAAGACTTAGTACA 1025
Qy      1077 GATGGCAATTCAGAGATCTCGGTTGTAGATACCAAGACAAAGATCTAAAGCAATTA 1136
Db      1026 GATGGCAATTCAGAGATCTCGGTTGTAGATACCAAGACAAAGATCTAAAGCAATTA 1085
Qy      1137 CTGGTAGTAGTAACCAAGATTAAGCATCCAAATAGACGCCAGAAACAGATGAAGAA 1196
Db      1086 CTGGTAGTAGTAACCAAGATTAAGCATCCAAATAGACGCCAGAAACAGATGAAGAA 1145
Qy      1197 TTGAAAAGATGAAGGGTTTGGTGAATATTCACGGCTCTCAATTTTGAATCTTTTAAAC 1256
Db      1146 TTGAAAAGATGAAGGGTTTGGTGAATATTCACGGCTCTCAATTTTGAATCTTTTAAAC 1205
Qy      1257 CTACACAGAGATTTTATTTTGGCTGATGGGTAAAGCCAAACATTTTCTATGTTTAA 1316
Db      1206 CTACACAGAGATTTTATTTTGGCTGATGGGTAAAGCCAAACATTTTCTATGTTTAA 1265
Qy      1317 CTATGTTGAGCTACTTGCAGTAGATTTGTTTCTATATGTTCACTGTTTGACATA 1376
Db      1266 CTATGTTGAGCTACTTGCAGTAGATTTGTTTCTATATGTTCACTGTTTGACATA 1325
Qy      1377 ATACACAGATTAATCTTAGTGCATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCT 1436
Db      1326 ATACACAGATTAATCTTAGTGCATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCT 1385
Qy      1437 TTTATTTCCAAACCTTTTTCACCTTTCACTTAAGTTGTTGAGGGGAAGGCTTAACAGA 1496
Db      1386 TTTATTTCCAAACCTTTTTCACCTTTCACTTAAGTTGTTGAGGGGAAGGCTTAACAGA 1445
Qy      1497 CACATCTTTAGAAATGGAAGATGAGACAGGACAGTGGCTCACACCTGTAATCCAG 1556
Db      1446 CACATCTTTAGAAATGGAAGATGAGACAGGACAGTGGCTCACACCTGTAATCCAG 1505
Qy      1557 CACTTAGGGAAGACAGATCAGAGATGATTAAGCTAGAGATTAGACACAGAGCTGGG 1616
Db      1506 CACTTAGGGAAGACAGATCAGAGATGATTAAGCTAGAGATTAGACACAGAGCTGGG 1565
Qy      1617 CAACGATTTGAGACATGCTATTAATAAATTAATGAAGACAGAAATAGCTTATTT 1676
Db      1566 CAACGATTTGAGACATGCTATTAATAAATTAATGAAGACAGAAATAGCTTATTT 1625
Qy      1677 TCAAAATATGAAAGAAATTTATATGAAATTTATCTGAGCTCATTAATAATCTCTTAAG 1736
Db      1626 TCAAAATATGAAAGAAATTTATATGAAATTTATCTGAGCTCATTAATAATCTCTTAAG 1685
Qy      1737 TGATACCTTTTGAAGTACATATGGCTAGAGTGGCAGATTAATAATGCGATATCAG 1796

```

```

Db      1686 TGATACCTTTTGAAGTACATTAATGCGTAGAGTTGCCAGATAAATGCTGATATCATG 1745
Qy      1797 CAATTAATTTGCACAAACATCATCTCTAAATTTAA 1830
Db      1746 CAATTAATTTGCACAAACATCATCTCTAAATTTAA 1779

RESULT 12
LOCUS AK023676 2719 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ13614 f1s, clone PLACE1010857.
ACCESSION AK023676
VERSION AK023676.1 GI:10435671
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Isegai,T., Ota,T., Hayaashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Ishibashi,T.,
Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoaka,S.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Maehuo,Y. and Kanehori,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2719)
AUTHORS Isegai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isegai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 282-0812, Japan
(B-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
Location/Qualifiers
source
1. 2719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1010857"
/tissue_type="placenta"
/clone_id="PLACE1"
/note="Cloning vector: pME18SFL3"
247248
misc_feature
/note="67 bases segment is present in AK022704."
293..1195
CDS
/notes="named protein product"
/codon_start=1
/protein_id="BAB14635.1"
/db_xref="GI:10435672"
/translation="MTFRERLHKNUOEHSNODLVLLTPSITTESCTHRLHSL
YKPOKGLFHVPLVAVNLGMSDQGYKTVSGSCWSTGFSRAVOTHSKFEEDGSLKE
VHKINEMVATSLQELKSIKCKVESDQAVDKLVQVRLKRIEKRGAQIOAAREKN
IQNDPQENITLCAALRFRPNSFLHSQWLSKNRHSKSCNVNHLIDVDVNTLLVY
EHTDIPASPSASTQILIKHKLALDIDPMQKRSRLDIDPKRSKADIDGSSNOKRASKM
SSPFDIEIKMKQFEYRSPTP"

ORIGIN
Query Match 80.2%; Score 1483; DB 9; Length 2719;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      297 AGAATGTGTGCTGTGGTGAACAAATCCGTCGTCTATTAGATGAGATGAGCGTTTGAAG 356
Db      246 AGAATGTGTGCTGTGGTGAACAAATCCGTCGTCTATTAGATGAGATGAGCGTTTGAAG 305
Qy      357 AGAGGCTGCTTCAACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTTTCTGC 416

```


Db 306 AGAGCTGCTTCAAAAACTTGACAGACATTTTTCACAAACCAAGACCTTGTTTCTGC 365
 QY 417 TATTAACACCAAGTATATATACAGAAAGGCTCTCATGCACTGAAACATTCCTTAT 476
 Db 366 TATTAACACCAAGTATATATACAGAAAGGCTCTCATGCACTGAAACATTCCTTAT 425
 QY 477 ATAAACCTCAAAAAGGACTTTTTCACAGGATCTTTAGTGTGCGAATCTGGGCAATG 536
 Db 426 ATAAACCTCAAAAAGGACTTTTTCACAGGATCTTTAGTGTGCGAATCTGGGCAATG 485
 QY 537 CTGAACAACGCGGTATTAATACTGTATCGGTTCCGTATGCTCACTGTTTACCGAG 596
 Db 486 CTGAACAACGCGGTATTAATACTGTATCGGTTCCGTATGCTCACTGTTTACCGAG 545
 QY 597 CAGTACAAAACACACAGCTCTAAATTTTGAAGAGATGATCTTTAAAGAGTACATA 656
 Db 546 CAGTACAAAACACACAGCTCTAAATTTTGAAGAGATGATCTTTAAAGAGTACATA 605
 QY 657 AGATAAATGAATAGTATGCTTCACTACAGAGAAATTAAGATATGCAAAAAAGTGG 716
 Db 606 AGATAAATGAATAGTATGCTTCACTACAGAGAAATTAAGATATGCAAAAAAGTGG 665
 QY 717 AAGACAGTGAACAGAGATAGATTAACCTAATGAAGATGTAACAGATTAAACGAGAA 776
 Db 666 AAGACAGTGAACAGAGATAGATTAACCTAATGAAGATGTAACAGATTAAACGAGAA 725
 QY 777 TTGAGAAAAGAGAGAGACAGATTCAGGACGACAGAGAGAAAGATCCCAAAAAAGAC 836
 Db 726 TTGAGAAAAGAGAGAGACAGATTCAGGACGACAGAGAGAAAGATCCCAAAAAAGAC 785
 QY 837 CTCAGAGAGACATTTTCTTCTTCTGACGACATTAAGGACCTTTTCCAAATTCGATTTG 896
 Db 786 CTCAGAGAGACATTTTCTTCTTCTGACGACATTAAGGACCTTTTCCAAATTCGATTTG 845
 QY 897 TTCATTCATGTGTATGTCTTTTAAAAATGACATGTTTCTAAAGTACTGTAATACA 956
 Db 846 TTCATTCATGTGTATGTCTTTTAAAAATGACATGTTTCTAAAGTACTGTAATACA 905
 QY 957 ACCACCACTCGATGTAGTGAACAATCTGACCTTAAATGGTGAAGACACATGACATTCCTG 1016
 Db 906 ACCACCACTCGATGTAGTGAACAATCTGACCTTAAATGGTGAAGACACATGACATTCCTG 965
 QY 1017 AAGCTAGTCCAGCTAGTACACCAAAATCACTTAAGCATTAAGCCTTAGACTTATGATGA 1076
 Db 966 AAGCTAGTCCAGCTAGTACACCAAAATCACTTAAGCATTAAGCCTTAGACTTATGATGA 1025
 QY 1077 GATGGCAATTCAGAGATCTCGGTTGTATGATACAAAGCAAAAGCATCTTAAGCAATA 1136
 Db 1026 GATGGCAATTCAGAGATCTCGGTTGTATGATACAAAGCAAAAGCATCTTAAGCAATA 1085
 QY 1137 CTGGTAGTAGTAAACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 1196
 Db 1086 CTGGTAGTAGTAAACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 1145
 QY 1197 TTGAAAAGATGAAGGTTTGGTGAATATCAAGGTCCTTACATTTTATCCTTTTAAAC 1256
 Db 1146 TTGAAAAGATGAAGGTTTGGTGAATATCAAGGTCCTTACATTTTATCCTTTTAAAC 1205
 QY 1257 CTTCAGAGAGATTTTATTTTGGCTGATGGTAAAGCCAAACATTTCTATTTGTTTAA 1316
 Db 1206 CTTCAGAGAGATTTTATTTTGGCTGATGGTAAAGCCAAACATTTCTATTTGTTTAA 1265
 QY 1317 CTATGTTGAGCTACTTGCAAGTAAGTCAATTTGTTTACTATGTTCCGTTTGAAGTA 1376
 Db 1266 CTATGTTGAGCTACTTGCAAGTAAGTCAATTTGTTTACTATGTTCCGTTTGAAGTA 1325
 QY 1377 ATACAGAGATTAAGCTTATGATGATCTTCAACAAAGTATCTTTTCAACATCAAGATGCT 1436
 Db 1326 ATACAGAGATTAAGCTTATGATGATCTTCAACAAAGTATCTTTTCAACATCAAGATGCT 1385
 QY 1437 TTATATTCGAAACCTTTTTCACCTTCACTAAGTGTGGAAGGGAAGGCTTAACAGAGA 1496
 Db 1386 TTATATTCGAAACCTTTTTCACCTTCACTAAGTGTGGAAGGGAAGGCTTAACAGAGA 1445

QY 1497 CACATTTCTTGAATTTGAAAAAGTGAACCAAGCAAGAGCTGCTCACTGTAATCCAG 1556
 Db 1446 CACATTTCTTGAATTTGAAAAAGTGAACCAAGCAAGAGCTGCTCACTGTAATCCAG 1505
 QY 1557 CACTTAGGAAAGCAAGTCAAGAGGATTTGATTTAGCTAGAGTTTGAAGCAAGCTGGG 1616
 Db 1506 CACTTAGGAAAGCAAGTCAAGAGGATTTGATTTAGCTAGAGTTTGAAGCAAGCTGGG 1565
 QY 1617 CAACGATTTGAGACCATGTCTATTTAAAAATTAATGAAGAAACCAAGAAATGACCTTATTT 1676
 Db 1566 CAACGATTTGAGACCATGTCTATTTAAAAATTAATGAAGAAACCAAGAAATGACCTTATTT 1625
 QY 1677 TCATAATATGAAAGAAATTTATATGAAATTTATCTGAGTCACTTAAATTTCTCTTAAG 1736
 Db 1626 TCATAATATGAAAGAAATTTATATGAAATTTATCTGAGTCACTTAAATTTCTCTTAAG 1685
 QY 1737 TGATACCTTTTATGAAAGTATATGCTAGAGTTCAGATTAATGCTGATATCATG 1796
 Db 1686 TGATACCTTTTATGAAAGTATATGCTAGAGTTCAGATTAATGCTGATATCATG 1745
 QY 1797 CAATAAATTTGCAAAAACATCATCTTAAATTTTAA 1830
 Db 1746 CAATAAATTTGCAAAAACATCATCTTAAATTTTAA 1779

RESULT 13

AC096768/c 180430 bp DNA linear PRI 01-MAR-2002

LOCUS AC096768 Homo sapiens BAC clone Rpl1-722p15 from 4, complete sequence.

DEFINITION AC096768 AC025517

AC096768.3 GI:18497264

VERSION HTG.

KEYWORDS Homo sapiens (human)

SOURCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 180430)

AUTHORS Sulston, J.E. and Waterston, R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

99063792

PUBMED 9847074

REFERENCE 2 (bases 1 to 180430)

AUTHORS Cedroni, M. and Hakenson, W.

TITLE The sequence of Homo sapiens BAC clone Rpl1-722p15

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 180430)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

REFERENCE 4 (bases 1 to 180430)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 5 (bases 1 to 180430)

AUTHORS Waterston, R.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Feb 5, 2002 this sequence version replaced gi:16259194.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>
 Contact: sepiens@wustl.wustl.edu
 ----- Summary Statistics
 Center Project name: H_NH0722P15
 Drafting Center: MIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tateo, M., Caranese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is RP11-767N15, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-722P15; actual end is at base position 5795 of RP11-767N15.

Data from AC069056 was used to finish the clone, AC096768. Polymorphisms have been identified between AC069056 and AC096768.

The sequence of AC025517 has been incorporated into AC096768.

FEATURES

source
 1. 180430
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="4"
 /map="4"
 /clone="RP11-722P15"
 /clone_1b="RPCI-11"
 1. 569
 repeat_region
 /rpt_family="ERV1"
 1106..1233
 repeat_region
 /rpt_family="ERV1"
 1234..1577
 repeat_region
 /rpt_family="MAIR"
 3175..3528
 repeat_region
 /rpt_family="MAIR"
 3529..3947
 repeat_region
 /rpt_family="ERV1"
 4059..4395
 repeat_region
 /rpt_family="ERV1"
 4426..4516
 repeat_region
 /rpt_family="ERV1"
 4873..4967
 repeat_region
 /rpt_family="ERV1"
 4968..5375
 repeat_region
 /rpt_family="ERV1"
 5414..5529
 repeat_region

repeat_region
 7106..7251
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 7252..7309
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 7310..7651
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 7657..7872
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 7876..8040
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 8062..8222
 /rpt_family="ERV1"
 /rpt_family="Alu"
 repeat_region
 9347..9389
 /rpt_family="AT_rich"
 /rpt_family="Alu"
 repeat_region
 9447..9747
 /rpt_family="Alu"
 /rpt_family="Alu"
 misc_feature
 9453..9466
 /note="match to EST A1864985 (NID:g5529092) wK06d01.x1"
 9909..10405
 /rpt_family="MAIR"
 /rpt_family="Alu"
 repeat_region
 10510..10812
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 12025..12333
 /rpt_family="L1"
 /rpt_family="L1"
 repeat_region
 12323..12514
 /rpt_family="L1"
 /rpt_family="L1"
 repeat_region
 12515..12544
 /rpt_family="L1"
 /rpt_family="L1"
 repeat_region
 12516..12539
 /rpt_family="L1"
 /rpt_family="L1"
 misc_feature
 12837..12861
 /note="match to EST BG208025 (NID:g13729712)"
 13396..13418
 /rpt_family="L1"
 /rpt_family="L1"
 repeat_region
 13664..14043
 /rpt_family="AT_rich"
 /rpt_family="AT_rich"
 repeat_region
 14068..14380
 /rpt_family="MIR"
 /rpt_family="Alu"
 repeat_region
 14384..14699
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 14675..14699
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 16512..16570
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 21257..21267
 /rpt_family="AT_rich"
 /rpt_family="AT_rich"
 repeat_region
 21448..21480
 /rpt_family="AT_rich"
 /rpt_family="AT_rich"
 repeat_region
 21517..21714
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 22206..22496
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 22366..22370
 /note="match to EST AA283800 (NID:g1928012) z644909.s1"
 22691..22732
 /rpt_family="TG)n"
 /rpt_family="TG)n"
 repeat_region
 22880..23140
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 23121..23148
 /rpt_family="Alu"
 /rpt_family="Alu"
 repeat_region
 23485..23721
 /rpt_family="MIR"
 /rpt_family="MIR"
 repeat_region
 24524
 /note="match to EST A1215621 (NID:g3784662) qh18d07.x1"
 24556..24773
 /note="match to EST AA283800 (NID:g1928012) z644909.s1"
 24585..24773
 /note="match to EST A1215621 (NID:g3784662) qh18d07.x1"
 24585..24773
 /note="match to EST AW084661 (NID:g6039813) xa46a03.x1"
 24657..24773
 /note="similar to Mus musculus EST BF465695

QY	1713	TGAGCTATTAAATTTCTCCCTTAAGTGAATCTTTTATAGAGTACATATAGGCTAGGTTG	1772
Db	79215	TGAGCTATTAAATTTCTCCCTTAAGTGAATCTTTTATAGAGTACATATAGGCTAGGTTG	79155
QY	1773	CCAGATAAATGCTGATATCATGCATATAATTTGGCAAAACATCATCTATAATTTAAA	1830
Db	79155	CCAGATAAATGCTGATATCATGCATATAATTTGGCAAAACATCATCTATAATTTAAA	79098
RESULT 14			
AX881436		1896 bp	DNA
LOCUS			linear
DEFINITION			PAT 17-DEC-2003
AX881436			
SEQUENCE			
AX881436			
GI:40036172			
ORGANISM			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
1			
Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, Y.,			
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.			
Primes for synthesising full-length cDNA and their use			
Patent: EP 1074617-A 1634.07-FEB-2001.			
Research Association for Biotechnology (JP)			
Location/Qualifiers			
1..1896			
/organism="Homo sapiens"			
/mol_type="unassigned DNA"			
/db_xref="taxon:9606"			
790..1512			
/note="unamed protein product"			
/codon_start=			
/protein_id="CAE91279.1"			
/db_xref="GI:40036173"			
/translation="MSBOLGYKTVSGSCWSTGFSRAYQVTHSSKFFEEBDSLEKVEHKIN			
EMVATLOEIKSICKVEDESOAVDKLVQVNLKREIERRGKQIOAERKIOQDP			
QENTFLCOALRTPEPNSPEFLFSCVMSKNHVSSESNVNHHLVDVNLTLVNEHDI			
PEASBPSTPOLIKKHTLIDLDRMQFKSRLLDPQDKSKADTGSNDKSKVSSPET			
DEEIEKKKGQFQEYRSRSPFSS"			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1135; Conservative			
44.1%; Score 815; DB 6; Length 1896;			
99.6%; Pred. No. 0;			
Mismatches 4; Indels 1; Gaps 1;			
QY	501	ACAGGATCCTTTAGTGGTGGCCATCTGGGATGTGGAACATCTGGGTATATAACTG	560
Db	758	ACAGGATCCTTTAGTGGTGGCCATCTGGGATGTGGAACATCTGGGTATATAACTG	817
QY	561	TATCAGGTTCCGTATGTCCACTGGTTTACCCGACGATGCAACACACACGCTCTAAT	620
Db	818	TATCAGGTTCCGTATGTCCACTGGTTTACCCGACGATGCAACACACAGCTCTAAT	877
QY	621	TTTTGAAGAAGATGGATCCTTAAAGAGGATCAATAGATAATAGAAATGATGCTTCAT	680
Db	878	TTTTGAAGAAGATGGATCCTTAAAGAGGATCAATAGATAATAGAAATGATGCTTCAT	937
QY	681	TACAAGAGAAATTAAAGATATATGCAAAAAAGTGGAAACATGTGAACAACAGATAGATA	740
Db	938	TACAAGAGAAATTAAAGATATATGCAAAAAAGTGGAAACATGTGAACAACAGATAGATA	997
QY	741	AACCTAGTAAAGATTAACAGATTAATAACAGAAATGAGAAAAAGAGAGAGACACAGA	800
Db	998	AACCTAGTAAAGATTAACAGATTAATAACAGAAATGAGAAAAAGAGAGAGACACAGA	1057
QY	801	TTACAGCAGCAAGAGAGAAACATCCAAAAAGACCTCAGAGAAACATTTTCTTCTTC	860
Db	1058	TTACAGCAGCAAGAGAGAAACATCCAAAAAGACCTCAGAGAAACATTTTCTTCTTC	1117
QY	861	AGGCAATACAGGACCTTTTTCCAATTCCTGAATTTCTTCATCATGTGTATGCTTTAA	920

```

Db 1118 AGGCATTAACGACCTTTTTCCTCAATTCCTGATTTCTTCACTCATGTGTTACTTTA 1177
QY 921 AAAATGACATGTTTCTTAAAGTAGCTGTACTACCAACCACTCGATGTAGTAGACA 980
Db 1178 AAAATGACATGTTTCTTAAAGTAGCTGTACTACCAACCACTCGATGTAGTAGACA 1237
QY 981 ATGTGACCTTAATGTAGAACACACATGACATTCCTGAGTGTCCAGCTAGTACACAC 1040
Db 1238 ATGTGACCTTAATGTAGAACACACATGACATTCCTGAGTGTCCAGCTAGTACACAC 1297
QY 1041 AAATCATTAAGCAATTAAGCTTGAAGTATGACAGATGGCAATTCAGAGATCTCGGT 1100
Db 1298 AAATCATTAAGCAATTAAGCTTGAAGTATGACAGATGGCAATTCAGAGATCTCGGT 1357
QY 1101 TGTTAGATACACAGACCAACGATCTTAAGCAATTCGTGTGTAGTACCAAGATAAG 1160
Db 1358 TGTTAGATACACAGACCAACGATCTTAAGCAATTCGTGTGTAGTACCAAGATAAG 1417
QY 1161 CATCCAAATAGACAGCCCAAGAACAGATGAGAAATGAAAAGATGAGAGGTTTGTG 1220
Db 1418 CATCCAAATAGACAGCCCAAGAACAGATGAGAAATGAAAAGATGAGAGGTTTGTG 1477
QY 1221 AATATTCACGCTCTCTCACTTTGATTCCTTTTAACTTACCAAGAGATTTTATTTG 1280
Db 1478 AATATTCACGCTCTCTCACTTTGATTCCTTTTAACTTACCAAGAGATTTTATTTG 1537
QY 1281 GCTGATGAGTAAAGCCAAATCTTATGTTTCTTATGTTGAGTACTTGCAGTAG 1340
Db 1538 GCTGATGAGTAAAGCCAAATCTTATGTTTCTTATGTTGAGTACTTGCAGTAG 1597
QY 1341 TTCATTTGTTTACTATGTTTCACTGTTTGCAGTAAACACAGATTAATCTTATGTCAT 1400
Db 1598 TTCATTTGTTTACTATGTTTCACTGTTTGCAGTAAACACAGATTAATCTTATGTCAT 1657
QY 1401 TTAATTCACAAAGTACTTTTCAACATGATGATGCTTTATTCCTTCAACCTTTTTCAC 1460
Db 1658 TTAATTCACAAAGTACTTTTCAACATGATGATGCTTTATTCCTTCAACCTTTTTCAC 1717
QY 1461 CTTCCTAATGTTGTTGAGGGGAGGCTTACACAGACATCTTTTGAATGGAAAGT 1520
Db 1718 CTTCCTAATGTTGTTGAGGGGAGGCTTACACAGACATCTTTTGAATGGAAAGT 1776
QY 1521 GAAACAGACAGCTGCTCACAACCTGTATCCACACCTTGGGAGGAGCAAGTCAAGAG 1580
Db 1777 GAAACAGACAGCTGCTCACAACCTGTATCCACACCTTGGGAGGAGCAAGTCAAGAG 1836
QY 1581 GATTGATTGAAGCTAGAGTTAGACACAGCTGAGGCAACGATTTGAGACCAATGCTATT 1640
Db 1837 GATTGATTGAAGCTAGAGTTAGACACAGCTGAGGCAACGATTTGAGACCAATGCTATT 1896

```

```

RESULT 15
BD159031 1896 bp DNA linear PAT 17-JAN-2003
LOCUS BD159031
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD159031
VERSION BD159031.1 GI:27864789
KEYWORDS JP 2002191363-A/13874.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1896)
Oca.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto.J.,
Ishii.S., Sugiyama.T., Makatsus.A., Nagai.K. and Otsuki.T.,
Patent: JP 2002191363-A 13874 09-JUL-2002;
HEPIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/13874
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
COMMENT
AUTHORS
JOURNAL
TITLE

```

```

PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUO OHSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (790)..(1509).
FEATURES
source
1..1896
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 44.1%; Score 815; DB 6; Length 1896;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1135; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 501 ACAGGGTACCTTATGTTGGTGGCCAACTGGGCAATGCTGAAACAACCTGGTTATTAACCTG 560
Db 758 ACAGGGTACCTTATGTTGGTGGCCAACTGGGCAATGCTGAAACAACCTGGTTATTAACCTG 817
QY 561 TATCAGGTTCTGTATGTCACCTGTTTAAAGCCAGAGATACCAACACAGCTCTAAT 620
Db 818 TATCAGGTTCTGTATGTCACCTGTTTAAAGCCAGAGATACCAACACAGCTCTAAT 877
QY 621 TTTTGAAGAAGATGATCCCTTAAAGAGTACCTAATGAATGAATGAATGATGCTCAT 680
Db 878 TTTTGAAGAAGATGATCCCTTAAAGAGTACCTAATGAATGAATGAATGATGCTCAT 937
QY 681 TACAAGAGAAATTAAGAGTATATGCAAAAAGTGAAGACAGTGAACAAAGCAGTAGATA 740
Db 938 TACAAGAGAAATTAAGAGTATATGCAAAAAGTGAAGACAGTGAACAAAGCAGTAGATA 997
QY 741 AACTAGTAAAGATGTAAACAGATTAACAGAAATTTGAGAAAGAGAGAGACAGAGA 800
Db 998 AACTAGTAAAGATGTAAACAGATTAACAGAAATTTGAGAAAGAGAGAGACAGAGA 1057
QY 801 TTCAGGACAGAGAGAGAGAAATCCAAAGAGCCCTCAGAGAGACATTTTCTTGTG 860
Db 1058 TTCAGGACAGAGAGAGAGAAATCCAAAGAGCCCTCAGAGAGACATTTTCTTGTG 1117
QY 861 AGGCATTACGACCTTTTTCCTCAATTTCTGATTTCTTCACTTCACTGTGTATGCTTTAA 920
Db 1118 AGGCATTACGACCTTTTTCCTCAATTTCTGATTTCTTCACTTCACTGTGTATGCTTTAA 1177
QY 921 AAAATGACATGTTTCTTAAAGTAGCTGTACTACCAACCACTCGATGTAGTAGACA 980
Db 1178 AAAATGACATGTTTCTTAAAGTAGCTGTACTACCAACCACTCGATGTAGTAGACA 1237
QY 981 ATGTGACCTTAATGTAGAACACACATGACATTCCTGAGTGTCCAGCTAGTACACAC 1040
Db 1238 ATGTGACCTTAATGTAGAACACACATGACATTCCTGAGTGTCCAGCTAGTACACAC 1297
QY 1041 AAATCATTAAGCAATTAAGCTTGAAGTATGACAGATGGCAATTCAGAGATCTCGGT 1100
Db 1298 AAATCATTAAGCAATTAAGCTTGAAGTATGACAGATGGCAATTCAGAGATCTCGGT 1357
QY 1101 TGTTAGATACACAGACCAACGATCTTAAGCAATTCGTGTGTAGTACCAAGATAAG 1160
Db 1358 TGTTAGATACACAGACCAACGATCTTAAGCAATTCGTGTGTAGTACCAAGATAAG 1417
QY 1161 CATCCAAATAGACAGCCCAAGAACAGATGAGAAATGAAAAGATGAGAGGTTTGTG 1220
Db 1418 CATCCAAATAGACAGCCCAAGAACAGATGAGAAATGAAAAGATGAGAGGTTTGTG 1477
QY 1221 AATATTCACGCTCTCTCACTTTGATTCCTTTTAACTTACCTTACAGAGATTTTATTTG 1280
Db 1478 AATATTCACGCTCTCTCACTTTGATTCCTTTTAACTTACCTTACAGAGATTTTATTTG 1537

```

QY 1281 GCTGATGGGTAAAGCCAAACATTCTATTGTTTTTACTATGTTAGCTTACCTGCACTAG 1340
DB 1538 GCTGATGGGTAAAGCCAAACATTCTATTGTTTTTACTATGTTAGCTTACCTGCACTAG 1597
QY 1341 TTGATTGTTTTTACTATGTTACCTGTTGCACTATACAGAGATTAATCTTAAGCAT 1400
DB 1598 TTGATTGTTTTTACTATGTTACCTGTTGCACTATACAGAGATTAATCTTAAGCAT 1657
QY 1401 TTACTTCACAAAGTACTTTTTCACAAATCATGATGCTTTTATTTCCAAACCTTTTTCAC 1460
DB 1658 TTACTTCACAAAGTACTTTTTCACAAATCATGATGCTTTTATTTCCAAACCTTTTTCAC 1717
QY 1461 CTTTCACTAAGTTGTTGAGGGGAAGCTTACACAGACATCTTTAGAAATGAAAAGT 1520
DB 1718 CTTTCACTAAGTTGTTGAGGGGAAGCTTACACACATCTTTAGAAATGAAAAGT 1776
QY 1521 GAGACGAGCAGAGTGGCTCACACCTGTATCCACACCTTAGGGAAGCAAGTCAGAG 1580
DB 1777 GAGACGAGCAGAGTGGCTCACACCTGTATCCACACCTTAGGGAAGCAAGTCAGAG 1836
QY 1581 GATTGATTGAAGTGAAGTTAGAGACCAAGCTGGGCAAGCTTAGAACCAATGCTATT 1640
DB 1837 GATTGATTGAAGTGAAGTTAGAGACCAAGCTGGGCAAGCTTAGAACCAATGCTATT 1896

RESULT 16

AK021582 1896 bp mRNA linear PRI 01-AUG-2002
LOCUS AK021582
DEFINITION Homo sapiens cDNA FLJ11520 fls, clone HEMBA1002381.
ACCESSION AK021582.1 GI:10432790
VERSION AK021582.1
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 Isegai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagaatsuma, M., Hosokita, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ichida, S., Murakawa, K., Ono, Y., Takiguchi, S., Matenabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Kakumatsu, A., Nakamura, Y., Negahara, K., Masuno, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1896)
AUTHORS Isegai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isegai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan (E-mail: genome@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

source 1. 1896
location/Qualifiers
organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
clone="HEMBA1002381"
cissue_type="whole embryo, mainly head"
clone_lib="HEMBA1"
dev_stage="embryo, 10 weeks"
note="cloning vector: pME18SFL3"

ORIGIN

Query Match 44.1%; Score 815; DB 9; Length 1896;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1135; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 501 ACAGGTAACCTTTAGTGTGTTGCTCAATCTGGGCAATGCTGAAACAAGGGTTATTAACAG 560
DB 758 ACAGGTAACCTTTAGTGTGTTGCTCAATCTGGGCAATGCTGAAACAAGGGTTATTAACAG 817
QY 561 TATCAGGTTCTGTATGTCATGCTGTTTAAAGGAGTAAATGAAATGAAATGAAATGAAATG 620
DB 818 TATCAGGTTCTGTATGTCATGCTGTTTAAAGGAGTAAATGAAATGAAATGAAATGAAATG 877
QY 621 TTTTGAAGAGATGATCCTTTAAAGAGTAAATGAAATGAAATGAAATGAAATGAAATGAAATG 680
DB 878 TTTTGAAGAGATGATCCTTTAAAGAGTAAATGAAATGAAATGAAATGAAATGAAATGAAATG 937
QY 681 TACAAGAGAAATTTAAAGATATATGCAAAAAGTGAAGACAGTGAACAAGCATAGATA 740
DB 938 TACAAGAGAAATTTAAAGATATATGCAAAAAGTGAAGACAGTGAACAAGCATAGATA 997
QY 741 AACTAGTAAAGATGTAAACAGATTTAAACGAGAAATTTGAAAAAGAGAGAGACAGAGA 800
DB 998 AACTAGTAAAGATGTAAACAGATTTAAACGAGAAATTTGAAAAAGAGAGAGACAGAGA 1057
QY 801 TTCAAGGACAG 860
DB 1058 TTCAAGGACAG 1117
QY 861 AGGCAATTAAGGACCTTTTTCACAAATTTCTGAATTTCTTCAATCATGTTATGCTTTAA 920
DB 1118 AGGCAATTAAGGACCTTTTTCACAAATTTCTGAATTTCTTCAATCATGTTATGCTTTAA 1177
QY 921 AAAATAGACATGTTTCTTAAAGTACGTGTATCTAACAACACATCTGATGATAGACA 980
DB 1178 AAAATAGACATGTTTCTTAAAGTACGTGTATCTAACAACACATCTGATGATAGACA 1237
QY 981 ATCTGACCTTAAAGTATGAACACACATGACATTTCTGAAAGTATGTCAGCTATGTCACAC 1040
DB 1238 ATCTGACCTTAAAGTATGAACACACATGACATTTCTGAAAGTATGTCAGCTATGTCACAC 1297
QY 1041 AAATATTAACCATTAACCTTGAATGATGACATGATGACATGATGATGATGATGATGATGATG 1100
DB 1298 AAATATTAACCATTAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1357
QY 1101 TGTATGATAC 1160
DB 1358 TGTATGATAC 1417
QY 1161 CATCCAAATGAGCAGCCACAGAAACAGTGAAGAAATGAAAGATGAAGGTTTGGTG 1220
DB 1418 CATCCAAATGAGCAGCCACAGAAACAGTGAAGAAATGAAAGATGAAGGTTTGGTG 1477
QY 1221 AATATTCACGGTCTCTCAATTTGATCTTTTAACTTAACTTAACTTAACTTAACTTAACTT 1280
DB 1478 AATATTCACGGTCTCTCAATTTGATCTTTTAACTTAACTTAACTTAACTTAACTTAACTT 1537
QY 1281 GCTGATGGGTAAAGCCAAACATTCTATTGTTTTTACTATGTTAGCTTACCTGCACTAG 1340
DB 1538 GCTGATGGGTAAAGCCAAACATTCTATTGTTTTTACTATGTTAGCTTACCTGCACTAG 1597
QY 1341 TTGATTGTTTTTACTATGTTACCTGTTGCACTATACAGAGATTAATCTTAAGCAT 1400
DB 1598 TTGATTGTTTTTACTATGTTACCTGTTGCACTATACAGAGATTAATCTTAAGCAT 1657
QY 1401 TTACTTCACAAAGTACTTTTTCACAAATCATGATGCTTTTATTTCCAAACCTTTTTCAC 1460
DB 1658 TTACTTCACAAAGTACTTTTTCACAAATCATGATGCTTTTATTTCCAAACCTTTTTCAC 1717
QY 1461 CTTTCACTAAGTTGTTGAGGGGAAGCTTACACAGACATCTTTAGAAATGAAAAGT 1520
DB 1718 CTTTCACTAAGTTGTTGAGGGGAAGCTTACACACATCTTTAGAAATGAAAAGT 1776
QY 1521 GAGACGAGCAGAGTGGCTCACACCTGTATCCACACCTTAGGGAAGCAAGTCAGAG 1580

Db	1777	AAAGCACAAGGACAGTGGGCTCCACCTGTAAATCCAGCACTTAAGGAAGCAAGTCAGGAG	183
Qy	1581	GATTGATTGAAGACTTGAAGATTAGAACACGCTTGGGCAACGTAATTGAAGCATTGTATT	1640
Db	1837	GATTGATTGAAGCTTGAAGATTAGAACACGCTTGGGCAACGTAATTGAAGCATTGTATT	1896
RESULT 17			
LOCUS	AX867484	736 bp	DNA
DEFINITION	Sequence 2389 from Patent EP1074617.		linear
ACCESSION	AX867484		
VERSION	AX867484.1	GI:40022347	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Makematsu,A., Nagai,K. and Otsuki,T.		
JOURNAL	Primers for synthesising full-length cDNA and their use		
FEATURES	Patent: EP 1074617-A 2389 07-FEB-2001; Research Association for Biotechnology (JP)		
source	Location/Qualifiers		
	1..736		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match	29.7%; Score 549; DB 6; Length 736;		
Best Local Similarity	99.7%; Pred. No. 8.1e-288;		
Matches	649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	1	CTGAGGCGGCGGTAGCAGTGAAGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCGTTTGCT	60
Db	36	CTGAGGCGGCGGTAGCAGTGAAGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCGTTTGCT	95
Qy	61	CGGCGCAGCTCGCTTTCGAGCAGCTCAACAGGAGCTCGGACAGGAGTTTCTTCTTG	120
Db	96	CGGCGCAGCTCGCTTTCGAGCAGCTCAACAGGAGCTCGGACAGGAGTTTCTTCTTG	155
Qy	121	GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTTCCAAATGGATGATTTGAAGT	180
Db	156	GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTTCCAAATGGATGATTTGAAGT	215
Qy	151	TGTTATACAAATGGACATTCAGAAATATTCAGATCACTGAGCTTTAGCTTTATTA	240
Db	216	TGTTATACAAATGGACATTCAGAAATATTCAGATCACTGAGCTTTAGCTTTATTA	275
Qy	241	TTCTTCAGGCGAAGTAATAGCAAGCACTGGAAGAAATATTATCAATGTCAAAAGAA	300
Db	276	TTCTTCAGGCGAAGTAATAGCAAGCACTGGAAGAAATATTATCAATGTCAAAAGAA	335
Qy	301	TGTGTAAGTTGGTACAAATTCCTGCTGATTCAGATCAATCAATGACGTTTGAAGAG	360
Db	336	TGTGTAAGTTGGTACAAATTCCTGCTGATTCAGATCAATCAATGACGTTTGAAGAG	395
Qy	361	GCTGCTTCAAAAACCTTGACAGAGCATTTTCAACCAAGACCTGTTTCTGTAT	420
Db	396	GCTGCTTCAAAAACCTTGACAGAGCATTTTCAACCAAGACCTGTTTCTGTAT	455
Qy	421	AACACCAAGTATATACAGAAAGCTGCTTACTCATGACATGGAACATTCCTTATATA	480
Db	456	AACACCAAGTATATATACAGAAAGCTGCTTACTCATGACATGGAACATTCCTTATATA	515
Qy	481	ACCTCAAAAAGACTTTTCAAGGAGTACTTAAGGTGTCGCAATCTGGAGATGCTGA	540
Db	516	ACCTCAAAAAGACTTTTCAAGGAGTACTTAAGGTGTCGCAATCTGGAGATGCTGA	575
Qy	541	ACAACCTGGTTATAAACTGTATCAGGTTCTGTATGTCACATGCTTTTGAACCAAGT	600

Db	576	ACAACTGGGTTATAAAACTGATATACAGTTCCTGTATGTCCACTGTGTTTAGCCGACAGT	635
Qy	601	ACAAACACACACGCTCTAAATTTTGAAGAAGATGATCCTTTAAGAAGAGT	651
Db	636	ACAAACACACACGCTCTAAATTTTGAAGAAGATGATCCTTTAAGAAGAGT	686
RESULT 18			
LOCUS	BD147546	736 bp	DNA linear PAT 17-JAN-2001
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD147546		
VERSION	BD147546.1	GI:27853304	
KEYWORDS	JP 2002191363-A/2389.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Cota,T., Ieogaki,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakematsu,A., Nagai,K. and Otsuki,T.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 2389 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/2389 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA,TAKAO ISOGAI,TEISUO NISHIKAWA,KOJI HAYASHI,KAORU PI SAITO, PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKEMATSU PI KEIICHI NAGAI,TEISUJI OTSUKI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10',C12P21/02,C12O1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key		
FEATURES	Location/Qualifiers		
source	FT source 1..736 /organism='Homo sapiens (human)'. 1..736 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'		
ORIGIN	Query Match 29.7%; Score 549; DB 6; Length 736; Best Local Similarity 99.7%; Pred. No. 8.1e-289; Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0		
Qy	1	CTGAGCGCGCGGTAGCATGAGGGGGAAGTACGTGGCGGTGCTCTCGGCGCTTTGTGT	60
Db	36	CTGAGCGCGCGGTAGCATGAGGGGGAAGTACGTGGCGGTGCTCTCGGCGCTTTGTGT	95
Qy	61	CGGCGCATCTCGCTTTCGACACCTCAACACGCACTCGACACGGAAGTTTCTTCTTG	120
Db	96	CGGCGCATCTCGCTTTCGACACCTCAACACGCACTCGACACGGAAGTTTCTTCTTG	155
Qy	121	GGAAGTAAAGGTGAAGCCAAAGACAGCATTACTGATTTCCAAATGATGATGTTGAAGT	180
Db	156	GGAAGTAAAGGTGAAGCCAAAGACAGCATTACTGATTTCCAAATGATGATGTTGAAGT	215
Qy	181	TGTTATATCAATGTGATTCAGAAATATATTCATGCTATGAGCTTTTAAAGCTTTATA	240
Db	216	TGTTATATCAATGTGATTCAGAAATATATTCATGCTATGAGCTTTTAAAGCTTTATA	275
Qy	241	TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAATGTCAAAAAGAA	300
Db	276	TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAATGTCAAAAAGAA	335
Qy	301	TGTGTAGGTGTGTCAAATTCCTGTCATTCAGATAGATCATGACGTTTAGAGAGAG	360

QY	417	TATTAACCAAGTCTAATAACAGAAAGCTGCTTACTCATCGACGGAACATCTCTAT	476
Db	366	TATTAACCAAGTCTAATAACAGAAAGCTGCTTACTCATCGACGGAACATCTCTAT	425
QY	477	ATPAACCTCAAAAAGACTTTTTCACAGGTAACCTTAGAGTTCGCAATCTGGGCACTG	536
Db	426	ATPAACCTCAAAAAGACTTTTTCACAGGTAACCTTAGAGTTCGCAATCTGGGCACTG	485
QY	537	CTGAACAACTGGGCTATATAAAGTGTATAGGTTCTGTATGTCACACTGGTTTATGGCCAG	596
Db	486	CTGAACAACTGGGCTATATAAAGTGTATAGGTTCTGTATGTCACACTGGTTTATGGCCAG	545
QY	597	CAGTACAAACACACAGCTCTAAATTTTGTGAAGAAGATGATCCTTAAAGAGAGTACATA	656
Db	546	CAGTACAAACACACAGCTCTAAATTTTGTGAAGAAGATGATCCTTAAAGAGAGTACATA	605
QY	657	AGATA 661	
Db	606	AGATA 610	

RESULT 23				
BD150128	BD150128	666 bp	DNA	linear PAT 17-JAN-2003
LOCUS				
DEFINITION	Primer for synthesizing			
ACCESSION	BD150128			
VERSION	BD150128.1	GI:27855886		
KEYWORDS	JP 2002191363-A/4971.			
SOURCE	Homo sapiens (human)			

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
1 (bases 1 to 668)					
Ots, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,					
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, Y. and Ohteki, T.					
Primer for synthesizing full-length cDNA and use thereof.					
Patent: JP 2002191363-A 4971 09-JUL-2002;					
HELIX RESEARCH INSTITUTE					
OS Homo sapiens (human)					
PN JP 2002191363-A/4971					

	PD	09-JUL-2002	
	PF	28-JUL-2000 JP 2000280990	
	PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU	
	PI	SAITO,	
	PI	MUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,	
	PI	KEIICHI NAGAI, TETSUJI OTSUKI	
	PC	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC	
	10,		
	PC	C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N5/00, C12N5/00 CC	
	Primer	for synthesizing full-length cDNA and use thereof FH	Key
FEATURES			
SOURCE	FT	source	
		1..668	
		/organism='Homo sapiens (human)'	
		Location/Qualifiers	
		1..668	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
ORIGIN			

Query Match	17.0%	Score 314	DB 6	Length 668
Beet Local Similarity	99.7%	Pred. No. 1,3e-159		
Matches 364	Conservative	0	Mismatches 1	Indels 0
				Gaps 0
QY	297	AGATGTGTGATGTTGGTCAAAATTCGTCGTCATTGACATGACATGACGTTTAGAG	356	
DB	246	AGAAATGTGTGATGTTGGTCAAAATTCGTCGTCATTGACATGACATGACGTTTAGAG	305	
QY	357	AGAGGCTGCTTACAAAAAATTGACAGAGACATTTTCAAAACCAAGACTTTGTTTTCTGC	416	
DB	306	AGAGGCTGCTTACAAAAAATTGACAGAGACATTTTCAAAACCAAGACTTTGTTTTCTGC	365	

QY	417	TATTAACACCAAGTATTAATAACAAGAAAGCTGCTTACTCATCGACTGGAACTTCTTAT	476
Db	366	TATTAACACCAAGTATTAATAACAGAAAGCTGCTTACTCATCGACTGGAACTTCTTAT	425
QY	477	ATAAACCTCAAAAAGACCTTTTTCACAGGGTACCTTTAGTGTGTTGCCAATCTGGGCATGT	536
Db	426	ATAAACCTCAAAAAGACCTTTTTCACAGGGTACCTTTAGTGTGTTGCCAATCTGGGCATGT	485
QY	537	CTGAACAACCTGGGTATTATPAAACGTATACAGGTTCCGTATGTCCACTGGTATTAGCCGAG	596
Db	486	CTGAACAACCTGGGTATTATPAAACGTATACAGGTTCCGTATGTCCACTGGTATTAGCCGAG	545
QY	597	CAGTACAAACACACAGCTCTMAATTTTTTTGAAAGAGATGATCCTTTAAAGAGGTACATA	656
Db	546	CAGTACAAACACACAGCTCTMAATTTTTTTGAAAGAGATGATCCTTTAAAGAGGTACATA	605
QY	657	AGATA 661	
Db	606	AGATA 610	

RESULT 24	AX870976/c	645 bp	DNA	linear	PAT 17-DEC-2003
LOCUS	AX870976				
DEFINITION	Sequence 5881 from Patent EP1074617.				
ACCESSION	AX870976				
VERSION	AX870976.1	GI:40025822			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

ORGANISM Homo sapiens; Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Carnivora; Homnidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuuki,T.

TITLE Primers for synthesising full-length cDNA and their use

JOURNAL Patent: JP 1074617-A 1998-07-28-1998-07-28

FEATURES Research Association for Biotechnology (JBP)

source Location/Qualifiers

1. 645

Query Match	Best Local Similarity	Score	DB	Length
Matches 335;	Conservative	0	Mismatches 0;	Indels 1; Gaps 1.
14.9%;		275;	DB 6;	Length 645;
99.7%;		Pred. No. 2.6e-138;		

ORIGIN	/organism="Homo sapiens"	/mol_type="unassigned DNA"	/db_xref="taxon:9606"
QY	1245	GAATCTTTAACTTACCAAGAGATTTT	1304
DB	395	GATCTTTTAACTTACCAAGAGATTTT	336
QY	1305	CTATTGTTTTACTATGTTAGCTTAC	1366
DB	335	CTATTGTTTTACTATGTTAGCTTAC	276
QY	1365	CTGTTGAGTAAACAGAGATTAAGCAT	142
DB	275	CTGTTGAGTAAACAGAGATTAAGCAT	216

Qy	1425	ACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGAA	148
Db	215	ACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGAA	156
Qy	1485	GGCTTACAGACACATCTTTAGATTGGAAGTGAACGAGGCACAGTGGCTCAC	154
Db	155	GGCTTACACA-AACATCTTTTGAATTGAAAAGTGAAACAGGCACAGTGGCTCAC	97
Qy	1545	CTGTATCCAGACCTTAGGAAAGCAAGTCAGAGATTTGAAAGCTAAGAGTTTGA	160
Db	96	CTGTATCCAGACCTTAGGAAAGCAAGTCAGAGATTTGAAAGCTAAGAGTTTGA	37

QY 1605 GACCAAGCTGGGCAAGCTATTGAGACCATGCTATT 1640
 DB 36 GACCAAGCTGGGCAAGCTATTGAGACCATGCTATT 1

RESULT 25
 LOCUS BD151038 645 bp DNA linear PAT 17-JUN-2003
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD151038
 VERSION BD151038.1 GI:27856796
 KEYWORDS JP 2002191363-A/5881.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 645)
 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., and Otsuki, T.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002191363-A 5881 09-JUL-2002;
 HELIX RESEARCH INSTITUTE

COMMENT
 OS Homo sapiens (human)
 PN JP 2002191363-A/5881
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 200280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SATO,
 PI JUNICHI YAMAMOTO, SHIZUO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUO OTSUKI

PC
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
 10,
 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key

FT source 1. .645
 Location/Qualifiers
 /organism="Homo sapiens (human)"
 1. .645
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Query Match 14.9%; Score 275; DB 6; Length 645;
 Best Local Similarity 99.7%; Pred. No. 2.6e-138;
 Matches 395; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1245 GATCCTTTTAACTTACAGAGAGATTTTATTTGGCTGATGGTAAAGCCAAACTTT 1304
 DB 395 GATCCTTTTAACTTACAGAGAGATTTTATTTGGCTGATGGTAAAGCCAAACTTT 336

QY 1305 CTATTTGTTTAACTTATGAGTACTTGGAGTAACTTATTTGTTTACTTATGTTTAC 1364
 DB 335 CTATTTGTTTAACTTATGAGTACTTGGAGTAACTTATTTGTTTACTTATGTTTAC 276

QY 1365 CTGTTTGAGTAACTTACAGATTAAGTCTTGTGATTTTACTTACAAAGTACTTTTCA 1424
 DB 275 CTGTTTGAGTAACTTACAGATTAAGTCTTGTGATTTTACTTACAAAGTACTTTTCA 216

QY 1425 ACATCAGATGCTTTTATTTCAAAAGCTTTTTCACCTTCACTAAGTTGTTAGGGGAA 1484
 DB 215 ACATCAGATGCTTTTATTTCAAAAGCTTTTTCACCTTCACTAAGTTGTTAGGGGAA 156

QY 1485 GGCTTACAGACAGACATTTCTTTGAAATGGAAAAGTGAACCCAGGACAGTGGCTTACAC 1544
 DB 155 GGCTTACAGACAGACATTTCTTTGAAATGGAAAAGTGAACCCAGGACAGTGGCTTACAC 97

QY 1545 CTGTAAATCCAGACCTTAGGGAAGACAGAGTCAAGAGATTGATTGAAGCTAAGAGTTAA 1604
 DB 96 CTGTAAATCCAGACCTTAGGGAAGACAGAGTCAAGAGATTGATTGAAGCTAAGAGTTAA 37

QY 1605 GACCAAGCTGGGCAAGCTATTGAGACCATGCTATT 1640
 DB 36 GACCAAGCTGGGCAAGCTATTGAGACCATGCTATT 1

RESULT 26
 LOCUS BC016905 1744 bp mRNA linear PRI 16-SEP-2003
 DEFINITION Homo sapiens hypothetical protein FLJ13614, mRNA (cDNA clone IMAGE:439205?), complete cds.
 ACCESSION BC016905
 VERSION BC016905.1 GI:16877293
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1744)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stopleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., Moewen, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Baulfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marz, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL MEDLINE
 22388257
 12477932
 2 (bases 1 to 1744)
 Strausberg, R.
 Direct Submission
 Submitted (05-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mdgapx1.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

REMARK
 Comment: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILMIL at: <http://image.llnl.gov>
 Series: IRAX Plate: 27 Row: B Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 20589960
 This clone has the following problem: The cds is short compared to
 the longest cds in the locus.

FEATURES
 source 1. .1744
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="IMAGE:4392057"
/issue_type="Breast, mammary adenocarcinoma."
/clone_id="N1H_MGC_87"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE6"
1. 1744
/gene="FLJ13614"
/note="synonyms: FLJ11520, FLJ12642"
/db_xref="LocusID:84142"
172. 393
/codon_start=1
/product="FLJ13614 protein"
/locus="AAH16905.1"
/db_xref="GI:16877294"
/db_xref="LocusID:84142"
/translation="MESHAYATGTVKMHDIQPLPVEKRFSCILGRSSMDYHHTQ
PCPAPFCIFSRDGVSPCPMGMSRTDPLK"

ORIGIN

Query Match 9.3%; Score 172; DB 9; Length 1744;
Best Local Similarity 100.0%; Pred. No. 4,3e-82;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GGGAGAGTACGTCGGCGGTGCTCTCGGCGCTTTGCTCGCGCACTGCTTCCAGCAC 83
DB 1 GGGAGAGTACGTCGGCGGTGCTCTCGGCGCTTTGCTCGCGCACTGCTTCCAGCAC 60
QY 84 TCACAGAGGACTCGGACACGGAAGGCTTTCTCTGCGGGAAGTAAAGGTGAAGCCAGA 143
DB 61 TCACAGAGGACTCGGACACGGAAGGCTTTCTCTGCGGGAAGTAAAGGTGAAGCCAGA 120
QY 144 ACAGCATTACTGATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 195
DB 121 ACAGCATTACTGATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 172

RESULT 27
AX071613 403 bp DNA linear PAT 25-JAN-2001
LOCUS Sequence 2085 from Patent WO01025568.
DEFINITION AX071613
ACCESSION AX071613
VERSION 1
KEYWORDS GI:12581964
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lansom, G., Drmanac, R., Crenkajko, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
Human genes and gene expression products
Patent: WO 0102568-A 2085 11-JAN-2001;
JOURNAL CHIRON CORPORATION (US); HYSEQ, INC. (US)

TITLE
JOURNAL
AUTHORS

FEATURES
source
1. 403
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 7.6%; Score 140; DB 6; Length 403;
Best Local Similarity 99.5%; Pred. No. 1.1e-64;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 GTGCTTGGGCTTTGCTGCTGCGGCACTGCTTCCAGCACCTCAACGAGCGCTCGGAC 100
DB 43 GTGCTTGGGCTTTGCTGCTGCGGCACTGCTTCCAGCACCTCAACGAGCGCTCGGAC 102
QY 101 ACGGAGGTTTCTCTCTGCGGGAAGTAAAGGTGAAGCCAGACGATTAATTC 160
DB 103 ACGGAGGTTTCTCTCTGCGGGAAGTAAAGGTGAAGCCAGACGATTAATTC 162

QY 161 CAATGATGATGTTGTAAGTTGTTTATATCAATTGACATTCAGAAATATATTCATGCTAT 220
DB 163 CAATGATGATGTTGTAAGTTGTTTATATCAATTGACATTCAGAAATATATTCATGCTAT 222
QY 221 CAGCTTTTAG 231
DB 223 CAGCTTTTAG 233

RESULT 28
AC124242 220818 bp DNA linear PRI 09-DEC-2002
LOCUS Homo sapiens chromosome 8, clone CTD-2547L16, complete sequence.
DEFINITION AC124242
ACCESSION AC124242
VERSION 1
KEYWORDS GI:26245914
HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barin, N., Bastein, V., Bloom, T., Boguslavsky, L.,
Bouckgalter, B., Brown, A., Camarata, J., Campolongo, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, M., Gage, D.,
Galligan, J., Gardyna, S., Gande, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
Menues, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicot, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riles, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.,
Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
AUTHORS
REFERENCE
Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 220818)

Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barin, N., Bastein, V., Bloom, T., Boguslavsky, L., Bouckgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, M., Gage, D.,
Galligan, J., Gardyna, S., Gande, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
Menues, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicot, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riles, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.,
Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

REFERENCE 4 (bases 1 to 220818)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguski, M., Boucknight, B.,
Camara, J., Chang, J., Chazaro, B., Choquet, Y., Collamore, A.,
Cook, A., Cooke, P., DeRubeis, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzgibbon, M., Gage, D., Galagan, J.,
Garday, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karas, A., Kelle, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,
Mathews, C., McCarthy, M., Meldrum, J., Meneses, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Noddu, C.,
Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, U., Testa, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Submitted (09-DEC-2002) Whitehead Institute/MIT Center for Genome
Journal Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 9, 2002 this sequence version replaced gi:25140057.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

COMMENT -----
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MMR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L27447
Center clone name: 2547_L_16

FEATURES
source 1..220818
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
/clone="CTD-2547L16"
/clone_lib="CTD2 Human BAC"
complement(38..593)
/rpt_family="MLT1F1"
2494..2614
/rpt_family="MER5A"
complement(2749..3041)
/rpt_family="LTR49-int"
complement(3112..4158)
/rpt_family="LTR49-int"
complement(4299..4371)
/rpt_family="LTR49-int"
complement(4431..4498)
/rpt_family="tRNA-Glu-GAG"
complement(4500..5443)
/rpt_family="LTR49-int"
complement(5526..5867)
/rpt_family="LTR49-int"
complement(5870..5962)
/rpt_family="LTR49"
complement(6012..6119)
/rpt_family="LTR48"
complement(6122..6439)
/rpt_family="LTR48B"
7625..7644
/rpt_family="(T)n"
7964..8160
/rpt_family="MIR"
complement(8290..8334)
/rpt_family="L3"
8600..8658

/rpt_family="(CA)n"
complement(8660..9602)
/rpt_family="LIMC"
complement(11351..11511)
/rpt_family="LIMA7"
complement(11534..13488)
/rpt_family="LIMA3"
13495..13525
/rpt_family="AT-rich"
complement(13526..14239)
/rpt_family="LIMA7"
complement(14309..15495)
/rpt_family="LIMA3"
complement(16109..16632)
/rpt_family="LIMA3"
16633..16652
/rpt_family="(GGGTG)n"
complement(16653..16966)
/rpt_family="LIMA3"
complement(17611..17990)
/rpt_family="MER92A"
17993..18150
/rpt_family="MER5B"
18170..18666
/rpt_family="L2"
18692..18841
/rpt_family="LIM4B"
complement(18835..20613)
/rpt_family="L1"
20614..20644
/rpt_family="(TTTG)n"
complement(20645..21957)
/rpt_family="L1"
complement(21958..22263)
/rpt_family="ALUSx"
complement(22264..22486)
/rpt_family="L1"
22957..23217
/rpt_family="MLT1F1"
25227..25428
/rpt_family="ALUo"
25587..26053
/rpt_family="L1"
26054..26334
/rpt_family="ALUSx"
26335..26635
/rpt_family="L1"
26636..26774
/rpt_family="ALUSg/x"
27131..27201
/rpt_family="MER74A"
27288..27480
/rpt_family="LINE"
complement(27848..28207)
/rpt_family="LIMA8"
28731..29079
/rpt_family="MER1B"
29142..30112
/rpt_family="L1"
30113..30413
/rpt_family="ALUSx"
30414..30560
/rpt_family="L1"
30684..30777
/rpt_family="MER89"
30778..31230

Query Match 7.2%; Score 134; DB 9; Length 220818;
Best Local Similarity 100.0%; Prid. No. 3e-61;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
548 GGTATATAACTGATCATGCTCTGATGTCACCTGTTTATGACGAGAGATCAACAA 607

Db 177714 GGTATATAACTGATATCGTTCCTGATGTCACATGCTTTTACGCCAGACGATACAAACA 177773
QY 608 CACAGCTCTAAATTTTGAAGAAAGATGATCTTTAAAGAGGTAATTAAGTAAAGAA 667
Db 177774 CACAGCTCTAAATTTTGAAGAAAGATGATCTTTAAAGAGGTAATTAAGTAAAGAA 177833
QY 668 ATGTATGCTCAT 681
Db 177834 ATGTATGCTCAT 177847
RESULT 29
G30051 346 bp DNA linear STS 05-OCT-1996
LOCUS human STS SHGC-36059, sequence tagged site.
DEFINITION G30051.1 GI:1593602
ACCESSION G30051.1 STS; STS sequence; primer; sequence tagged site.
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 346)
AUTHORS Myers, R.M.
JOURNAL Unpublished (1996)
COMMENT Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: GCTTTATTTCCAAACCTTTT
Primer B: TGTCCTGCTCCTCCTTTTC
STS size: 100
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3
Prepared with primer pairs provided by Sandoz, derived from F08936
-- Washington University/Merck EST sequence.
FEATURES
Source
1. .346
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4"
STS
13. .112
13. .35
primer_bind complement(93. .112)
ORIGIN
Query Match 6.5%; Score 121; DB 11; Length 346;
Best Local Similarity 99.4%; Pred. No. 2.6e-54;

Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1474 GTTGAAGGGAAGGCTTACAGAGACATCTTTAGAAATGGAAAAAGTACAGACGACCA 1533
Db 53 GTTGAAGGGAAGGCTTACAGAGACATCTTTAGAAATGGAAAAAGTACAGACGACCA 112
QY 1534 GTGGCTCACACCTGTATCCAGCACTTAGGAGACAAAGTCAGAGAGATTGTAAGC 1593
Db 113 GTGGCTCACACCTGTATCCAGCACTTAGGAGACAAAGTCAGAGAGATTGTAAGC 172
QY 1594 TAGAGCTTAGAGACCAAGCTGGGCAAGGATATGAGACCATGTCTATTAATAA 1645
Db 173 TAGAGCTTAGAGACCAAGCTGGGCAAGGATATGAGACCATGTCTATTAATAA 224
RESULT 30
AB020868/c 153472 bp DNA linear PRI 21-MAY-1999
LOCUS Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
DEFINITION hepatocellular colorectal and non-small cell lung cancer, segment
11/11.
ACCESSION AB020868
VERSION AB020868.1 GI:4003388
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 153472)
AUTHORS Nakamura, Y. and Iwamura, M.
JOURNAL Title
Homo sapiens 1,210,381bp genomic DNA of 8p21.3-p22 anti-oncogene of
hepatocellular colorectal and non-small cell lung cancer region
Published only in Database (1998)
2 (bases 1 to 153472)
Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
Direct Submission
Submitted (30-NOV-1998) Mika Hirakawa, Japan Science and Technology
Corporation (JST), Advanced Database Department; 5-3, Yonban-cho,
Chiyoda-ku, Tokyo 102-0028, Japan (E-mail: mika@tokyo.jst.go.jp,
Tel:81-3-5214-8491, Fax:81-3-5214-8470)
This sequence is conducted by Japanese Foundation for Cancer
Research as a JST sequencing team
Principal Investigator: Yusuke Nakamura Ph.D.
Phone: +81-3-5449-5372, Fax: +81-3-5449-5433,
yusuke@hgc.ims.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing in AUIS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive web site
(http://www-ais.tokyo.jst.go.jp/HGS/top.html)
or send email to webmaster@www-ais.tokyo.jst.go.jp.
Location/Qualifiers
1. .153472
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p21.3-p22"
7141. .7378
/note="sbsG1568: The location is between each flanking site
of PCR primers "
/db_xref="GDB:4564419"
ORIGIN
Query Match 4.9%; Score 91; DB 9; Length 153472;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30022 AATTAAAGATATATGCAAAAAAGTGGAGACAGTGAACAGCTAGATAACTAGTAA 29963
 QY 750 AGGATGTAAACAGATTAAACGGAATTGA 780
 Db 29962 AGGATGTAAACAGATTAAACGGAATTGA 29932

RESULT 31
 AP006203/c 168921 bp DNA linear PRI 18-FEB-2003
 LOCUS Homo sapiens genomic DNA, chromosome 8, clone:RP11-110N16, complete
 DEFINITION sequence.
 ACCESSION AP006203
 VERSION AP006203.1 GI:28411639
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Hattori, M., Toyoda, A., Taylor, T.D., Fujiyama, A., Yada, T.,
 Totsuki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2003)
 REFERENCE 2 (bases 1 to 168921)
 AUTHORS Hattori, M., Toyoda, A., Taylor, T.D., Fujiyama, A., Yada, T.,
 Totsuki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki-shi, Yokohama-shi, Kanagawa-shi, Japan
 (E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9117, Fax:81-45-503-9170)
 FEATURES
 source
 1.168921
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /clone="RP11-110N16"

ORIGIN
 Query Match 4.9%; Score 91; DB 9; Length 168921;
 Best Local Similarity 100.0%; Pred. No. 8, 6e-38;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AATTAAAGATATATGCAAAAAAGTGGAGACAGTGAACAGCTAGATAACTAGTAA 749
 Db 86292 AATTAAAGATATATGCAAAAAAGTGGAGACAGTGAACAGCTAGATAACTAGTAA 86233
 QY 750 AGGATGTAAACAGATTAAACGGAATTGA 780
 Db 86232 AGGATGTAAACAGATTAAACGGAATTGA 86202

RESULT 32
 AP006208 177888 bp DNA linear PRI 18-FEB-2003
 LOCUS Homo sapiens genomic DNA, chromosome 8, clone:RP11-815A6, complete
 DEFINITION sequence.
 ACCESSION AP006208
 VERSION AP006208.1 GI:28411644
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Hattori, M., Toyoda, A., Taylor, T.D., Fujiyama, A., Yada, T.,
 Totsuki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2003)
 REFERENCE 2 (bases 1 to 177888)

AUTHORS Hattori, M., Toyoda, A., Taylor, T.D., Fujiyama, A., Yada, T.,
 Totsuki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki-shi, Yokohama-shi, Kanagawa-shi, Japan
 (E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9117, Fax:81-45-503-9170)
 FEATURES
 source
 1.177888
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /clone="RP11-815A6"

ORIGIN
 Query Match 4.9%; Score 91; DB 9; Length 177888;
 Best Local Similarity 100.0%; Pred. No. 8, 7e-38;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AATTAAAGATATATGCAAAAAAGTGGAGACAGTGAACAGCTAGATAACTAGTAA 749
 Db 19507 AATTAAAGATATATGCAAAAAAGTGGAGACAGTGAACAGCTAGATAACTAGTAA 19448
 QY 750 AGGATGTAAACAGATTAAACGGAATTGA 780
 Db 19447 AGGATGTAAACAGATTAAACGGAATTGA 19417

RESULT 33
 AC080014 163111 bp DNA linear PRI 25-FEB-2003
 LOCUS Homo sapiens 3 BAC RP11-301G23 (Roswell Park Cancer Institute Human
 BAC library) complete sequence.
 DEFINITION AC080014
 ACCESSION AC080014
 VERSION AC080014.13 GI:19033395
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 163111)
 Murny, D.M., Adams, C., Adio-Oluola, B., Ali-Osman, F.R., Allen, C.,
 Albrooks, S.L., Amaral, H.C., Ayre, V.R., Ayala, M., Banks, T.,
 Barbieri, J., Benton, J., Bimberg, K., Blackebury, K., Bryant, D.,
 Bouchard, J., Bowie, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P.,
 Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dabonne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Decker, D.A.,
 Delaney, K.R., Delgado, O., Dunn, A.L., Ding, Y., Dinh, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
 Gabisi, A., Geo, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gattelli, J.H., Guevara, W., Gunatane, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., He, X.,
 Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
 Hollins, B., Homs, F., Howard, S., Huber, J., Huyl, S., Hune, D.,
 Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolyvet, S.,
 Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Koryah, J.,
 Kovar, C., Kratovic, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.C.,
 Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W.,
 Louisse, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
 Ma, J., Maheswari, M., Mapa, P., Martin, R., Martindale, A.,
 Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M.,
 Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Monabati, K.,
 Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, N., Neal, D.,
 Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N.,
 Nickerson, E., Nocken, K., Ogun, N., Okunju, G., Oragunye, N.,
 Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L.,

http://gc.bcm.tmc.edu:8088/quality.info/genbank_annotation.html.

Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sison, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tameris, A., Tameris, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umani, K., Vazquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczek, R., Wodden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Naylor, S. L., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 163111)
Worley, K. C.

Direct Submission
Submitted (23-SEP-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 163111)
Worley, K. C.

Direct Submission
Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 163111)
Worley, K. C.

Direct Submission
Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 163111)
Worley, K. C.

Direct Submission
Submitted (25-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 1, 2002 this sequence version replaced gi:18449677.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

FEATURES	QUALSTAT REPORT
source	Location/Qualifiers
repeat_region	1. .163111 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="3" /clone="RP11-301G23" 121. .431 /rpt_family="AluY" repeat_region 1709. .1765 /rpt_family="MIR" 2435. .3244 /rpt_family="L1ME2" repeat_region complement(3663. .3842) /rpt_family="MER5A" 4566. .4612 /rpt_family="(TATATG)n" repeat_region complement(5831. .5920) /rpt_family="MIR" 6108. .6141 /rpt_family="AT_rich" repeat_region 6940. .7252 /rpt_family="AluY" repeat_region complement(7727. .7943) /rpt_family="MIR" 8764. .8795 /rpt_family="AT_rich" 8826. .8856 /rpt_family="AT_rich" complement(9534. .9670) /rpt_family="MIR" repeat_region complement(9671. .10122) /rpt_family="MER45B" 10124. .10873 /rpt_family="L1PA4" repeat_region complement(10873. .11461) /rpt_family="MER45B" 12515. .12659 /rpt_family="MIR" repeat_region 12671. .12948 /rpt_family="AluYb" repeat_region 13282. .13603 /rpt_family="AluY" repeat_region 13825. .13965 /rpt_family="L1P" repeat_region 13961. .15866 /rpt_family="L1PA7" complement(16016. .16132) /rpt_family="FLAM_C" 17586. .17734 /standard_name="6896" 17735. .17762 /rpt_family="(A)n" repeat_region 19317. .19411 /rpt_family="L2" repeat_region 20418. .20620 /rpt_family="MER45C" 20906. .21327 /rpt_family="MER45C" 21963. .22111 /rpt_family="MIR" 23721. .23816 /rpt_family="(CCCA)n" 24296. .24443 /rpt_family="MIR" complement(25826. .25871) /rpt_family="MIR" complement(25872. .26178) /rpt_family="AluSg1" complement(26179. .26349) repeat_region

feature	1409. .2850
1409. .2850	

REFERENCE
AUTHORS

REFERENCE	AUTHORS
2 (bases 1 to 92134)	Birren, B., Linton, L., Nusbam, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bedd, F., Boguslavsky, L., Boukngalter, B., Brown, A., Caestele, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domingo, M., Doyle, M., Fenebor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardina, S., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karataas, A., Klein, J., Landers, T., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGuck, A., McKernan, K., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stenge-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodor, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J. Zimmerman, A. and Zody, M.
	Direct Submission

```

* 51795: gap of 100 bp
* 51796: contig of 910 bp in length
* 52705: gap of 100 bp
* 52706: contig of 925 bp in length
* 53730: gap of 100 bp
* 53731: contig of 883 bp in length
* 54713: gap of 100 bp
* 54714: contig of 914 bp in length
* 55727: gap of 100 bp
* 55728: contig of 902 bp in length
* 56729: gap of 100 bp
* 56730: contig of 894 bp in length
* 57724: gap of 100 bp
* 57725: contig of 920 bp in length
* 58744: gap of 100 bp
* 58745: contig of 855 bp in length
* 59702: gap of 100 bp
* 59703: contig of 912 bp in length
* 59803: gap of 100 bp
* 60714: contig of 841 bp in length
* 60815: gap of 100 bp
* 61755: contig of 876 bp in length
* 61756: gap of 100 bp
* 62731: contig of 847 bp in length
* 62732: gap of 100 bp
* 63578: contig of 912 bp in length
* 63579: gap of 100 bp
* 64590: contig of 922 bp in length
* 64591: gap of 100 bp
* 65612: contig of 900 bp in length
* 65713: gap of 100 bp
* 66712: contig of 867 bp in length
* 66713: gap of 100 bp
* 67579: contig of 883 bp in length
* 67580: gap of 100 bp
* 68562: contig of 925 bp in length
* 68563: gap of 100 bp
* 69587: gap of 100 bp
* 69588: contig of 890 bp in length
* 70577: gap of 100 bp
* 70578: contig of 923 bp in length
* 71600: gap of 100 bp

```

Query Match 3.9%; Score 73; DB 2; Length 92134;

Best Local Similarity 100.0%; Pred. No. 5.5e-28; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCATTACTGATTCGCAATGATGATGTTGAAGTTTATACATTGACATTGAGAA 205

Db 24070 AGCATTACTGATTCGCAATGATGATGTTGAAGTTTATACATTGACATTGAGAA 24011

QY 206 TATATTCGATGCT 218

Db 24010 TATATTCGATGCT 23998

RESULT 37
AX199349/c 51 bp DNA 1linear PAT 29-AUG-2001
LOCUS AX199349
DEFINITION Sequence 279 from Patent WO0151670.
ACCESSION AX199349
VERSION AX199349.1 GI:15389733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 Shimkets, R.A. and Leach, M.D.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0151670-A 279 19-JUL-2001;
FEATURES Curagen Corporation (US)
Location/Qualifiers

SOURCE

1. 51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/note="1 of 2 allelic variants (280 is other entry)"
Accession number CG3041720"

ORIGIN

Query Match 2.8%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 ACCAAGTATATATACAGAAAGCTGCTCTACTCATCGATCGAATTCCTT 474

Db 51 ACCAAGTATATATACAGAAAGCTGCTCTACTCATCGATCGAATTCCTT 1

RESULT 38

AC124267/c 70659 bp DNA 1linear HTG 14-JUN-2002
LOCUS AC124267
DEFINITION Homo sapiens chromosome 8 clone CTD-230215 map 8, LOW-PASS SEQUENCE
SAMPLING:
AC124267
AC124267.1 GI:21426288
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 70659)
AUTHORS Birtten, B., Linton, J., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 8, clone CTD-230215
UNPUBLISHED
2 (bases 1 to 70659)
REFERENCE Birtten, B., Linton, J., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguski, L.,
Borkholder, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, S., Choquet, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Gardy, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K.,
Lamas, R., Landers, T., Lehoczy, J., Levine, R., Linblad-Toh, K.,
Lin, G., Maclean, C., Macdonald, P., Major, J., Margulis, N.,
Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Nayler, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strause, N., Subramanian, A., Talamas, J., Testa, S.,
Theodore, J., Topham, K., Travers, M., Trivis, N., Trigglio, J., Ye, M.J.,
Vassiliev, H., Veli, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/km/RepeatMasker.html

COMMENT
TITLE JOURNAL
JOURNAL

GENOME CENTER

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIR
Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu
Project Information
Center Project name: L27437
Center clone name: 2302_1_5

* NOTE: This record contains 82 individual

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 747: contig of 747 bp in length
* 748 847: gap of 100 bp
* 848 1604: contig of 757 bp in length
* 1605 1704: gap of 100 bp
* 1705 2470: contig of 766 bp in length
* 2471 2570: gap of 100 bp
* 2571 3334: contig of 764 bp in length
* 3335 3444: gap of 100 bp
* 3445 4187: contig of 753 bp in length
* 4188 4287: gap of 100 bp
* 4288 5078: contig of 791 bp in length
* 5079 5178: gap of 100 bp
* 5179 5965: contig of 787 bp in length
* 5966 6065: gap of 100 bp
* 6066 6860: contig of 795 bp in length
* 6861 6960: gap of 100 bp
* 6961 7724: contig of 764 bp in length
* 7725 7824: gap of 100 bp
* 7825 8582: contig of 758 bp in length
* 8583 8682: gap of 100 bp
* 8683 9438: contig of 756 bp in length
* 9439 9538: gap of 100 bp
* 9539 10195: contig of 657 bp in length
* 10196 10295: gap of 100 bp
* 10296 11048: contig of 753 bp in length
* 11049 11148: gap of 100 bp
* 11149 11931: contig of 783 bp in length
* 11932 12031: gap of 100 bp
* 12032 12808: contig of 777 bp in length
* 12809 13689: gap of 100 bp
* 13690 13789: contig of 781 bp in length
* 13790 14588: contig of 799 bp in length
* 14589 14688: gap of 100 bp
* 14689 15448: contig of 760 bp in length
* 15449 15548: gap of 100 bp
* 15549 16299: contig of 751 bp in length
* 16300 16399: gap of 100 bp
* 16400 17160: contig of 761 bp in length
* 17161 17260: gap of 100 bp
* 17261 18013: contig of 753 bp in length
* 18014 18113: gap of 100 bp
* 18114 18863: contig of 750 bp in length
* 18864 18963: gap of 100 bp
* 18964 19729: contig of 766 bp in length
* 19730 19829: gap of 100 bp
* 19830 20577: contig of 748 bp in length
* 20578 20677: gap of 100 bp
* 20678 21439: contig of 762 bp in length
* 21440 21539: gap of 100 bp
* 21540 22324: contig of 785 bp in length
* 22325 22424: gap of 100 bp
* 22425 23182: contig of 768 bp in length
* 23183 23292: gap of 100 bp
* 23293 24069: contig of 777 bp in length
* 24070 24169: gap of 100 bp
* 24170 24959: contig of 790 bp in length
* 24960 25059: gap of 100 bp
* 25060 25801: contig of 742 bp in length
* 25802 25901: gap of 100 bp
* 25902 26659: contig of 758 bp in length
* 26660 26759: gap of 100 bp
* 26760 27513: contig of 754 bp in length

27514 27613: gap of 100 bp
* 27614 28362: contig of 749 bp in length
* 28363 28462: gap of 100 bp
* 28463 29220: contig of 758 bp in length
* 29221 29320: gap of 100 bp
* 29321 30072: contig of 752 bp in length
* 30073 30172: gap of 100 bp
* 30173 30945: contig of 777 bp in length
* 30950 31045: gap of 100 bp
* 31050 31832: contig of 783 bp in length
* 31833 31932: gap of 100 bp
* 31934 32689: contig of 757 bp in length
* 32690 32789: gap of 100 bp
* 32790 33544: contig of 755 bp in length
* 33545 33644: gap of 100 bp
* 33645 34407: contig of 763 bp in length
* 34408 34507: gap of 100 bp
* 34508 35259: contig of 752 bp in length
* 35260 35359: gap of 100 bp
* 35360 36108: contig of 749 bp in length
* 36109 36208: gap of 100 bp
* 36209 36944: contig of 736 bp in length
* 36945 37044: gap of 100 bp
* 37045 37816: contig of 772 bp in length
* 37817 37917: gap of 100 bp
* 37918 38699: contig of 783 bp in length
* 38700 38799: gap of 100 bp
* 38800 39522: contig of 723 bp in length
* 39523 39622: gap of 100 bp
* 39623 40407: contig of 785 bp in length
* 40408 40507: gap of 100 bp
* 40508 41287: contig of 780 bp in length
* 41288 41387: gap of 100 bp
* 41388 42155: contig of 768 bp in length
* 42156 42255: gap of 100 bp
* 42256 43012: contig of 757 bp in length
* 43013 43112: gap of 100 bp
* 43113 43880: contig of 768 bp in length
* 43881 43980: gap of 100 bp
* 43981 44755: contig of 775 bp in length
* 44756 44855: gap of 100 bp
* 44856 45619: contig of 764 bp in length
* 45620 45719: gap of 100 bp
* 45720 46457: contig of 738 bp in length
* 46458 46557: gap of 100 bp
* 46558 47341: contig of 784 bp in length
* 47342 47441: gap of 100 bp
* 47442 48218: contig of 777 bp in length
* 48219 48318: gap of 100 bp
* 48319 49107: contig of 785 bp in length
* 49108 49207: gap of 100 bp
* 49209 50007: contig of 800 bp in length
* 50010 50107: gap of 100 bp
* 50108 50876: contig of 769 bp in length
* 50877 50976: gap of 100 bp
* 50977 51734: contig of 758 bp in length
* 51735 51834: gap of 100 bp
* 51835 52598: contig of 764 bp in length
* 52599 52698: gap of 100 bp
* 52699 53431: contig of 733 bp in length
* 53432 53531: gap of 100 bp
* 53532 54250: contig of 719 bp in length
* 54251 54350: gap of 100 bp
* 54351 55113: contig of 763 bp in length
* 55114 55213: gap of 100 bp
* 55214 55974: contig of 761 bp in length
* 55975 56074: gap of 100 bp
* 56075 56816: contig of 742 bp in length
* 56817 56916: gap of 100 bp
* 56917 57559: contig of 743 bp in length
* 57560 57760: gap of 100 bp
* 57761 58540: contig of 781 bp in length
* 58541 58640: gap of 100 bp

```

* 58641 59413: contig of 773 bp in length

Query Match      2.7%; Score 49; DB 2; Length 70659;
Best Local Similarity 100.0%; Pred.NC.6.8e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TGAAGTTGTTTATACATTCAGCAATTCAGAAATATATTCATGCTATCAG 223
      |||
Db 14849 TGAAGTTGTTTATACATTCAGCAATTCAGAAATATATTCATGCTATCAG 14801

RESULT 39
AF220172S1 9630 bp DNA linear PRI 02-AUG-2000
LOCUS Homo sapiens acid ceramidase (ASAH) gene, exon 1.
ACCESSION AF220172
VERSION AF220172.1 GI:9651699
KEYWORDS
SEGMENT 1 of 3
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9630)
AUTHORS Mukherjee, A.B.
JOURNAL Human acid ceramidase gene
TITLE Unpublished
REFERENCE 2 (bases 1 to 9630)
AUTHORS Mukherjee, A.B.
JOURNAL Direct Submission
TITLE Submitted (29-DEC-1999) HDB, NICHD/NIH, 9000 Rockville Pike,
JOURNAL Bethesda, MD 20892-1830, USA
FEATURES
    source
        1. 9630
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="8"
            /map="q22-21.2"
            <1.5429
            /gene="ASAH"
            /note="contains promoter and 5' UTR"
            5430..5507
            /gene="ASAH"
            /number=1
    exon
        misc_feature
            <1.5429
            /gene="ASAH"
            /note="contains promoter and 5' UTR"
            5430..5507
            /gene="ASAH"
            /number=1
    ORIGIN
        Query Match      2.4%; Score 44; DB 9; Length 9630;
        Best Local Similarity 100.0%; Pred.NC.3.3e-12;
        Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 ACCACATCTCGATGTAGTACATCTGACCTTAATGCTAGAA 1000
      |||
Db 68 ACCACATCTCGATGTAGTACATCTGACCTTAATGCTAGAA 111

RESULT 40
AC079355/c 140241 bp DNA linear PRI 15-OCT-2003
LOCUS Homo sapiens BAC clone CTD-2526L21 from 7, complete sequence.
AC079355 AC079355.6 GI:15638962
VERSION AC079355.6 GI:15638962
KEYWORDS HIT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 140241)
AUTHORS Sulston, J.E. and Wilson, R.
JOURNAL Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

REFERENCE 2 (bases 1 to 140241)
AUTHORS All, J., Boyer, E., Dixon, R., Elliott, G. and Naupin, R.
JOURNAL The sequence of Homo sapiens BAC clone CTD-2526L21
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 140241)
AUTHORS Waterston, R.H.
JOURNAL Direct Submission
TITLE Submitted (28-AUG-2000) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL MO 63108, USA
REFERENCE 4 (bases 1 to 140241)
AUTHORS Waterston, R.H.
JOURNAL Direct Submission
TITLE Submitted (18-SEP-2001) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL MO 63108, USA
REFERENCE 5 (bases 1 to 140241)
AUTHORS Waterston, R.
JOURNAL Direct Submission
TITLE Submitted (09-JUN-2002) Department of Genetics, Washington
JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 140241)
AUTHORS Wilson, R.
JOURNAL Direct Submission
TITLE Submitted (15-OCT-2003) Department of Genetics, Washington
JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Sep 18, 2001 this sequence version replaced GI:14702090.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: saplens@wustl.wustl.edu
----- Summary Statistics -----
Center project name: H_T2526L21

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/CTB/CHR7, send
mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu

SOURCE INFORMATION:
Clone CTD-2526L21 is from a release of the human BAC library CTD.
The library contains cloned DNA from human sperm. See: Shinya et
al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al.,
Genomics 34:213-8 (1996). The clone is available from Research
Genetics, Inc. (http://www.reagen.com).
VECTOR: pBelBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-965K10, 2000 bp overlap the
clone sequenced to the right is RP11-340I6, 2000 bp overlap.
Actual start of this clone is at base position 106086 of
RP5-965K10.

```

FEATURES
source

Location/Qualifiers
1. 140241
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="CTD-2526L21"
/clone_1b="CTD"
245. 544
/rpt_family="Alu"
658. 968
/rpt_family="Alu"
1018. 1070
/rpt_family="L2"
1112. 1202
/rpt_family="L2"
1240. 1537
/rpt_family="Alu"
1757. 1936
/rpt_family="L1"
1937. 2020
/rpt_family="Alu"
2076. 2140
/rpt_family="L2"
2293. 2422
/rpt_family="Alu"
2429. 2568
/rpt_family="Alu"
2569. 2862
/rpt_family="Alu"
2863. 3036
/rpt_family="Alu"
3375. 3676
/rpt_family="Alu"
4188. 4312
/rpt_family="Alu"
5671. 5730
/rpt_family=" (TA) n"
5731. 5845
/rpt_family="Alu"
6494. 6788
/rpt_family="Alu"
7363. 7657
/rpt_family="Alu"
8026. 8341
/rpt_family="Alu"
8580. 8872
/rpt_family="Alu"
8876. 8906
/rpt_family=" (CAAA) n"
9425. 9719
/rpt_family="Alu"
9737. 9782
/rpt_family=" (CA) n"
10303. 10438
/rpt_family="Alu"
12039. 12144
/rpt_family="MIR"
12189. 12492
/rpt_family="Alu"
13020. 13130
/rpt_family="GA-rich"
13737. 14033
/rpt_family="Alu"
14751. 15056
/rpt_family="Alu"
15244. 15543
/rpt_family="Alu"
15507. 16812
/rpt_family="Alu"
17801. 18042
/rpt_family="Alu"

repeat_region 18053. 18313
/rpt_family="Alu"
repeat_region 19116. 19403
/rpt_family="Alu"
repeat_region 19410. 19699
/rpt_family="Alu"
repeat_region 20261. 20432
/rpt_family="MIR"
repeat_region 20752. 21000
/rpt_family="Alu"
repeat_region 21001. 21125
/rpt_family="Alu"
repeat_region 21163. 21455
/rpt_family="Alu"
misc_feature 21602. 22059
/note="CpG island (%GC=62.7, o/e=1.07, #CpGs=49)"
repeat_region 22097. 22200
/rpt_family="Alu"
repeat_region 22264. 22393
/rpt_family="Alu"
repeat_region 22401. 22532
/rpt_family="Alu"
repeat_region 22568. 22744
/rpt_family="Alu"
repeat_region 23462. 23762
/rpt_family="Alu"
repeat_region 23961. 24235
/rpt_family="Alu"
repeat_region 24520. 24615
/rpt_family="Alu"
repeat_region 24982. 25288
/rpt_family="Alu"
repeat_region 25419. 25718
/rpt_family="Alu"
repeat_region 25867. 25977
/rpt_family="Alu"
repeat_region 25978. 26140
/rpt_family="Alu"
repeat_region 26164. 26450

Query Match 2.3%; Score 43; DB 9; Length 140241;
Best Local Similarity 100.0%; Pred. No. 1,3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1519 GTGAGACGACGACAGTGCTCACCTGTAAATCCCGACCTT 1561
Db 132627 GTGAGACGACGACAGTGCTCACCTGTAAATCCCGACCTT 132585

RESULT 41
AC146373/c 156131 bp DNA linear HTG 19-DEC-2003
LOCUS Pan troglodytes chromosome 7 clone RP43-60G24, WORKING DRAFT
DEFINITION
SEQUENCE, 5 unordered pieces.
AC146373
AC146373.3 GI:40217772
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 156131)
AUTHORS Wilson, R. K.
TITLE The sequence of Pan troglodytes clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 156131)
REFERENCE Wilson, R. K.
TITLE Direct Submission
AUTHORS Wilson, R. K.
JOURNAL Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 156131)
AUTHORS Wilson, R. K.
TITLE Direct Submission

JOURNAL Submitted (19-DEC-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Dec 19, 2003 this sequence version replaced gi:38154121.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
Project Information -----
Center project name: C_PT060G24

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152805 bases at least Q40
Consensus quality: 153535 bases at least Q30
Consensus quality: 153919 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1611: contig of 1611 bp in length
1612 1711: gap of unknown length
1712 3208: contig of 1497 bp in length
3209 3308: gap of unknown length
3309 12806: contig of 9498 bp in length
12807 12906: gap of unknown length
12907 56903: contig of 43997 bp in length
56904 57004: gap of unknown length
57004 156131: contig of 99128 bp in length.

FEATURES
source
1. 156131
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/clone="RP43-60G24"

misc_feature
1. 1611
/note="assembly_name:Contig3"
misc_feature
1712. 3208
/note="assembly_name:Contig4"
misc_feature
3309. 12806
/note="assembly_name:Contig7"
misc_feature
12907. 56903
/note="assembly_name:Contig8"
misc_feature
57004. 156131
/note="assembly_name:Contig9"

ORIGIN
Query Match 2.3% Score 43; DB 2; Length 156131;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1519 GTGAGACCGAGCAGTGGCTCACCTGTATCCAGCACTT 1561
48422 GTGAGACCGAGCAGTGGCTCACCTGTATCCAGCACTT 48380
RESULT 42
AC130708 192281 bp DNA linear HTG 24-APR-2003
LOCUS Homo sapiens chromosome UNK clone RP11-114D19, WORKING DRAFT
DEFINITION
SEQUENCE, 9 unsorted pieces.
AC130708 AC023016

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

AC130708.2 GI:30089848
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 192281)
Waterson, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 192281)
Waterson, R.H.
Direct Submission
Submitted (13-NOV-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 192281)
Waterson, R.H.
Direct Submission
Submitted (24-APR-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 24, 2003 this sequence version replaced gi:22213488.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
Project Information -----
Center project name: H_NH0114D19
Drafting center: WIBR

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 191695 bases at least Q40
Consensus quality: 192780 bases at least Q30
Consensus quality: 193441 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1650: contig of 1650 bp in length
1651 1750: gap of unknown length
1751 4098: contig of 2348 bp in length
4099 4198: gap of unknown length
4199 7036: contig of 2838 bp in length
7037 7136: gap of unknown length
7137 9466: contig of 2330 bp in length
9467 9566: gap of unknown length
9567 23520: contig of 13954 bp in length
23521 23620: gap of unknown length
23621 36330: contig of 12610 bp in length
36331 36330: gap of unknown length
36331 47687: contig of 11357 bp in length
47688 47788: gap of unknown length
47789 77485: contig of 29698 bp in length
77486 77585: gap of unknown length
77586 192281: contig of 114696 bp in length.

FEATURES
source
1. 192281
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

```
/chromosome="UNK"
/clone="RP11-114D19"
1. 1650
misc_feature /note="assembly_name:Contig87"
1751.4098
misc_feature /note="assembly_name:Contig88"
4199.7036
misc_feature /note="assembly_name:Contig89"
7137.9466
misc_feature /note="assembly_name:Contig90"
9567.23520
misc_feature /note="assembly_name:Contig91"
23621.36230
misc_feature /note="assembly_name:Contig92"
36331.47687
misc_feature /note="assembly_name:Contig93"
47788.77485
misc_feature /note="assembly_name:Contig94"
77586.192281
misc_feature /note="assembly_name:Contig95"

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 192281;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GTGAGACGACGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 149380 GTGAGACGACGACAGTGGCTCACACCTGTATCCGACACTT 149422

RESULT 43
LOCUS AC137779 211395 bp DNA linear HTG 03-DEC-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-1017J6, WORKING DRAFT
ACCESSION AC137779
VERSION AC137779.1 GI:26006521
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 211395)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 211395)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Project Name: 1685254
Center clone name: RP11-11_1017J6
-----
Summary Statistics
Consensus quality: 206323 bases at least Q40
Consensus quality: 207293 bases at least Q30
Consensus quality: 208070 bases at least Q20
Estimated insert size: 160000; agarose-gel estimation
Estimated insert size: 210595; sum-of-contigs estimation
Quality coverage: 13.72 in Q20 bases; agarose-gel estimation
Quality coverage: 10.42 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
```

```
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1073: contig of 1073 bp in length
1074 1173: gap of unknown length
1173 2512: contig of 1339 bp in length
2513 2612: gap of unknown length
2613 9193: contig of 6581 bp in length
9194 9293: gap of unknown length
9294 20310: contig of 11016 bp in length
20310 20409: gap of unknown length
20410 32219: contig of 11810 bp in length
32219 32320: gap of unknown length
32320 52904: contig of 20585 bp in length
52905 53004: gap of unknown length
53005 83155: contig of 30151 bp in length
83156 83255: gap of unknown length
83256 140865: contig of 57610 bp in length
140866 140965: gap of unknown length
140966 211395: contig of 70430 bp in length.
Location/Qualifiers
1. 211395
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1017J6"
/clone_id="RP11-1017J6"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 211395;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GTGAGACGACGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 45615 GTGAGACGACGACAGTGGCTCACACCTGTATCCGACACTT 45573

RESULT 44
LOCUS AC091321 45415 bp DNA linear PRI 20-APR-2002
DEFINITION Homo sapiens, clone RP11-261112, complete sequence.
ACCESSION AC091321
VERSION AC091321.8 GI:20219139
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 45415)
Britten, B., Linton, L., Nussbaum, C. and Lander, E.
Unpublished
2 (bases 1 to 45415)
Britten, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, S.,
Barnett, N., Baetsen, V., Boguslavsky, L., Bouknight, B., Brown, A.,
Camarata, J., Campobiano, A., Chang, D., Choquet, Y., Colangelo, M.,
Collins, S., Collymore, A., Cooke, P., DeArrelano, K., Dewar, K.,
Diaz, D.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardy, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Harford, A., Horton, L., Hulme, W.,
Iliev, I., Johnson, R., Jones, C., Kartas, A., LaRoque, K.,
Lamaze, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Margulis, N., McCarthy, M.,
McGowan, P., McKernan, K., McSheeters, R., Meltram, J., Meneus, L.,
Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., North, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rice, C., Rogov, P., Roman, J.,
Roettig, M., Roy, A., Santos, R., Schauer, S., Schnupp, R., Seaman, S.,
Severy, P., Sougnuez, C., Spencer, B., Strange-Thomann, N.,
```


Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
Direct Submission
JOURNAL
Submitted (15-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
3 (bases 1 to 45415)
AUTHORS
Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gird, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczeky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Margits, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, D., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnepack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
Direct Submission
JOURNAL
Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
4 (bases 1 to 45415)
AUTHORS
Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gird, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczeky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Margits, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, D., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnepack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL
On Apr 20, 2002 this sequence version replaced gi:20143615.
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: Sequence_Submissions@genome.wi.mit.edu
Project Information
Center project name: L13165
Center clone name: 261_I_12

T7 overlaps with AC074237 [WIGR project L9084] by 106x bp. We are only submitting 45.4 kilobases of the project.
Location/Qualifiers

FEATURES
Source
1..45415
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-261112"
/clone_11b="RPC1-11 Human Male BAC"
49..319
/rpt_family="ERVU"
repeat_region
603..935
/rpt_family="MLT1A1"
repeat_region
1153..1451
/rpt_family="ERVU"
repeat_region
1452..1472
/rpt_family="(TTG)n"
repeat_region
1473..1506
/rpt_family="ERVU"
repeat_region
1521..1880
/rpt_family="MLT1I"
repeat_region
1919..1946
/rpt_family="(GA)n"
repeat_region
1963..2107
/rpt_family="(TA)n"
repeat_region
2715..2739
/rpt_family="AT_rich"
repeat_region
complement(3092..3398)
/rpt_family="AluDo"
3662..3746
/rpt_family="MLT1I-int"
repeat_region
3789..4174
/rpt_family="MLT1I"
repeat_region
4246..4783
/rpt_family="ERVU"
repeat_region
5449..5568
/rpt_family="L1"
repeat_region
complement(5835..6183)
/rpt_family="MLT1D"
6184..6257
/rpt_family="MSTU"
repeat_region
6311..6519
/rpt_family="MSTU"
repeat_region
complement(6520..6633)
/rpt_family="MLT1D"
7058..7319
/rpt_family="L1ME"
repeat_region
7361..7733
/rpt_family="L1ME"
repeat_region
complement(8460..8596)
/rpt_family="MER69A"
8640..9001
/rpt_family="L1"
repeat_region
complement(9319..9655)
/rpt_family="L1MBS"
9656..9684
/rpt_family="(TG)n"
repeat_region
complement(9685..9839)
/rpt_family="L1MBS"
10297..10340
/rpt_family="AT_rich"
repeat_region
10379..10458
/rpt_family="MADE1"
10387..10417
/note="single clone coverage"
10865..10930
/rpt_family="(TA)n"
repeat_region
complement(10936..11017)
/rpt_family="r1ggers5"
11008..11084
/rpt_family="r1ggers5"
11235..11271
/rpt_family="AT_rich"
repeat_region

```

repeat_region 11627..11834
                /rpt_family="Alu0c"
repeat_region 11934..12003
                /rpt_family="GA-rich"
repeat_region 12430..12455
                /rpt_family="AT-rich"
repeat_region complement(14097..14174)
                /rpt_family="MR"
repeat_region 14804..14830
                /rpt_family="(TA)n"
repeat_region complement(14902..15116)
                /rpt_family="HAL1"
repeat_region 15117..15424
                /rpt_family="AluY"
repeat_region complement(15425..15583)
                /rpt_family="HAL1"
repeat_region complement(16005..16373)
                /rpt_family="MER31-int"
repeat_region complement(18006..18304)
                /rpt_family="T1MA10"
repeat_region complement(18896..19783)
                /rpt_family="L1PA9"
repeat_region 19790..20673

Query Match      2.3%; Score 42; DB 9; Length 45415;
Best Local Similarity 100.0%; Pred. No. 4,4e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1520 TGAGACGACGACAGTGGCTCACACCTGTATCCAGACACTT 1561
DB 35160 TGAGACGACGACAGTGGCTCACACCTGTATCCAGACACTT 35201

RESULT 45
AL606475/c 83585 bp DNA linear PRI 22-OCT-2001
LOCUS Human DNA sequence from clone RPI3-168N19 on chromosome X, complete
DEFINITION
ACCESSION AL606475
VERSION AL606475.7 GI:16415583
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 83585)
Whitehead, S.
Direct Submission
Submitted (20-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requester: clonerequest@sanger.ac.uk
On Oct 24, 2001 this sequence version replaced gi:15983962.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Emi, EMBL; Swi,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone configs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at

```

```

FEATURES
    source
        location/Qualifiers
            1..83585
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="X"
            /clone="RPI3-168N19"
            /clone_1lb="RPCT-13.1"

ORIGIN
Query Match      2.3%; Score 42; DB 9; Length 83585;
Best Local Similarity 100.0%; Pred. No. 4,5e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACACTTAAAGGA 1566
DB 16013 CCAGGACAGTGGCTCACACCTGTATCCAGACACTTAAAGGA 15972

RESULT 46
AC025435 98939 bp DNA linear PRI 23-AUG-2001
LOCUS Homo sapiens chromosome 5 clone CTC-424X3, complete sequence.
DEFINITION
ACCESSION AC025435
VERSION AC025435.6 GI:15281222
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 98939)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 98939)
DOE Joint Genome Institute.
Direct Submission
Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 98939)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 98939)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 23, 2001 this sequence version replaced gi:10954351.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.hgsc.stanford.edu
Quality: Phrap Quality >=40 99.4% of Sequence;
Estimated Total Number of Errors is 1.
Location/Qualifiers
    1..98939
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="5"

```

ORIGIN /clone="CTC-424K13"

Query Match 2.3%; Score 42; DB 9; Length 99339;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTTAGGGA 1566
DB 79617 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTTAGGGA 79658

RESULT 47
LOCUS AC008671.c 99335 bp DNA linear PRI 25-MAR-2003
DEFINITION Homo sapiens chromosome 5 clone CTB-38P19, complete sequence.
ACCESSION AC008671
VERSION AC008671.6 GI:29171385
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 99335)
TITLE Direct Submission
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Unpublished
DOI 10.1101/000000

REFERENCE 2 (bases 1 to 99335)
TITLE Direct Submission
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 99335)
TITLE Direct Submission
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 99335)
TITLE Direct Submission
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
Submitted (25-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 25, 2003 this sequence version replaced gi:19224654.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
www.shgc.stanford.edu

COMMENT Finishing Completed at Stanford Human Genome Center
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 150,935). It is clipped by the overlap with AC024561.
The number of bases overlapped is 20072.
Location/Qualifiers
1. 99335
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-38P19"

FEATURES
source

ORIGIN

Query Match 2.3%; Score 42; DB 9; Length 99335;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTTAGGGA 1566
DB 81122 CCAGGACAGTGGCTCAGACCTGTATCCAGCACTTAGGGA 81081

RESULT 48
LOCUS AC129623 133581 bp DNA linear PRI 25-SEP-2002

DEFINITION Homo sapiens 12 BAC CTD-2107C6 (Cal Tech Human BAC Library D) complete sequence.
ACCESSION AC129623
VERSION AC129623.4 GI:23307942
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 133581)
AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, P.R., Allen, C., Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayala, M., Banks, T., Barbieri, J., Benton, J., Bimagne, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhey, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cartron, T.F., Carter, M., Cavazos, S.R., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., David, R., Cleveland, C.D., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Din, H.H., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Din, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Biscotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabris, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homel, F., Howard, S., Huber, U., Huliy, S., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C., Kravovic, J., Kureishi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lien, C., Liu, J., Liu, W., Lonsdale, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapu, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Marshney, E., McLeod, M.P., Meador, M., Mei, G., Mescher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Monabadi, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwckenko, S., Ogih, M., Okumura, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pul, L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shm, C., Shochet, R., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tanerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G., and Gibbs, R.

TITLE Direct Submission
JOURNAL Unpublished
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 133581)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 133581)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 25, 2002 this sequence version replaced gi:22474785.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

source

Location/Qualifiers

1..133581

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="12"

/clone="CTD-2107C6"

2433..2713

/standard_name="D11S3206"

46450..46603

/standard_name="D18S965"

79573..79590

/note="variable size of repeat (polyA) in subclone, size 17-18, deletion at 79590"

/function="unresolved homopolymeric run"

128155..128360

/standard_name="RH36462"

STS

STS

ORIGIN

Query Match

Best Local Similarity

Matches

42; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

2.3%; Score 42; DB 9; Length 133581;

Pred. No. 4.6e-11;

100.0%;

17693

17693

17693

17693

17693

COMMENT

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

FEATURES
 * 91593 105981: contig of 14389 bp in length
 * 105982 106081: gap of unknown length
 * 106082 120503: contig of 14422 bp in length
 * 120504 120603: gap of unknown length
 * 120604 147812: contig of 27209 bp in length.
 Location/Qualifiers
 1. 147812
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="18"
 /clone="RP11-261112"
 1. 1170
 /note="assembly_name:Contig3"
 1271. 2991
 /note="assembly_name:Contig4"
 3092. 6547
 /note="assembly_name:Contig6"
 6648. 8714
 /note="assembly_name:Contig7"
 8815. 13890
 /note="assembly_name:Contig8"
 13991. 20037
 /note="assembly_name:Contig9"
 20138. 26761
 /note="assembly_name:Contig10"
 26862. 33528
 /note="assembly_name:Contig11"
 clone_end:SP6
 vector_side:left"
 33629. 40043
 /note="assembly_name:Contig12"
 40144. 49133
 /note="assembly_name:Contig13"
 49234. 56452
 /note="assembly_name:Contig14"
 clone_end:T7
 vector_side:left"
 56553. 63837
 /note="assembly_name:Contig15"
 63938. 71629
 /note="assembly_name:Contig16"
 71730. 81272
 /note="assembly_name:Contig17"
 81373. 91492
 /note="assembly_name:Contig18"
 91593. 105981
 /note="assembly_name:Contig19"
 106082. 120503
 /note="assembly_name:Contig20"
 120604. 147812
 /note="assembly_name:Contig21"

misc_feature
 /note="assembly_name:Contig3"
 1271. 2991
 /note="assembly_name:Contig4"
 3092. 6547
 /note="assembly_name:Contig6"
 6648. 8714
 /note="assembly_name:Contig7"
 8815. 13890
 /note="assembly_name:Contig8"
 13991. 20037
 /note="assembly_name:Contig9"
 20138. 26761
 /note="assembly_name:Contig10"
 26862. 33528
 /note="assembly_name:Contig11"
 clone_end:SP6
 vector_side:left"
 33629. 40043
 /note="assembly_name:Contig12"
 40144. 49133
 /note="assembly_name:Contig13"
 49234. 56452
 /note="assembly_name:Contig14"
 clone_end:T7
 vector_side:left"
 56553. 63837
 /note="assembly_name:Contig15"
 63938. 71629
 /note="assembly_name:Contig16"
 71730. 81272
 /note="assembly_name:Contig17"
 81373. 91492
 /note="assembly_name:Contig18"
 91593. 105981
 /note="assembly_name:Contig19"
 106082. 120503
 /note="assembly_name:Contig20"
 120604. 147812
 /note="assembly_name:Contig21"

Query Match 2.3%; Score 42; DB 2; Length 147812;
 Best Local Similarity 100.0%; Pred.No. 4.7e-11;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1520 TGAGACGAGGACAGTGGCTCAGACCTGTAATCCAGACACTT 1561
 |||||
 DB 82010 TGAGACGAGGACAGTGGCTCAGACCTGTAATCCAGACACTT 81969

RESULT 50
 AC007683/c 155735 bp DNA linear PRI 07-OCT-2000
 LOCUS AC007683 Homo sapiens BAC clone RP11-401113 from 7, complete sequence.
 DEFINITION AC007683
 ACCESSION AC007683.5 GI:9755494
 VERSION AC007683.5
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 9847074
 2 (bases 1 to 155735)
 Nelson,D., Scott,K., Kalicki,J. and Stumpf,J.
 The sequence of Homo sapiens BAC clone RP11-401113
 Unpublished
 3 (bases 1 to 155735)
 Waterston,R.H.
 Direct Submission
 Submitted (29-MAY-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 155735)
 Waterston,R.H.
 Direct Submission
 Submitted (30-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 155735)
 Waterston,R.H.
 Direct Submission
 Submitted (01-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 6 (bases 1 to 155735)
 Waterston,R.H.
 Direct Submission
 Submitted (09-AUG-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 7 (bases 1 to 155735)
 Waterston,R.H.
 Direct Submission
 Submitted (07-OCT-2000) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2000 this sequence version replaced gi:8844167.
 COMMENT
 Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_NH0401113

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and
 sequencing collaboration between the NHGRI Chromosome 7 Mapping
 Project (Eric D. Green, Director), John D. McPherson in the
 Department of Genetics (Washington University), and the Washington
 University Genome Sequencing Center. For additional information
 about the map position of this sequence, see
 http://www.nhgri.nih.gov/DIR/GRB/CHR7, send
 mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPEC1-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Moon, P. Y., Zhao, B., Frangsen, E., Tareno, M., Catanesse, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is CTA-27603. Actual start of this clone is at base position 76429 of CTA-27603; actual end is at base position 155735 of RP11-401L13.

The sequence from position 62351 to 62375 is represented by a single M13 subclone sequenced with two chemistries. The assembly in this region is supported by size information obtained by PCR of RP11-401L13 clone DNA.

The sequence from base position 37464 to 38534 represents the best possible assembly of an imperfect tandem repeat. Estimates from HindIII and EcoRV digest suggest that approximately 1500 to 2000 bases may be missing in this area.

FEATURES

source

Location/Qualifiers

1..155735

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="7"

/map="7"

/clone="RP11-401L13"

/clone_lib="RPEC1-11"

56..284

/note="similar to EST N71439 (NID:G1228019) za38h07.s1"

repeat_region

217..295

/rpt_family="L2"

367..662

/rpt_family="Alu"

1643..1791

/note="similar to EST A1678054 (NID:G4868236) wd35c03.x1"

repeat_region

1804..2059

/rpt_family="Alu"

2832..3129

/rpt_family="Alu"

4443..4542

/note="similar to EST AM894409 (NID:G8058614)"

repeat_region

4565..5070

/rpt_family="L1"

5269..5657

/note="similar to EST A1239570 (NID:G3834967) qh31h07.x1"

repeat_region

5976..6267

/rpt_family="Alu"

6483..6635

/rpt_family="Alu"

6747..6901

/rpt_family="MER1_type"

7572..7649

/note="similar to EST AM894409 (NID:G8058614)"

misc_feature

8412..8495

/note="similar to EST AM894409 (NID:G8058614)"

repeat_region

8792..9102

/rpt_family="Mariner"

9049..9165

/rpt_family="Mariner"

9623..9831

/rpt_family="MER2_type"

9862..9940

/rpt_family="MER2_type"

10125..10479

/rpt_family="L1"

10491..10585

/rpt_family="L1"

repeat_region 10618..10977 /rpt_family="L1"

repeat_region 11607..11917 /rpt_family="Alu"

repeat_region 12294..13353 /rpt_family="L1"

repeat_region 13354..14644 /rpt_family="L1"

repeat_region 14648..14926 /rpt_family="L1"

repeat_region 14972..15347 /rpt_family="L1"

repeat_region 15333..15430 /rpt_family="L1"

repeat_region 15432..15919 /rpt_family="L1"

repeat_region 16112..16477 /rpt_family="L1"

repeat_region 16478..16588 /rpt_family="MALR"

repeat_region 17878..18139 /rpt_family="L1"

misc_feature 18365..18813 /note="similar to EST N34516 (NID:G1155658) yy55a04.s1"

misc_feature 18483..19117 /note="similar to EST AM977887 (NID:G8169040)"

repeat_region 19067..19402 /rpt_family="L1"

repeat_region 19511..19830 /rpt_family="L1"

repeat_region 20100..20340 /rpt_family="L1"

repeat_region 20435..21129 /rpt_family="L1"

repeat_region 21130..21432 /rpt_family="Alu"

repeat_region 21433..21964 /rpt_family="L1"

repeat_region 21967..22087 /rpt_family="L1"

repeat_region 22089..22307 /rpt_family="L1"

repeat_region 22310..22754 /rpt_family="L1"

repeat_region 22755..22847 /rpt_family="L1"

Query Match 2.3%; Score 42; DB 9; Length 155735;

Best Local Similarity 100.0%; Pred. No. 4.7e-11; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 1525 CCAGGCAAGTGGCTCACACCTGTATCCAGACTTAGGGA 1566

Db 3127 CCAGGCAAGTGGCTCACACCTGTATCCAGACTTAGGGA 3086

RESULT 51

AC020898 164498 bp DNA linear PRI 03-OCT-2001

LOCUS Homo sapiens chromosome 5 clone CTC-451P13, complete sequence.

DEFINITION AC020898

ACCESSION AC020898.6 GI:15887298

VERSION

KEYWORDS

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 164498)

DOE Joint Genome Institute and Stanford Human Genome Center.

ATTN Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 164498)

DOE Joint Genome Institute.

TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 164498)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Submitted (23-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 164498)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Oct 3, 2001 this sequence version replaced gi:10280746.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99% of Sequence;
 Estimated Total Number of Errors is 1.2.
 STS Content:
 SHGC-57966 G37545.
FEATURES
 source
 Location/Qualifiers
 1..164498
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTC-451P13"
ORIGIN
 Query Match 2.3%; Score 42; DB 9; Length 164498;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1525 CCAGGACAGTGGCTCACACCTGTATCCGACACTTAGGGA 1566
 Db 93196 CCAGGACAGTGGCTCACACCTGTATCCGACACTTAGGGA 93237
RESULT 52
AC027523 172917 bp DNA linear HTG 06-MAR-2003
LOCUS Papio hamadryas clone RP41-171B5, WORKING DRAFT SEQUENCE.
DEFINITION AC140973
ACCESSION AC140973.1 GI:28867005
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Papio hamadryas (hamadryas baboon)
SOURCE Papio hamadryas
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 172917)
AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT
 Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Project Name: B009
 Bac Clone Name: RP41-171B5
 This sequence has been compared to sequences of other species using Vsta (<http://www.gsd.lbl.gov/VISTA>). The results can be viewed at:

http://pga.lbl.gov/cgi-bin/search_cvsget?type=nk&value=NR113
 The order-orientation of the draft sequence was accomplished by using:
 Avid (<http://baboon.math.berkeley.edu/avid/>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.
 Funding agent: Programs for Genomic Applications (NHBLI)
Summary Statistics:
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 1 172917: contig of 172917 bp in length.
FEATURES
 source
 Location/Qualifiers
 1..172917
 /organism="Papio hamadryas"
 /mol_type="genomic DNA"
 /db_xref="taxon:9557"
 /clone="RP41-171B5"
ORIGIN
 Query Match 2.3%; Score 42; DB 2; Length 172917;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1520 TGAGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
 Db 13161 TGAGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 13202
RESULT 53
AC027523 182834 bp DNA linear HTG 04-JUL-2001
LOCUS Homo sapiens chromosome 18 clone RP11-311F3 map 18, WORKING DRAFT SEQUENCE. 7 unordered pieces.
DEFINITION AC027523
ACCESSION AC027523.3 GI:14595932
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 182834)
AUTHORS Birren, B., Linton, L., Nussbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 18, clone RP11-311F3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 182834)
AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, S., Boguslavsky, L., Boucknight, B., Brown, A., Burkett, G., Collins, S., Compagno, A., Cooke, P., Deaile, A., Choepel, K., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Deaile, A., Dewar, K., Diaz, D., S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardys, S., Ginde, S., Goyette, M., Graham, L., Grand, J., Grant, N., Grant, J., Hager, B., Heaford, A., Horton, L., Howland, J., C., Iliev, I., Johnson, R., Jones, C., Kamm, L., Karatas, A., Klein, J., Labèque, K., Lamazares, R., Landers, T., Lebecky, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPherson, R., Meldrum, D., Menais, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

TITLE
JOURNAL
COMMENT

Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teefaye, S., Theodore, J., Tirrell, A., Travers, M., Triggilio, J.,
Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 4, 2001 this sequence version replaced gi:7630712.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project information

Center project name: L8515

Center clone name: 311.P.3

Summary Statistics

Sequencing vector: M13; M77815, 41% of reads
Sequencing vector: Plasmid; n/a; 59% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 180288 bases at least Q40
Consensus quality: 181523 bases at least Q30
Consensus quality: 181936 bases at least Q20

Insert size: 183000; agarose-fp

Insert size: 182234; sum-of-coverage
Quality coverage: 9.8 in Q20 bases; agarose-fp
Quality coverage: 9.8 in Q20 ba.

NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 23100: contig of 23100 bp in length
* 23101 23200: gap of 100 bp
* 23201 28150: contig of 4950 bp in length
* 28151 28250: gap of 100 bp
* 28251 35485: contig of 7235 bp in length
* 35486 35585: gap of 100 bp
* 35586 55234: contig of 19649 bp in length
* 55235 55334: gap of 100 bp
* 55335 78764: contig of 23430 bp in length
* 78765 78864: gap of 100 bp
* 78865 107181: contig of 28317 bp in length
* 107182 107282: gap of 100 bp
* 107282 182834: contig of 75553 bp in length.

FEATURES

source

1. 182834

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="18"

/map="18"

/clone="RP11-311F3"

/clone_lib="RPC1-11 Human Male BAC"

1. 23100

/note="assembly_fragment"

/clone_end:56

vector_side:left"

23201..28150

/note="assembly_fragment"

28251..35485

/note="assembly_fragment"

35586..55234

/note="assembly_fragment"

55335..78764

/note="assembly_fragment"

misc_feature 78865..107181
/note="assembly_fragment"
misc_feature 107282..182834
/note="assembly_fragment"

ORIGIN

Query Match 2.3%; Score 42; DB 2; Length 182834;
Best Local Similarity 100.0%; Pred. No. 4/7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGCACTTAGGA 1566
DB 60160 CCAGGACAGTGGCTCACACCTGTATCCAGCACTTAGGA 60119

RESULT 54

AC146901

LOCUS

DEFINITION

ORDERED

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

COMMENT

Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABRK
Center Project Name: J031
Bac Clone Name: CH259-132H12

This sequence has been compared to sequences of other species
using Vista (http://www.gsdlbl.gov/VISTA). The results can be
viewed at:
http://pga.lbl.gov/cgi-bin/search_cvsgrd?type=navalue=RM113

The order-orientation of the draft sequence was accomplished by
using:
Avid (http://paboon.math.berkeley.edu/mauid),
Lagan (http://lagan.stanford.edu/) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:

Sequencing vector: Plasmid; pUC18

Chemistry: Dye-terminator Big Dye

Assembly program: Phrap version 0.990329.

NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 56236: contig of 56236 bp in length

56237 56336: gap of unknown length

REFERENCES

4 (Issues 1 to 2005/57)

Birren, B., Nisbaum, C., Lader, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavsky, U., Boulton, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collamore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S.,

```

Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardayana, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mienga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nobu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talama, J.,
Testa, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 28, 2002 this sequence version replaced gi:22123309.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIMR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: 12424
Center clone name: 380_C_8

FEATURES
source
-----
location/Qualifiers
1..208039
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-380C8"
/clone_1fb="RP11-380C8 Human Male BAC"
1..58
/repeat_region
/rpt_family="AluSg/x"
59..271
/repeat_region
/rpt_family="Aluub"
complement(501..802)
/rpt_family="AluSx"
complement(2674..2963)
/rpt_family="Aluub"
complement(3308..3607)
/rpt_family="AluSx"
complement(4322..4515)
/rpt_family="Charlie1"
complement(4516..4631)
/rpt_family="FLAM_A"
complement(4653..5018)
/rpt_family="Charlie1"
complement(5185..5474)
/rpt_family="AluSx"
5511..5545
/rpt_family="AluSx"
/rpt_family="AT_rich"
complement(5681..5754)
/rpt_family="Charlie1"
complement(5788..5918)
/rpt_family="Aluub"
complement(6017..6343)
/rpt_family="AluY"
complement(6346..6636)
/rpt_family="AluY"
complement(6639..6719)
/rpt_family="AluSg/q"
6873..7038
/rpt_family="Aluub"
7059..7099
/rpt_family="Aluub"
/rpt_family="(CA)n"

repeat_region complement(7311..7545)
/rpt_family="AluSx"
repeat_region 7849..8082
/rpt_family="MER20"
repeat_region 8354..8427
/rpt_family="(TCTCCC)n"
repeat_region 8432..10358
/rpt_family="SVA"
repeat_region complement(10609..11016)
/rpt_family="MLT1D"
repeat_region complement(11059..11356)
/rpt_family="AluSc"
repeat_region 11381..11447
/rpt_family="(TTAA)n"
repeat_region 11506..11804
/rpt_family="AluSg"
repeat_region 11899..12192
/rpt_family="AluY"
repeat_region complement(12772..13065)
/rpt_family="AluSx"
repeat_region complement(13114..13390)
/rpt_family="Aluub"
repeat_region complement(13581..13653)
/rpt_family="MER41A"
repeat_region complement(13654..13900)
/rpt_family="FLM4"
repeat_region complement(13910..14081)
/rpt_family="FAM"
repeat_region complement(14110..14369)
/rpt_family="Aluub"
repeat_region 14402..15503
/rpt_family="FLM4"
repeat_region 15513..16122
/rpt_family="FLM4A"
repeat_region 16131..16353
/rpt_family="Aluub"
repeat_region 16355..16400
/rpt_family="FLAM_A"
repeat_region 16403..16636
/rpt_family="FLM4"
repeat_region complement(16867..17140)
/rpt_family="AluSg1"
repeat_region complement(17187..17500)
/rpt_family="Aluub"
repeat_region complement(17931..18115)
/rpt_family="FLM4a"
repeat_region complement(18143..18363)
/rpt_family="FLME1"
repeat_region complement(18364..18663)
/rpt_family="AluSx"
repeat_region complement(18709..18823)
/rpt_family="FLME1"
repeat_region complement(18826..19115)
/rpt_family="AluSx"
repeat_region complement(19222..19321)
/rpt_family="FLME1"
repeat_region 19499..19792
/rpt_family="AluSg"
repeat_region complement(19935..20153)
/rpt_family="Aluub"
repeat_region complement(20165..20273)
/rpt_family="FLAM_A"
repeat_region complement(20386..20573)
/rpt_family="AluSg/x"
repeat_region complement(20689..20995)
/rpt_family="AluY"
repeat_region complement(21037..21317)
/rpt_family="AluSg"
repeat_region complement(21438..21826)

Query Match 2.3%; Score 42; DB 9; Length 208039;
Best Local Similarity 100.0%; Pred. No. 4,8e-11; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 0;

```

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCGACCTTAGGGA 1566
DB 122626 CCAGGACAGTGGCTCACACCTGTATCCGACCTTAGGGA 122585

RESULT 57
AF001848/c 224010 bp DNA linear HTG 08-Aug-2000
LOCUS Homo sapiens chromosome 18 clone RP11-814018 map 18p11.2, WORKING
DEFINITION DRAFT SEQUENCE, 32 unordered pieces.
ACCESSION AP001848
VERSION AP001848.3 GI:9757461
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 224,010 genomic DNA of 18p11.2
2 (bases 1 to 224010)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (18-Apr-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN) Genomic Sciences Center (GSC),
1-15-1 Katsushika, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Aug 9, 2000 this sequence version replaced gi:8117511.
----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrat18
Center clone name: RP11-814018
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly
Program: Phrap; Version 0.990329
Consensus quality: 212358 bases at least Q40
Consensus quality: 218536 bases at least Q30
Insert size: 220910; sum-of-contigs
Quality coverage: 9.03x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
32 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 15221 contig of 15221 bp in length
15322 30276 contig of 14955 bp in length
30377 40753 contig of 10377 bp in length
40854 53793 contig of 12940 bp in length
53894 65011 contig of 11118 bp in length
65112 75224 contig of 10113 bp in length
75325 84814 contig of 9490 bp in length
84915 96348 contig of 11434 bp in length
96449 106172 contig of 9724 bp in length
106273 114921 contig of 8649 bp in length
114922 132606 contig of 8045 bp in length
132607 131751 contig of 8045 bp in length
131752 138950 contig of 7099 bp in length
138951 144550 contig of 5500 bp in length
144551 146503 contig of 8303 bp in length
146504 152953 contig of 4328 bp in length
152954 159224 contig of 6171 bp in length
159225 159325 contig of 6171 bp in length
159326 165737 contig of 6412 bp in length
165738 173107 contig of 7271 bp in length
173108 173207 contig of 100 bp
173208 178488 contig of 5281 bp in length
178489 178588 contig of 100 bp
178589 183587 contig of 4999 bp in length
183588 187911 contig of 4224 bp in length
187912 188011 contig of 100 bp
188012 192483 contig of 4372 bp in length
192484 196811 contig of 100 bp
196812 201215 contig of 4304 bp in length
201216 201315 contig of 4304 bp in length

153054 159224 contig of 6171 bp in length
159325 165736 contig of 6412 bp in length
165837 173107 contig of 7271 bp in length
173208 178488 contig of 5281 bp in length
178589 183587 contig of 4999 bp in length
183688 187911 contig of 4224 bp in length
188012 192483 contig of 4372 bp in length
192484 196811 contig of 4304 bp in length
196912 201315 contig of 4603 bp in length
201316 205918 contig of 4603 bp in length
206019 210031 contig of 4013 bp in length
210132 213781 contig of 3650 bp in length
213882 217164 contig of 3283 bp in length
217265 219263 contig of 1999 bp in length
219364 220624 contig of 1261 bp in length
220725 221858 contig of 1134 bp in length
221959 224010 contig of 2052 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 15221: contig of 15221 bp in length
15222 15321: gap of 100 bp
15322 15321: gap of 100 bp
15322 30276: contig of 14955 bp in length
30277 30276: gap of 100 bp
30277 40753: contig of 10377 bp in length
40754 40853: gap of 100 bp
40854 53793: contig of 12940 bp in length
53794 53894: gap of 100 bp
53894 65011: contig of 11118 bp in length
65012 65112: gap of 100 bp
65112 75224: contig of 10113 bp in length
75225 75325: gap of 100 bp
75325 84814: contig of 9490 bp in length
84815 84915: gap of 100 bp
84915 96348: contig of 11434 bp in length
96349 96449: gap of 100 bp
96449 106172: gap of 9724 bp in length
106173 106273: gap of 100 bp
106273 114921: contig of 8649 bp in length
114922 115021: gap of 100 bp
115021 123606: contig of 8585 bp in length
123607 123706: gap of 100 bp
123707 131751: contig of 8045 bp in length
131752 138950: gap of 100 bp
138951 139050: contig of 7099 bp in length
139051 144550: gap of 100 bp
144551 144650: contig of 5500 bp in length
144651 146503: gap of 100 bp
146504 152953: contig of 8303 bp in length
152954 159224: gap of 100 bp
159225 159325: gap of 6171 bp in length
159326 165737: contig of 6412 bp in length
165738 173107: contig of 7271 bp in length
173108 173207: gap of 100 bp
173208 178488: contig of 5281 bp in length
178489 178588: gap of 100 bp
178589 183587: contig of 4999 bp in length
183588 187911: gap of 100 bp
187912 188011: contig of 4224 bp in length
188012 192483: contig of 4372 bp in length
192484 196811: gap of 100 bp
196812 201215: contig of 4328 bp in length
201216 201315: gap of 100 bp
201315: gap of 100 bp

the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

```

source
    Location/Qualifiers
    1..94508
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="12"
    /clone="RP3-329B11"
    1..2077
    /note="Overlap bases 179021..181097 of clone AC004216"
    /function="clone overlap"
    1..306
    /rpt_family="AluSg"
    repeat_region
    479..667
    /rpt_family="L1MC4a"
    repeat_region
    668..982
    /rpt_family="AluSx"
    repeat_region
    983..1074
    /rpt_family="L1MC4a"
    repeat_region
    1083..1384
    /rpt_family="AluSx"
    repeat_region
    1385..1679
    /rpt_family="AluSg"
    repeat_region
    2018..2310
    /rpt_family="AluYo"
    repeat_region
    2311..2443
    /rpt_family="FLAM_C"
    repeat_region
    2452..2472
    /rpt_family="AT_rich"
    repeat_region
    3245..3547
    /rpt_family="AluSp"
    STS
    3334..3450
    /standard_name="D1S2560"
    repeat_region
    3558..3756
    /rpt_family="L1MC4"
    repeat_region
    3757..4041
    /rpt_family="AluSx"
    repeat_region
    4042..4101
    /rpt_family="L1MC4"
    repeat_region
    4102..4142
    /rpt_family="(CA)n"
    repeat_region
    4143..4492
    /rpt_family="L1MC4"

```

```

repeat_region 4519..4544
/rpt_family="L1M3"
repeat_region 4545..4643
/rpt_family="AluSx"
repeat_region 4644..5054
/rpt_family="L1M3"
repeat_region 5094..5230
/rpt_family="AluYb"
repeat_region 5231..5530
/rpt_family="AluYb"
repeat_region 5531..5624
/rpt_family="AluYb"
repeat_region 5625..6212
/rpt_family="AluSp"
repeat_region 6215..6326
/rpt_family="L1MC4"
repeat_region 6327..6356
/rpt_family="(TA)n"
repeat_region 6357..6381
/rpt_family="L1MD3"
repeat_region 6382..6392
/rpt_family="(GA)n"
repeat_region 6393..6432
/rpt_family="L1MD3"
repeat_region 6433..6723
/rpt_family="MER46A"
repeat_region 6724..6919
/rpt_family="AluSx"
repeat_region 6920..7028
/rpt_family="MER46A"
repeat_region 7108..7401
/rpt_family="L1MD3"
repeat_region 7622..7920
/rpt_family="AluY"
repeat_region 7921..8232
/rpt_family="AluYb"
repeat_region 8311..8620
/rpt_family="AluSp"
repeat_region 8621..8907
/rpt_family="AluSx"
repeat_region 9370..9399
/rpt_family="AluY"
repeat_region 9415..9723
/rpt_family="(TTTTG)n"
repeat_region 9724..9897
/rpt_family="AluSx"
repeat_region 9911..10166
/rpt_family="AluSg"
/rpt_family="MTR"

```

Query Match 2.2%; Score 41; DB 9; Length 94508;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1521 GAGACCGAGCAQAGTGGCTCACTGATATCCAGCACTT 1561
Db 7620 GAGACCGAGCAQAGTGGCTCACTGATATCCAGCACTT 7660

```

```

RESULT 60
HSDJ263J7/c HSDJ263J7 104081 bp DNA linear PRI 04-MAR-2003
LOCUS Human DNA sequence from clone RPI-263J7 on chromosome 6q14.3-15,
DEFINITION complete sequence.
ACCESSION AL049545
VERSION AL049545.6 GI:5002650
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 104081)
AUTHORS Smith,S.
TITLE Direct Submission

```

JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 humquerry@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
 On Jun 7, 1999 this sequence version replaced gi:14835284.

COMMENT ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RPI1-2637 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.choi.org/bacpac/home.htm> VECTOR: pcypac2.

FEATURES
 source Location/Qualifiers
 1..104081
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="q14.3-15"
 /clone="RPI-2637"
 /clone_1ib="RPCI-1"

ORIGIN
 Query Match 2.2%; Score 41; DB 9; Length 104081;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1521 GAGACGAGGACGAGCTGCTCAGCCTGTATCCGACACTT 1561
 37815 GAGACGAGGACGAGCTGCTCAGCCTGTATCCGACACTT 37775

RESULT 61
 AP000446/c 110580 bp DNA linear PRI 15-MAR-2003
 LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:CMB9-8L6, complete
 DEFINITION
 sequence.
 AP000446
 VERSION AP000446 GI:13359351
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 Homo sapiens genomic DNA

JOURNAL Published Only in Database (1999)
 REFERENCE 2 (bases 1 to 110580)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

COMMENT -----
 Submitted (13-SEP-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 E-mail: hattori@gsc.riken.go.jp, URL: <http://hsp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170
 On Mar 16, 2001 this sequence version replaced gi:10130052.

COMMENT
 Location/Qualifiers
 1..110580
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q"
 /clone="CMB9-8L6"

ORIGIN
 Query Match 2.2%; Score 41; DB 9; Length 110580;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1521 GAGACGAGGACGAGCTGCTCAGCCTGTATCCGACACTT 1561
 93761 GAGACGAGGACGAGCTGCTCAGCCTGTATCCGACACTT 93721

RESULT 62
 AC008086 157504 bp DNA linear HTG 04-MAY-2001
 LOCUS Homo sapiens clone RP11-441L4, WORKING DRAFT SEQUENCE, 25 unordered
 DEFINITION
 pieces.
 AC008086
 VERSION AC008086.2 GI:7131136
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 157504)
 Birten, B., Linton, L., Nussbaum, C. and Lander, E.
 Homo sapiens, clone RP11-441L4
 Unpublished
 2 (bases 1 to 157504)
 Birten, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckert, R., Benn, D., Brown, A., Castle, A., Cerny, D., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Depayre, E., Devoy, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Headford, A., Horton, L., Howland, J. C., Jones, C., Kamm, L., Karakas, A., Lehoczy, J., Lien, C., Locke, K., Macdonald, P., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, F., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Teseaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.

Direct Submission
 Submitted (21-UTL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 1, 2000 this sequence version replaced gi:1552047.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1093
Center clone name: 44.L14
----- Summary Statistics
Sequencing vector: M13: M77815; 99% of reads
1.1342155094518echemistry: dye-primer-amerham; 99% of reads
Chemistry: Dye-terminator Big Dye; 1% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 121785 bases at least Q40
Consensus quality: 139703 bases at least Q30
Consensus quality: 148379 bases at least Q20
Insert size: 170000; agarose-ep
Insert size: 155104; sum-of-contigs
Quality coverage.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1398: contig of 1398 bp in length
* 1399 1498: gap of 100 bp
* 1499 2569: contig of 1071 bp in length
* 2570 2669: gap of 100 bp
* 2670 3715: contig of 1046 bp in length
* 3716 3815: gap of 100 bp
* 3816 4982: contig of 1167 bp in length
* 4983 5082: gap of 100 bp
* 5083 7548: contig of 2466 bp in length
* 7549 7649: gap of 100 bp
* 7649 8855: contig of 1207 bp in length
* 8856 8955: gap of 100 bp
* 8956 10690: contig of 1735 bp in length
* 10691 10790: gap of 100 bp
* 10791 12073: contig of 1283 bp in length
* 12074 12173: gap of 100 bp
* 12174 14379: contig of 2206 bp in length
* 14380 14479: gap of 100 bp
* 14480 17943: contig of 3464 bp in length
* 17944 18043: gap of 100 bp
* 18044 21826: contig of 3783 bp in length
* 21827 21926: gap of 100 bp
* 21927 27359: contig of 5433 bp in length
* 27360 27459: gap of 100 bp
* 27460 30113: contig of 2654 bp in length
* 30114 30213: gap of 100 bp
* 30214 35192: contig of 4979 bp in length
* 35193 35292: gap of 100 bp
* 35293 41089: contig of 5797 bp in length
* 41090 41189: gap of 100 bp
* 41190 46410: contig of 5221 bp in length
* 46411 46510: gap of 100 bp
* 46511 52192: contig of 5682 bp in length
* 52193 52292: gap of 100 bp
* 52293 60495: contig of 8203 bp in length
* 60496 60595: gap of 100 bp
* 60596 68130: contig of 7535 bp in length
* 68131 68230: gap of 100 bp
* 68231 74345: contig of 6015 bp in length
* 74346 82056: gap of 100 bp
* 82057 82156: gap of 100 bp
* 82157 91897: contig of 9741 bp in length
* 91898 91997: gap of 100 bp
* 91998 104359: contig of 12362 bp in length
* 104360 104459: gap of 100 bp
* 104460 124116: contig of 19657 bp in length
* 124117 124216: gap of 100 bp
* 124217 157504: contig of 33288 bp in length.

FEATURES
source
Location/Qualifiers
1. .157504
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-44114"
/clone_11b="RP11-11 Human Male BAC"
1. .1398
/note="assembly_fragment"
1499. .2569
/note="assembly_fragment"
2670. .3715
/note="assembly_fragment"
3816. .4982
/note="assembly_fragment"
5083. .7548
/note="assembly_fragment"
7649. .8855
/note="assembly_fragment"
8956. .10690
/note="assembly_fragment"
10791. .12073
/note="assembly_fragment"
12174. .14379
/note="assembly_fragment"
14480. .17943
/note="assembly_fragment"
18044. .21826
/note="assembly_fragment"
21927. .27359
/note="assembly_fragment"
27460. .30113
/note="assembly_fragment"
clone_end:T7
vector_side:left"
30214. .35192
/note="assembly_fragment"
35293. .41089
/note="assembly_fragment"
41190. .46410
/note="assembly_fragment"
46511. .52192
/note="assembly_fragment"
52293. .60495
/note="assembly_fragment"
60596. .68130
/note="assembly_fragment"
68231. .74245
/note="assembly_fragment"
74346. .82056
/note="assembly_fragment"
82157. .91897
/note="assembly_fragment"
91998. .104359
/note="assembly_fragment"
104460. .124116
/note="assembly_fragment"
124217. .157504
/note="assembly_fragment"
clone_end:SP6
vector_side:left"

ORIGIN
Query Match 2.2%; Score 41; DB 2; Length 157504;
Best Local Similarity 100.0%; Pred.No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1521 GAGACGAGGACAGTGGCTACACCTGTATATCCAGACACTT 1561
DB 45859 GAGACGAGGACAGTGGCTACACCTGTATATCCAGACACTT 45899
RESULT 63

AC147284 161251 bp DNA linear HTG 07-NOV-2003
 LOCUS Pan troglodytes chromosome UNK clone RP43-81H17, *** SEQUENCING IN
 DEFINITION PROGRAMS ***, 32 unordered pieces.
 AC147284
 AC147284.1 GI:38198822
 VERSION HTG; HTGS_PHASE1.
 KEYWORDS Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 1 (bases 1 to 161251)
 Wilson, R.K.
 The sequence of Pan troglodytes clone
 Unpublished
 2 (bases 1 to 161251)
 Wilson, R.K.
 Direct Submission
 Submitted (07-NOV-2003) Genetics, Genome Sequencing Center, 4444
 Forest Park Parkway, St. Louis, MO 63108, USA
 COMMENT
 ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submissions@wustl.edu
 ----- Project Information -----
 Center project name: C_PT081H17
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 32 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of 'N', but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 1502: contig of 1502 bp in length
 * 1503 1602: gap of unknown length
 * 1603 3113: contig of 1511 bp in length
 * 3114 3213: gap of unknown length
 * 3214 4285: contig of 1072 bp in length
 * 4286 4385: gap of unknown length
 * 4386 6085: contig of 1700 bp in length
 * 6086 6185: gap of unknown length
 * 6186 7615: contig of 1430 bp in length
 * 7616 7715: gap of unknown length
 * 7716 9203: contig of 1487 bp in length
 * 9203 9302: gap of unknown length
 * 9303 11567: contig of 2265 bp in length
 * 11568 11667: gap of unknown length
 * 11668 14947: contig of 3280 bp in length
 * 14948 15047: gap of unknown length
 * 15048 17560: contig of 2513 bp in length
 * 17561 17660: gap of unknown length
 * 17661 19904: contig of 2244 bp in length
 * 19905 20004: gap of unknown length
 * 20005 23814: contig of 3810 bp in length
 * 23815 23914: gap of unknown length
 * 23915 27270: contig of 3356 bp in length
 * 27271 27370: gap of unknown length
 * 27371 31537: contig of 4167 bp in length
 * 31538 31637: gap of unknown length
 * 31638 34389: contig of 2752 bp in length
 * 34390 34489: gap of unknown length
 * 34490 38795: contig of 4306 bp in length
 * 38796 38895: gap of unknown length
 * 38896 43707: contig of 4812 bp in length
 * 43708 43807: gap of unknown length
 * 43808 48001: contig of 4194 bp in length
 * 48002 48101: gap of unknown length
 * 48102 51182: contig of 5081 bp in length
 * 51183 53282: gap of unknown length

FEATURES
 source
 * 53283 57687: contig of 4405 bp in length
 * 57688 57787: gap of unknown length
 * 57788 62026: contig of 4239 bp in length
 * 62027 62126: gap of unknown length
 * 62127 68654: contig of 6528 bp in length
 * 68655 68754: gap of unknown length
 * 68755 74806: contig of 6032 bp in length
 * 74807 74906: gap of unknown length
 * 74907 82737: contig of 7831 bp in length
 * 82738 82837: gap of unknown length
 * 82838 91224: contig of 8387 bp in length
 * 91225 91325: gap of unknown length
 * 91326 9443: contig of 8119 bp in length
 * 9444 99543: gap of unknown length
 * 99544 108161: contig of 8618 bp in length
 * 108162 108262: gap of unknown length
 * 108263 117841: contig of 9580 bp in length
 * 117842 117941: gap of unknown length
 * 117942 126968: contig of 9027 bp in length
 * 126969 127068: gap of unknown length
 * 127069 138945: contig of 11877 bp in length
 * 138946 139046: gap of unknown length
 * 139047 158658: contig of 19613 bp in length
 * 158659 158758: gap of unknown length
 * 158759 159883: contig of 1125 bp in length
 * 159884 161251: gap of unknown length
 * 159984 161251: contig of 1268 bp in length.
 Location/Qualifiers
 1..161251
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /chromosome="UNK"
 /clone="RP43-81H17"
 1..1502
 /note="assembly_name:Contig12"
 1603..3113
 /note="assembly_name:Contig15"
 3214..4285
 /note="assembly_name:Contig23"
 4386..6085
 /note="assembly_name:Contig25"
 6186..7615
 /note="assembly_name:Contig26"
 7716..9202
 /note="assembly_name:Contig27"
 9303..11567
 /note="assembly_name:Contig28"
 11668..14947
 /note="assembly_name:Contig29"
 15048..17560
 /note="assembly_name:Contig30"
 17661..23814
 /note="assembly_name:Contig31"
 23915..27270
 /note="assembly_name:Contig32"
 27371..31537
 /note="assembly_name:Contig33"
 31638..34389
 /note="assembly_name:Contig34"
 34490..38795
 /note="assembly_name:Contig35"
 38896..43707
 /note="assembly_name:Contig36"
 43808..48001
 /note="assembly_name:Contig37"
 48102..51182
 /note="assembly_name:Contig38"
 51183..53282
 /note="assembly_name:Contig39"
 53283..57687
 /note="assembly_name:Contig40"
 57688..62026
 /note="assembly_name:Contig41"
 62027..68654
 /note="assembly_name:Contig42"
 68655..74806
 /note="assembly_name:Contig43"
 74807..74906
 /note="assembly_name:Contig44"
 74907..82737
 /note="assembly_name:Contig45"
 82738..82837
 /note="assembly_name:Contig46"
 82838..91224
 /note="assembly_name:Contig47"
 91225..91325
 /note="assembly_name:Contig48"
 91326..9443
 /note="assembly_name:Contig49"
 9444..99543
 /note="assembly_name:Contig50"
 99544..108161
 /note="assembly_name:Contig51"
 108162..108262
 /note="assembly_name:Contig52"
 108263..117841
 /note="assembly_name:Contig53"
 117842..117941
 /note="assembly_name:Contig54"
 117942..126968
 /note="assembly_name:Contig55"
 126969..127068
 /note="assembly_name:Contig56"
 127069..138945
 /note="assembly_name:Contig57"
 138946..139046
 /note="assembly_name:Contig58"
 139047..158658
 /note="assembly_name:Contig59"
 158659..158758
 /note="assembly_name:Contig60"
 158759..159883
 /note="assembly_name:Contig61"
 159884..161251
 /note="assembly_name:Contig62"
 161252..161251: contig of 1268 bp in length.

misc_feature /note="assembly_name:Contig41"
62127..66854
/note="assembly_name:Contig42"
misc_feature /note="assembly_name:Contig43"
68755..74806
/note="assembly_name:Contig43"
74907..82737
/note="assembly_name:Contig44"
misc_feature /note="assembly_name:Contig45"
82838..91224
/note="assembly_name:Contig45"
91325..99443
/note="assembly_name:Contig46"
misc_feature /note="assembly_name:Contig47"
99544..108161
/note="assembly_name:Contig47"
108262..117841
/note="assembly_name:Contig48"
misc_feature /note="assembly_name:Contig48"
117942..126968
/note="assembly_name:Contig49"
misc_feature /note="assembly_name:Contig50"
127069..138945
/note="assembly_name:Contig51"
139046..158658
/note="assembly_name:Contig51"
misc_feature /note="assembly_name:Contig51"
158759..159883
/note="assembly_name:Contig51"
159884..161251
/note="assembly_name:Contig51"
misc_feature /note="assembly_name:Contig51"
159884..161251
/note="assembly_name:Contig51"

ORIGIN
Query Match 2.2%; Score 41; DB 2; Length 161251;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1521 GAGACGAGGCTCACCTGTATCCGACCTTGGGAG 1561
Db 150764 GAGACGAGGCTCACCTGTATCCGACCTTGGGAG 150804

RESULT 64
AC027121 162771 bp DNA linear PRI 02-AUG-2000
LOCUS Homo sapiens chromosome 3 clone RP11-25C11 map 3p, complete
DEFINITION sequence.
AC027121
VERSION AC027121.5 GI:9653120
KEYWORDS HTG
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Wu, Q., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, G., Li, W., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.
Chromosome 3p genomic sequence
Unpublished
2 (bases 1 to 162771)
JOURNAL
REFERENCE
AUTHORS Kang, N., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, W., Li, L., Feng, X., Yu, J. and Yang, H.
Direct Submission
Submitted (28-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P. R. China
3 (bases 1 to 162771)

AUTHORS Wu, Q., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, G., Li, W., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.
Direct Submission
Submitted (02-AUG-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P. R. China
On Aug 2, 2000 this sequence version replaced gi:8101165.

COMMENT -----Genome Center
Center: Beijing Center
Center code: Beijing
Website: http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgsc@igtp.ac.cn
----- Project Information
Center project name: 13 project
Center clone name: RP11-25C11
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 5% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 165893 bases at least Q40
Consensus quality: 165987 bases at least Q30
Consensus quality: 166025 bases at least Q20
Insert size: 162771; sum-of-contrigs
Quality coverage: 11.38x in Q20 bases; sum-of-contrigs

FEATURES
source
Location/Qualifiers
1..162771
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-25C11"

ORIGIN
Query Match 2.2%; Score 41; DB 9; Length 162771;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1521 GAGACGAGGCTCACCTGTATCCGACCTT 1561
Db 75726 GAGACGAGGCTCACCTGTATCCGACCTT 75766

RESULT 65
AC012567 163157 bp DNA linear HTG 24-AUG-2002
LOCUS Homo sapiens chromosome 3 clone RP11-53F7 map 3, WORKING DRAFT
DEFINITION SEQUENCE. 7 unordered pieces.
AC012567
AC012567.3 GI:8072484
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
2 (bases 1 to 163157)
JOURNAL
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,

TITLE
JOURNAL
REFERENCE
AUTHORS

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gage, D.,
Galligan, J., Gargy, S., Grant, C., Hago, B., Heaford, A., Horton, L.,
Howard, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Liu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melidrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (30-Oct-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 163157)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Balwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouknight, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choe, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galligan, J., Gargy, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hago, B., Heaford, A., Horton, L.,
Howard, J., Iley, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Lacroque, K., Lamazares, R., Lander, E., Lehoczky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,
Melidrim, J., Menus, L., Mihov, T., Miranda, C., Mlenka, J., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trifoglio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

TITLE
JOURNAL
COMMENT

Submitted (24-Aug-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced g117657782.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project information

Center project name: L2013

Center clone name: 53 F 7

Sequencing vector: M13, M7815, 100% of reads

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 159367 bases at least Q40

Consensus quality: 159342 bases at least Q30

Consensus quality: 16162 bases at least Q20

Insert size: 21000; agarose-efp

Insert size: 162557; sum-of-coverage

Quality coverage: 3.8 in Q20 bases; agarose-efp

Quality coverage: 4.9 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 2124: contig of 2124 bp in length

FEATURES

source

2125 2224: gap of 100 bp
2225 8840: contig of 6616 bp in length
2226 8841 8941: gap of 100 bp
2227 8841 18299: contig of 9359 bp in length
2228 18300 18301: gap of 100 bp
2229 18301 18302: gap of 16153 bp in length
2230 18302 3453: gap of 100 bp
2231 3453 3454: gap of 100 bp
2232 3454 51735: contig of 17083 bp in length
2233 51735 51736: gap of 100 bp
2234 51736 82945: contig of 31110 bp in length
2235 82945 83045: gap of 100 bp
2236 83045 83046: gap of 100 bp
2237 83046 163157: contig of 80112 bp in length.

Location/Qualifiers

1. 163157

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="3"

/map="3"

/clone="RP11-53F7"

/clone_lib="RP11-11 Human Male BAC"

1. 2124

/note="assembly_fragment"

2225. 8840

/note="assembly_fragment"

clone_end:SP6

vector_side:right"

/note="assembly_fragment"

8941. 18299

/note="assembly_fragment"

18400. 3453

/note="assembly_fragment"

3453. 51735

/note="assembly_fragment"

51735. 82945

/note="assembly_fragment"

83046. 163157

/note="assembly_fragment"

vector_side:right"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 166-10;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1521 GAGACGACGACAGTGGCTCAGACCTGTATCCACACTT 1561

Db 92576 GAGACGACGACAGTGGCTCAGACCTGTATCCACACTT 92616

RESULT 66

AC026165

LOCUS

DEFINITION

AC026165

VERSION

KEYWORDS

SOURCE

ORGANISM

HTG

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 166338)

REFERENCE

AUTHORS

Wu, Q., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, G., Chen, J., Ding, H.,
Dong, W., Fan, H., Fang, X., Gong, J., Guan, O., Gu, X., Guo, D., He, L.,
Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G., Li, J., Li, W.,
Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W.,
Li, Y., Luo, D., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M.,
Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, L.,
Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Bao, J., Xie, F.,
Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G.,
Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X.,
Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

```

TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 166338)
Wang,R., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,M., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.
Direct Submission
Submitted (21-MAR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
3 (bases 1 to 166338)
Wu,Q., Bao,Q., Bao,W., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,G.,
Li,L., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,W., Li,Y., Luo,J., Niu,Y., Qiu,Q., Qiu,X., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (02-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
4 (bases 1 to 166338)
Wu,Q., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L.,
Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,D.,
Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,Y., Luo,J., Niu,Y., Qiu,Q., Qiu,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Bao,J., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (16-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
5 (bases 1 to 166338)
Wu,Q., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L.,
Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,D.,
Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,Y., Luo,J., Niu,Y., Qiu,Q., Qiu,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Bao,J., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (17-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Aug 16, 2000 this sequence version replaced gi:19653118.
-----Genome Center
Center:Beijing Center
Website:http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgsc@igtp.ac.cn
-----Project Information
Center project name:11 project
Center clone name: RP11-124L8
-----Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990325

```

```

Consensus quality: 166323 bases at least Q40
Consensus quality: 16906 bases at least Q30
Consensus quality: 169276 bases at least Q20
Insert size: 166338; sum-of-ctrls
Quality coverage: 11.33x in Q20 bases; sum-of-ctrls
-----
Location/Qualifiers
1. 166338
/organism="Homo sapiens"
/mol_type="genomic DNA"
/ID_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-124L8"

```

```

ORIGIN
Query Match 2.2%; Score 41; DB 9; Length 166338;
Best Local Similarity 100.0%; Pred.No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1521 GAGACGAGGACAGTGGCTCACACCTGTATCCACGACACTT 1561
Db 132297 GAGACGAGGACAGTGGCTCACACCTGTATCCACGACACTT 132337

```

```

RESULT 67
AC073363
LOCUS
DEFINITION
Homo sapiens 3 BAC RP11-293N1 (Roswell Park Cancer Institute Human
BAC library) complete sequence.
AC073363
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
1 (bases 1 to 184092)
Muzny,D.M., Adams,C., Adio-Oduola,B., All-ouman,F.R., Allen,C.,
Alsbrooks,S.L., Anarlunga,H.C., Are,J.R., Banks,T., Barbetta,J.,
Benton,D., Bimaga,K., Blankenburg,K., Bonin,D., Bouck,J.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burck,P., Burckett,C., Burrell,K.L., Byrd,N.C., Cartron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Donthwaite,K.J., Diaper,H.,
Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C.,
Elhai,C., Becotto,M., Falls,T., Ferrazuto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Geo,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A.,
He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
Holloway,C., Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudas,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J.,
Kovar,C., Krawiec,J., Kureishi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Luiseger,H., Lozano,R.U., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawliny,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabac,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Niedero,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M.,
Rojae,A., Rojudoakan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S.,
Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,B.,
Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Sytek,A.,
Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telrod,B., Thomas,N., Thomas,S., Umanal,K., Vasquez,L.,

```

<http://gc.bcm.tmc.edu/quality/info/genbank.annotation.html>.

Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Naylor, S. L., Weinstein, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 184092)
Worley, K. C.

Direct Submission
Submitted (15-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184092)
Worley, K. C.

Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 184092)
Worley, K. C.

Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 184092)
Worley, K. C.

Direct Submission
Submitted (01-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 184092)
Worley, K. C.

Direct Submission
Submitted (29-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 23, 2002 this sequence version replaced gi:117933800.
INFORMATION: <http://www.hgsc.bcm.tmc.edu> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at <http://www.hgsc.bcm.tmc.edu/quality/info/genbank.annotation.html>.

FEATURES	QUALSTAT	REPORT
source	location/Qualifiers	1..184092
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
	/chromosome="3"	
	/clone="RP11-293N1"	
	/complement(1..20306)	
	/note="overlaps bases 1..2005 of clone AC079847"	
	/function="clone overlap"	
misc_feature	/complement(82..435)	
repeat_region	/rpt_family="LIPAV"	
repeat_region	/complement(647..712)	
repeat_region	/rpt_family="MIR"	
repeat_region	/complement(1092..1512)	
repeat_region	/rpt_family="MSTB"	
repeat_region	2757..2975	
repeat_region	/rpt_family="MIR"	
repeat_region	/complement(2981..3357)	
repeat_region	/rpt_family="MSTA"	
repeat_region	5345..5418	
repeat_region	/rpt_family="TTCA)n"	
repeat_region	6126..6170	
repeat_region	/rpt_family="TG)n"	
repeat_region	/complement(6470..6594)	
repeat_region	/rpt_family="L2"	
repeat_region	7183..7356	
repeat_region	/rpt_family="MIR"	
repeat_region	7471..7691	
repeat_region	/rpt_family="MIR"	
repeat_region	/complement(8404..8558)	
repeat_region	/rpt_family="MIR"	
repeat_region	9804..9925	
repeat_region	/rpt_family="MERSA"	
STS	10519..10797	
repeat_region	/standard_name="136095"	
repeat_region	11579..11654	
repeat_region	/rpt_family="GA-rich"	
repeat_region	11958..12011	
repeat_region	/rpt_family="GC-rich"	
repeat_region	12802..12842	
repeat_region	/rpt_family="TTCC)n"	
repeat_region	13425..13450	
repeat_region	/rpt_family="GC-rich"	
repeat_region	14170..14194	
repeat_region	/rpt_family="TTCA)n"	
repeat_region	14219..14263	
repeat_region	/rpt_family="(TTCA)n"	
repeat_region	/complement(16760..16856)	
repeat_region	/rpt_family="MIR"	
repeat_region	19107..19148	
repeat_region	/rpt_family="AT-rich"	
repeat_region	19795..19936	
repeat_region	/rpt_family="MIR"	
repeat_region	/complement(19950..20360)	
repeat_region	/rpt_family="L2"	
repeat_region	20361..20543	
repeat_region	/rpt_family="Charlie1"	
repeat_region	20540..20977	
repeat_region	/rpt_family="Charlie1"	
repeat_region	21241..21541	
repeat_region	/rpt_family="Alusx"	
repeat_region	/complement(21880..21995)	
repeat_region	/rpt_family="MER2"	
repeat_region	/complement(22155..22217)	
repeat_region	/rpt_family="MERSB"	
repeat_region	/complement(22402..22762)	
repeat_region	/rpt_family="MLT1A1"	
repeat_region	23234..23528	
repeat_region	/rpt_family="Alusx"	

repeat_region 26030..26299
/rpt_family="L2"
repeat_region 27254..27306
/rpt_family="MIR"
repeat_region 28688..28747
/rpt_family="L2"
repeat_region 29227..29310
/rpt_family="CT-rich"

Query Match 2.2%; Score 41; DB 9; Length 184092;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGGACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 43491 GAGACCGGACAGTGGCTCACACCTGTATCCGACACTT 43531

RESULT 68
AC024171/ 208881 bp DNA linear PRI 08-NOV-2002
LOCUS Homo sapiens chromosome 3 clone RP11-794G3 map 3p, complete
DEFINITION
AC024171
VERSION
AC024171.5 GI:24270682
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 208881)
Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, G.,
Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L.,
Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,
Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X.,
Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X.,
Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, L., Zhang, M.,
Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,
Yu, J. and Yang, H.

TITLE
JOURNAL
Unpublished
Chromosome 3p genomic sequence

2 (bases 1 to 208881)
Liu, Y., Hu, S., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Wang, X., Cheng, C., Wang, Y.,
Liu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, B., Fan, H.,
Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L.,
Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L.,
Feng, X., Yu, J. and Yang, H.
Direct Submission
Submitted (25-FEB-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China

TITLE
JOURNAL
Unpublished
Chromosome 3p genomic sequence

3 (bases 1 to 208881)
Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G.,
Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W.,
Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L., Song, S., Sun, M.,
Sun, Y., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, L.,
Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F.,
Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G.,
Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X.,
Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.
Direct Submission
Submitted (09-OCT-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China
4 (bases 1 to 208881)
Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G.,
Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W.,
Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L., Song, S., Sun, M.,
Sun, Y., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, L.,
Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F.,
Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G.,
Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X.,
Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

TITLE
JOURNAL
Submitted (13-OCT-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China
5 (bases 1 to 208881)
Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C.,
Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L.,
Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,
Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y.,
Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B.,
Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M.,
Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,
Yu, J. and Yang, H.

TITLE
JOURNAL
Submitted (23-OCT-2002) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China
6 (bases 1 to 208881)
Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C.,
Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L.,
Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,
Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y.,
Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B.,
Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M.,
Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,
Yu, J. and Yang, H.

TITLE
JOURNAL
Submitted (08-NOV-2002) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P. R. China
On Oct 23, 2002 this sequence version replaced gi:10719851.

-----Genome Center
Center: Beijing Center
Center code: Beijing
Website: http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgsc@igtp.ac.cn
-----Project Information
Center project name: 1% project
Center clone name: RP11-794G3
-----Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 212441 bases at least Q40
Consensus quality: 212441 bases at least Q40
Consensus quality: 212735 bases at least Q20
Insert size: 208881; sum-of-contrigs
Quality coverage: 9.75x in Q20 bases; sum-of-contrigs

FEATURES
SOURCE
1. 208881
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-794G3"

ORIGIN

Query Match 2.2%; Score 41; DB 9; Length 208881;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACGAGCAGAGTGCTCACACTGTATCCAGCACTT 1561
 |||
 DB 187874 GAGACGAGCAGAGTGCTCACACTGTATCCAGCACTT 187834

RESULT 69
 AL354652 226572 bp DNA linear HTG 24-AUG-2000
 LOCUS Homo sapiens chromosome X clone RP11-368D24, WORKING DRAFT
 DEFINITION
 SEQUENCE
 AL354652.1 GI:9581622
 ACCESSION
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 XKEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Wilson, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jul 28, 2000 this sequence version replaced gi:9501193.

COMMENT
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA368D24
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye 3; 87% of reads
 Chemistry: Dye-terminator Big Dye 3; 87% of reads
 quality: 225240 bases at least Q40
 Consensus quality: 225683 bases at least Q30
 Consensus quality: 225849 bases at least Q20
 Insert size: 226572; sum-of-contigs
 Insert size: 229844; 7.6% error; agarose-fp
 Quality coverage: 7.84x in Q20 bases; sum-of-contigs Quality
 Coverage: 7.73x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 226572: contig of 226572 bp in length.
 Location/Qualifiers
 1..226572
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="X"
 /clone_1id="RP11-368D24"
 /clone_1id="RP11-368D24"
 1..226572
 /note="assembly_fragment:03393
 clone_end:T7
 vector_side:right"

misc_feature
 misc_feature

ORIGIN

Query Match 2.2%; Score 41; DB 2; Length 226572;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACGAGCAGAGTGCTCACACTGTATCCAGCACTT 1561
 |||
 DB 50268 GAGACGAGCAGAGTGCTCACACTGTATCCAGCACTT 50228

RESULT 70
 HSE129H9 37170 bp DNA linear PRI 04-MAR-2003
 LOCUS Human DNA sequence from clone LL22NC01-129H9 on chromosome 22,
 complete sequence.
 DEFINITION
 SEQUENCE
 HSE129H9 37170 bp DNA linear PRI 04-MAR-2003
 ACCESSION
 HTG. 268224.1 GI:1122885
 XKEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Hunt, S.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep/LL22NC01-129H9
 is from the human chromosome 22-specific conoid library LL22NC01,
 constructed at the Biomedical Sciences Division, Lawrence Livermore
 National Laboratory, Livermore, CA 94550 under the auspices of the
 National Laboratory Gene Library Project sponsored by the US
 Department of Energy. The source of the flow sorted chromosomes
 was a human/hamster hybrid containing chromosomes Y, 22 and 9.
 VECTOR: lawr16

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk

* This sequence was finished as follows unless otherwise noted: all
 * regions were either double-stranded or sequenced with an alternate
 * chemistry or covered by high quality data (i.e., phred quality >= 30);
 * an attempt was made to resolve all sequencing problems, such
 * as compressions and repeats; all regions were covered by at least
 * one plasmid subclone or more than one M13 subclone; and the
 * assembly was confirmed by restriction digest, except on the rare
 * occasion of the clone being a YAC.
 * This sequence was generated from part of bacterial clone contigs of
 * human chromosome 22, constructed by the Sanger Centre Chromosome 22
 * Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr22.
 Location/Qualifiers
 1..37170
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="22"
 /clone_1id="LL22NC01-129H9"
 /clone_1id="LL22NC01"

ORIGIN

Query Match 2.2%; Score 40; DB 9; Length 37170;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCACCCTGTATCCAGACTT 1561
Db AGACGAGGACAGTGGCTCACCCTGTATCCAGACTT 3959

RESULT 71 AC135786 39400 bp DNA linear HTG 22-OCT-2002
LOCUS Homo sapiens chromosome 16 clone CTD-3160F3, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
AC135786
AC135786.1 GI:24211106
VERSION HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1 (bases 1 to 39400)
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 16
AUTHORS 2 (bases 1 to 39400)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
AUTHORS Submitted (22-OCT-2002) Production Sequencing Facility, DOE Joint
TITLE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL

COMMENT Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 917592
Center clone name: CITB-E1_3160F3

Summary Statistics
Consensus quality: 37563 bases at least Q40
Consensus quality: 38007 bases at least Q30
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 39200; sum-of-coverage estimation
Quality coverage: 14.17 in Q20 bases; agarose-fp estimation
Quality coverage: 57.83 in Q20 bases; sum-of-coverage estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1105: contig of 1105 bp in length
1106 1205: gap of unknown length
1206 2818: contig of 1613 bp in length
2819 2918: gap of unknown length
2919 39400: contig of 36482 bp in length.

FEATURES
source
1. 39400
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTD-3160F3"
/clone_lib="Caltech human BAC library D"

ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 39400;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACGAGGACAGTGGCTCACCCTGTATCCAGACTT 1560
Db GAGACGAGGACAGTGGCTCACCCTGTATCCAGACTT 7688

RESULT 72 AC036154 55100 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens chromosome 17, clone RP11-346N15, complete sequence.
AC036154
AC036154.1 GI:18855116
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS 1 (bases 1 to 55100)
TITLE Homo sapiens chromosome 17, clone RP11-346N15
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 55100)
TITLE Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Boguslavsky, L., Bouckgeater, B., Brown, A., Burkett, G.,
Campiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hago, B., Heald, R., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kam, L., Karakas, A.,
Klein, J., Larocque, K., Lamazares, R., Lander, E., Lehoczy, J.,
Levine, R., Liu, G., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeckers, R.,
Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Miya, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teefave, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

REFERENCE Direct Submission
JOURNAL Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 55100)

REFERENCE Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckgeater, B.,
Brown, A., Camarata, J., Campiano, A., Chang, J., Chararo, B.,
Choquet, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamak, A., Karakas, A., Kells, C., Labocque, K., Lamazares, R.,
Lander, E., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneses, L., Mihova, T.,
Miyata, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Roselli, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Stratus, N., Subramanian, A., Talamas, J., Teefave, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 55100)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguski, J., Bouckgeater, B.,
 Brown, A., Camarero, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choquet, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
 Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Fato, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karas, A., Kelle, C., Larocque, K., Lamazares, R.,
 Landers, T., Lechoczy, J., Levine, R., Liu, G., Maclean, C.,
 Macdonald, P., Major, J., Margus, N., Matthews, C., McCarthy, M.,
 McKernan, P., McKernan, K., Meidrim, U., Menais, L., Mihova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppback, R., Seaman, S.,
 Severy, P., Spencer, B., Stange, Thomas, N., Stefany, S., Theodore, J.,
 Strauss, N., Sudramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
 Viet, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (21-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 21, 2002 this sequence version replaced g11863526.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L9091

Center clone name: 346_N_15

Only the first 55.1 kilobases of this clone are being submitted.
 The remainder overlaps AC005207 (WICKR project L329).

FEATURES

source

1. 55100

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="17"

/map="17"

/clone="RP11-346N15"

/clone_1lb="RP11-11 Human Male BAC"

repeat_region complement(922..1094)

repeat_region /rpt_family="AluSg/X"

repeat_region complement(1096..1346)

repeat_region /rpt_family="AluSg"

repeat_region complement(1831..2101)

repeat_region /rpt_family="AluUo"

repeat_region 2496..2804

repeat_region /rpt_family="AluSg"

repeat_region complement(3607..3953)

repeat_region /rpt_family="HALLb"

repeat_region complement(3951..4012)

repeat_region /rpt_family="L1MB8"

repeat_region 4426..4460

repeat_region /rpt_family="AT_rich"

repeat_region complement(5087..5251)

repeat_region /rpt_family="Char11e1"

repeat_region complement(5256..5390)

repeat_region /rpt_family="L1MB7"

repeat_region complement(5393..5558)

repeat_region /rpt_family="Char11e1"

repeat_region 5569..6339

repeat_region /rpt_family="L1MEC"

repeat_region 6344..6581

repeat_region /rpt_family="AluU" complement(6582..6606)
 repeat_region /rpt_family="L1M4" complement(6607..6883)
 repeat_region /rpt_family="AluSg" complement(6884..7031)
 repeat_region /rpt_family="L1M4" complement(7097..7397)
 repeat_region /rpt_family="AluUo" complement(7428..7785)
 repeat_region /rpt_family="L1PAL4" 8150..8450
 repeat_region /rpt_family="AluSg" 8466..8755
 repeat_region /rpt_family="AluSg" complement(9228..9525)
 repeat_region /rpt_family="AluY" 9633..9766
 repeat_region /rpt_family="FLAM_A" complement(10030..10263)
 repeat_region /rpt_family="L1PAL3" complement(10264..10559)
 repeat_region /rpt_family="AluY" complement(10560..10600)
 repeat_region /rpt_family="L1PAL3" complement(10614..10918)
 repeat_region /rpt_family="AluSg" 11008..11336
 repeat_region /rpt_family="AluSg" 11372..11680
 repeat_region /rpt_family="AluSg" complement(12024..12154)
 repeat_region /rpt_family="FLAM_C" 12365..13015 (ATTG)n
 repeat_region /rpt_family="AluY" complement(13016..13300)
 repeat_region /rpt_family="AluSg" 13744..13767
 repeat_region /rpt_family="AT_rich" 14067..14238
 repeat_region /rpt_family="AluYa5" complement(14915..14961)
 repeat_region /rpt_family="MER3" complement(14962..15275)
 repeat_region /rpt_family="AluY" complement(15278..15562)
 repeat_region /rpt_family="AluUo" complement(15563..15690)
 repeat_region /rpt_family="MER3" 16113..16139
 repeat_region /rpt_family="AT_rich" 16177..16475
 repeat_region /rpt_family="AluUo" 17077..17378
 repeat_region /rpt_family="AluSg" complement(17741..18037)
 repeat_region /rpt_family="L12" complement(18648..18797)
 repeat_region /rpt_family="L1MC4a" complement(18798..19100)
 repeat_region /rpt_family="AluY" complement(19101..19133)

Query Match

Best Local Similarity 100.0%; Pred.No.5.4e-10;

Matches 40; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

DB 15522 AGACGAGCAGTGTCTCACACCTGTATCCGACACTT 1561

DB 15563 AGACGAGCAGTGTCTCACACCTGTATCCGACACTT 15524

RESULT 73

AC015782/c
 LOCUS AC015782 59903 bp DNA linear HTG 06-JAN-2001
 DEFINITION Homo sapiens clone RP11-207, LOW-PASS SEQUENCE SAMPLING.
 ACCESSION AC015782.5 GI:12043617
 VERSION AC015782.5
 KEYWORDS HTG; PHASEO.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 59903)
 Birten,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens, clone RP11-207
 Unpublished
 2 (bases 1 to 59903)
 Birten,B., Linton,L., Nusbaum,C., Bender,E., Allen,N., Anderson,M.,
 Baldwin,J., Barna,N., Beckert,R., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Castle,A., Colangelo,N., Collins,S., Colymore,A.,
 Cooke,P., Dearrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Lebecky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
 McMan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
 Morron,J., Naylor,U., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Teefaye,S., Turrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 6, 2001 this sequence version replaced gi:11120869.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information
 Center project name: L1537
 Center clone name: 2_J_7

 * NOTE: This record contains 74 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.
 * 1
 * 724 823: contig of 723 bp in length
 * 824 823: gap of 100 bp
 * 1546 1545: contig of 722 bp in length
 * 1646 1645: gap of 100 bp
 * 2346 2345: contig of 700 bp in length
 * 2446 2445: gap of 100 bp
 * 3162 3161: contig of 716 bp in length
 * 3262 3261: gap of 100 bp
 * 3992 3991: contig of 731 bp in length
 * 4092 4091: gap of 100 bp
 * 4784 4783: contig of 692 bp in length
 * 4785 4784: gap of 100 bp
 * 4885 4884: gap of 100 bp
 * 5589 5588: contig of 705 bp in length
 * 5690 5689: gap of 100 bp
 * 6391 6390: contig of 702 bp in length
 * 6491 6490: gap of 100 bp
 * 6492 7200: contig of 709 bp in length

7201 7300: gap of 100 bp
 7301 8009: contig of 709 bp in length
 8010 8109: gap of 100 bp
 8110 8832: contig of 723 bp in length
 8833 8932: gap of 100 bp
 8933 9620: contig of 688 bp in length
 9621 9720: gap of 100 bp
 9721 10401: contig of 681 bp in length
 10402 10501: gap of 100 bp
 10502 11217: contig of 716 bp in length
 11218 11317: gap of 100 bp
 11318 12017: contig of 700 bp in length
 12018 12117: gap of 100 bp
 12118 12785: contig of 668 bp in length
 12786 12885: gap of 100 bp
 12886 13598: contig of 713 bp in length
 13599 13698: gap of 100 bp
 13699 14398: contig of 700 bp in length
 14399 14498: gap of 100 bp
 14499 15208: contig of 710 bp in length
 15309 15308: gap of 100 bp
 15309 16010: contig of 702 bp in length
 16011 16110: gap of 100 bp
 16111 16828: contig of 718 bp in length
 16829 16928: gap of 100 bp
 16929 17624: contig of 696 bp in length
 17625 17724: gap of 100 bp
 17725 18443: contig of 719 bp in length
 18444 18543: gap of 100 bp
 18544 19267: contig of 724 bp in length
 19268 19367: gap of 100 bp
 19368 20074: contig of 707 bp in length
 20075 20174: gap of 100 bp
 20175 20870: contig of 696 bp in length
 20871 21672: contig of 702 bp in length
 20971 21772: gap of 100 bp
 21673 22487: contig of 715 bp in length
 22488 22587: gap of 100 bp
 22588 23289: contig of 702 bp in length
 23290 23389: gap of 100 bp
 23390 24107: contig of 718 bp in length
 24108 24207: gap of 100 bp
 24208 24972: contig of 765 bp in length
 24973 25072: gap of 100 bp
 25073 25785: contig of 713 bp in length
 25786 25885: gap of 100 bp
 25886 26591: contig of 706 bp in length
 26592 27400: contig of 709 bp in length
 27401 27500: gap of 100 bp
 27501 28190: contig of 690 bp in length
 28191 28290: gap of 100 bp
 28291 28989: contig of 693 bp in length
 28990 29089: gap of 100 bp
 29090 29791: contig of 702 bp in length
 29792 29891: gap of 100 bp
 29892 30640: contig of 749 bp in length
 30641 30740: gap of 100 bp
 30741 31471: contig of 731 bp in length
 31472 31571: gap of 100 bp
 31572 32298: contig of 727 bp in length
 32299 32398: gap of 100 bp
 32399 33105: contig of 707 bp in length
 33106 33205: gap of 100 bp
 33206 33925: contig of 720 bp in length
 33926 34025: gap of 100 bp
 34026 34747: contig of 722 bp in length
 34748 34847: gap of 100 bp
 34848 35553: contig of 706 bp in length
 35554 36345: gap of 100 bp
 36345 36445: contig of 692 bp in length
 36446 36445: gap of 100 bp

```

* 36446 37142: contig of 697 bp in length
* 37143 37242: gap of 100 bp
* 37243 37545: contig of 703 bp in length
* 37946 38045: gap of 100 bp
* 38046 38783: contig of 738 bp in length
* 38784 38883: gap of 100 bp
* 38884 39581: contig of 698 bp in length
* 39582 39681: gap of 100 bp
* 39682 40411: contig of 730 bp in length
* 40412 40511: gap of 100 bp
* 40512 41219: contig of 708 bp in length
* 41220 41319: gap of 100 bp
* 41320 42018: contig of 699 bp in length
* 42019 42118: gap of 100 bp
* 42119 42818: contig of 700 bp in length
* 42819 42918: gap of 100 bp
* 42919 43606: contig of 688 bp in length
* 43607 43706: gap of 100 bp
* 43707 44428: contig of 722 bp in length
* 44429 44528: gap of 100 bp
* 44529 45263: contig of 735 bp in length
* 45264 45363: gap of 100 bp
* 45364 46051: contig of 688 bp in length
* 46052 46151: gap of 100 bp
* 46152 46856: contig of 705 bp in length
* 46857 46956: gap of 100 bp
* 46957 47687: contig of 731 bp in length
* 47688 47788: gap of 100 bp
* 47789 48504: contig of 717 bp in length
* 48505 48604: gap of 100 bp
* 48605 49329: contig of 725 bp in length
* 49330 49429: gap of 100 bp
* 49430 50135: contig of 706 bp in length
* 50136 50235: gap of 100 bp
* 50236 50930: contig of 695 bp in length
* 50931 51030: gap of 100 bp
* 51031 51716: contig of 686 bp in length
* 51717 51816: gap of 100 bp
* 51817 52514: contig of 698 bp in length
* 52515 52614: gap of 100 bp
* 52615 53342: contig of 728 bp in length
* 53343 53442: gap of 100 bp
* 53443 54169: contig of 727 bp in length
* 54170 54269: gap of 100 bp
* 54270 54983: contig of 714 bp in length
* 54984 55083: gap of 100 bp
* 55084 55805: contig of 722 bp in length
* 55806 55905: gap of 100 bp
* 55906 56609: contig of 704 bp in length
* 56610 56709: gap of 100 bp
* 56710 57421: contig of 712 bp in length
* 57422 57521: gap of 100 bp
* 57522 58246: contig of 725 bp in length
* 58247 58346: gap of 100 bp
* 58347 59072: contig of 726 bp in length

```

Query Match 2.2%; Score 40; DB 2; Length 59903;
 Best Local Similarity 100.0%; Pred. No. 5.5e-10;
 Matches 40; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGTGGCTCACACCTGATCCAGCACTT 1561
 DB 12500 AGACGAGCAGTGGCTCACACCTGATCCAGCACTT 12461

RESULT 74
 AC136358
 LOCUS Homo sapiens chromosome 18 clone RP11-42J14 map 18, LOW-PASS
 DEFINITION SEQUENCE SAMPLING.
 AC136358
 AC136358.1 GI:24431824
 KEYWORDS HTG; HTGS_PHASE0.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 64706)
 Birren, B., Nuebaum, C., and Lander, E.
 Homo sapiens chromosome 18, clone RP11-42J14
 Unpublished
 2 (bases 1 to 64706)
 Birren, B., Nuebaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., D'Arliano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fairo, S., Ferreira, P., Fitzgerald, H., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hales, N.,
 Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,
 Matthews, C., McCarthy, M., Meldrum, J., Meneses, L., Mihova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunhphang, P., Pierre, N., Raymond, C., Retva, R.,
 Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupback, R.,
 Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Talamas, J., Testfay, S., Theodore, J., Topham, K.,
 Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT
 Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/MV/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WISR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L28549
 Center clone name: 42_J_14

NOTE: This record contains 84 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

```

1 644: contig of 644 bp in length
* 645 744: gap of 100 bp
* 745 1428: contig of 684 bp in length
* 1429 1528: gap of 100 bp
* 1529 2220: contig of 692 bp in length
* 2221 2320: gap of 100 bp
* 2321 3013: contig of 693 bp in length
* 3014 3113: gap of 100 bp
* 3114 3768: contig of 655 bp in length
* 3769 3868: gap of 100 bp
* 3869 4504: contig of 636 bp in length
* 4505 4604: gap of 100 bp
* 4605 5273: contig of 669 bp in length
* 5274 5373: gap of 100 bp
* 5374 6043: contig of 670 bp in length
* 6044 6143: gap of 100 bp
* 6144 6823: contig of 680 bp in length
* 6824 6923: gap of 100 bp
* 6924 7601: contig of 678 bp in length
* 7602 7701: gap of 100 bp

```

```

* 7702 8380: contig of 679 bp in length
* 8480: gap of 100 bp
* 8481 9151: contig of 671 bp in length
* 9152 9251: gap of 100 bp
* 9252 9945: contig of 694 bp in length
* 9946 10045: gap of 100 bp
* 10046 10733: contig of 688 bp in length
* 10734 10834 11516: contig of 683 bp in length
* 11517 12270: contig of 654 bp in length
* 12271 13029: contig of 659 bp in length
* 13030 13129: gap of 100 bp
* 13130 13796: contig of 667 bp in length
* 13797 13896: gap of 100 bp
* 13897 14586: contig of 690 bp in length
* 14587 15356: contig of 670 bp in length
* 15357 15456: gap of 100 bp
* 15457 16108: contig of 652 bp in length
* 16109 16208: gap of 100 bp
* 16209 16893: contig of 685 bp in length
* 16894 17683: contig of 690 bp in length
* 17684 17783: gap of 100 bp
* 17784 18422: contig of 639 bp in length
* 18423 18522: gap of 100 bp
* 18523 19212: contig of 690 bp in length
* 19213 20007: contig of 695 bp in length
* 20008 20764: contig of 657 bp in length
* 20765 20864: gap of 100 bp
* 20865 21523: contig of 659 bp in length
* 21524 22275: contig of 652 bp in length
* 22276 23055: contig of 680 bp in length
* 23056 23155: gap of 100 bp
* 23156 23803: contig of 648 bp in length
* 23804 24577: contig of 674 bp in length
* 24578 25362: contig of 685 bp in length
* 25363 25462: gap of 100 bp
* 25463 26246: contig of 684 bp in length
* 26247 26871: contig of 625 bp in length
* 26872 27661: contig of 690 bp in length
* 27662 28385: contig of 624 bp in length
* 28386 28485: gap of 100 bp
* 28486 29143: contig of 658 bp in length
* 29144 29243: gap of 100 bp
* 29244 29905: contig of 662 bp in length
* 29906 30682: contig of 677 bp in length
* 30683 30782: gap of 100 bp
* 30783 31455: contig of 673 bp in length
* 31456 32237: contig of 672 bp in length
* 32238 32327: gap of 100 bp
* 32328 33011: contig of 684 bp in length
* 33012 33111: gap of 100 bp
* 33112 33800: contig of 689 bp in length
* 33801 34590: contig of 690 bp in length
* 34591 34690: gap of 100 bp
* 34691 35378: contig of 688 bp in length
* 35379 35478: gap of 100 bp
* 35479 36135: contig of 657 bp in length

```

```

* 36136 36235: gap of 100 bp
* 36236 36893: contig of 658 bp in length
* 36894 36993: gap of 100 bp
* 36994 37665: contig of 672 bp in length
* 37666 37765: gap of 100 bp
* 37766 38433: contig of 668 bp in length
* 38434 38533: gap of 100 bp
* 38534 39217: contig of 684 bp in length
* 39218 39317: gap of 100 bp
* 39318 39956: contig of 679 bp in length
* 39957 40096: gap of 100 bp
* 40097 40786: contig of 690 bp in length
* 40787 40886: gap of 100 bp
* 40887 41547: contig of 661 bp in length
* 41548 41647: gap of 100 bp
* 41648 42337: contig of 690 bp in length
* 42338 42437: gap of 100 bp
* 42439 43119: contig of 682 bp in length
* 43120 43219: gap of 100 bp
* 43220 43913: contig of 694 bp in length
* 43914 44013: gap of 100 bp
* 44014 44660: contig of 647 bp in length
* 44661 44760: gap of 100 bp
* 44761 45430: contig of 670 bp in length
* 45431 45530: gap of 100 bp
* 45531 46207: contig of 677 bp in length
* 46208 46307: gap of 100 bp
* 46308 46986: contig of 679 bp in length
* 46987 47086: gap of 100 bp
* 47087 47768: contig of 682 bp in length
* 47769 47868: gap of 100 bp
* 47869 48526: contig of 658 bp in length
* 48527 48626: gap of 100 bp
* 48627 49306: contig of 680 bp in length
* 49307 49406: gap of 100 bp
* 49407 50055: contig of 649 bp in length
* 50056 50155: gap of 100 bp
* 50156 50845: contig of 690 bp in length
* 50846 50945: gap of 100 bp
* 50946 51648: contig of 703 bp in length
* 51649 51748: gap of 100 bp
* 51749 52449: contig of 701 bp in length
* 52450 52549: gap of 100 bp
* 52550 53209: contig of 660 bp in length
* 53210 53309: gap of 100 bp
* 53310 53946: contig of 637 bp in length
* 53947 54046: gap of 100 bp
* 54047 54704: contig of 658 bp in length

Query Match      2.2%  Score 40; DB 2; Length 64706;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACCGAGCACAGTGGCTCACACCTGTATATCCAGACACTT 1561
DB      11756 AGACCGAGCACAGTGGCTCACACCTGTATATCCAGACACTT 11795

RESULT 75
LOCUS      AC027403              77879 bp    DNA      linear      HTG 30-MAR-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-813018 map 11, LOW-PASS
SEQUENCE FEATURES
ACCESSION  AC027403
VERSION    AC027403.1 GI:7342095
KEYWORDS   HTG; HTGS-PHASE0.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 77879)
AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE     Homo sapiens chromosome 11, clone RP11-813018

```

JOURNAL
REFERENCE
AUTHORS

unpublished
2 (bases 1 to 77879)
Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bede, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choe, P., Colangelo, M., Collins, S., Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L., Howard, J.C., Iliev, I., Johnson, R., Jones, C., Kahn, L., Karlzas, A., Klein, J., Lacroque, K., Lamazares, R., Landers, T., Lechocz, J., Levine, R., Lien, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R., Meltrin, J., Menus, L., Mihova, T., Mitchell, A., Travers, M., Triggillo, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6954
Center clone name: 813_O_18

* NOTE: This record contains 88 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
800 899: gap of 100 bp in length
900 1706: contig of 807 bp in length
1707 1806: gap of 100 bp in length
1807 2610: contig of 804 bp in length
2611 2710: gap of 100 bp in length
2710 3502: contig of 792 bp in length
3503 3602: gap of 100 bp in length
3603 4383: contig of 781 bp in length
4384 4483: gap of 100 bp in length
4484 5273: contig of 790 bp in length
5274 5373: gap of 100 bp in length
5374 6165: contig of 792 bp in length
6166 6265: gap of 100 bp in length
6266 7025: contig of 760 bp in length
7026 7125: gap of 100 bp in length
7126 7905: contig of 780 bp in length
7906 8005: gap of 100 bp in length
8006 8780: contig of 775 bp in length
8781 8880: gap of 100 bp in length
8881 9656: contig of 776 bp in length
9657 9756: gap of 100 bp in length
9757 10551: contig of 795 bp in length
10552 10651: gap of 100 bp in length

10652 11460: contig of 809 bp in length
11461 11560: gap of 100 bp in length
11561 12357: contig of 797 bp in length
12358 12457: gap of 100 bp in length
12458 13235: contig of 778 bp in length
13236 13335: gap of 100 bp in length
13336 14233: contig of 788 bp in length
14234 14233: gap of 100 bp in length
14234 15010: contig of 787 bp in length
15011 15110: gap of 100 bp in length
15111 15887: contig of 777 bp in length
15888 15987: gap of 100 bp in length
15989 16773: contig of 786 bp in length
16774 16873: gap of 100 bp in length
16874 17655: contig of 782 bp in length
17656 17755: gap of 100 bp in length
17756 18541: contig of 786 bp in length
18542 18641: gap of 100 bp in length
18642 19433: contig of 792 bp in length
19434 19533: gap of 100 bp in length
19534 20304: contig of 771 bp in length
20305 20404: gap of 100 bp in length
20405 21186: contig of 792 bp in length
21187 21286: gap of 100 bp in length
21297 22100: contig of 804 bp in length
22101 22200: gap of 100 bp in length
22201 22961: contig of 761 bp in length
22962 23061: gap of 100 bp in length
23062 23795: contig of 734 bp in length
23796 23895: gap of 100 bp in length
23896 24688: contig of 793 bp in length
24689 24788: gap of 100 bp in length
24789 25564: contig of 776 bp in length
25565 25664: gap of 100 bp in length
25665 26437: contig of 773 bp in length
26438 26537: gap of 100 bp in length
26538 27319: contig of 782 bp in length
27320 27419: gap of 100 bp in length
27420 28218: contig of 799 bp in length
28219 28318: gap of 100 bp in length
28319 29101: contig of 783 bp in length
29102 29201: gap of 100 bp in length
29202 30004: contig of 803 bp in length
30005 30104: gap of 100 bp in length
30105 30887: contig of 783 bp in length
30888 30987: gap of 100 bp in length
30988 31776: contig of 789 bp in length
31777 31876: gap of 100 bp in length
31877 32651: contig of 775 bp in length
32652 32751: gap of 100 bp in length
32752 33536: contig of 785 bp in length
33537 33636: gap of 100 bp in length
33637 34429: contig of 793 bp in length
34430 34529: gap of 100 bp in length
34530 35004: contig of 775 bp in length
35005 35404: gap of 100 bp in length
35406 36164: contig of 760 bp in length
36165 36264: gap of 100 bp in length
36266 37050: contig of 786 bp in length
37051 37150: gap of 100 bp in length
37151 37959: contig of 809 bp in length
37960 38059: gap of 100 bp in length
38060 38834: contig of 775 bp in length
38835 38934: gap of 100 bp in length
38936 39714: contig of 780 bp in length
39715 39814: gap of 100 bp in length
39814 40531: contig of 817 bp in length
40532 40731: gap of 100 bp in length
40732 41534: contig of 803 bp in length
41535 42408: contig of 774 bp in length
42409 42508: gap of 100 bp in length
42509 43302: contig of 794 bp in length

```

* 43303 43402: gap of 100 bp
* 43403 44195: contig of 793 bp in length
* 44196 44295: gap of 100 bp
* 44296 45089: contig of 794 bp in length
* 45090 45189: gap of 100 bp
* 45190 45976: contig of 787 bp in length
* 45977 46076: gap of 100 bp
* 46077 46866: contig of 780 bp in length
* 46867 46966: gap of 100 bp
* 46967 47753: contig of 789 bp in length
* 47756 47855: gap of 100 bp
* 47856 48654: contig of 799 bp in length
* 48655 48754: gap of 100 bp
* 48755 49571: contig of 817 bp in length
* 49572 49671: gap of 100 bp
* 49672 50459: contig of 788 bp in length
* 50460 50559: gap of 100 bp
* 50560 51350: contig of 791 bp in length
* 51351 51450: gap of 100 bp
* 51451 52248: contig of 798 bp in length
* 52249 52348: gap of 100 bp
* 52349 53124: contig of 776 bp in length
* 53125 53225: gap of 100 bp
* 53225 54008: contig of 784 bp in length
* 54009 54108: gap of 100 bp
* 54109 54899: contig of 791 bp in length
* 54900 54999: gap of 100 bp
* 55000 55770: contig of 771 bp in length
* 55771 55870: gap of 100 bp
* 55871 56660: contig of 790 bp in length
* 56661 56760: gap of 100 bp
* 56761 57568: contig of 808 bp in length
* 57569 57669: gap of 100 bp
* 57669 58445: contig of 777 bp in length
* 58446 58545: gap of 100 bp
* 58546 59338: contig of 793 bp in length
* 59339 59438: gap of 100 bp
* 59439 60246: contig of 808 bp in length
* 60247 60346: gap of 100 bp
* 60347 61141: contig of 795 bp in length
* 61142 61241: gap of 100 bp

```

Query Match 2.2%; Score 40; DB 2; Length 77879;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCAGACCTGTATCCGACACTT 1561
 Db 39943 AGACGAGGACAGTGGCTCAGACCTGTATCCGACACTT 39982

RESULT 76
 LOCUS AL731577 91516 bp DNA linear PRI 21-JUN-2002
 DEFINITION Human DNA sequence from clone RPl1-298J20 on chromosome 10,
 complete sequence.
 ACCESSION AL731577 AC010158
 VERSION AL731577.7 GI:21540114
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 91516)
 Laylor, S.
 Direct Submission
 Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Jun 23, 2002 this sequence version replaced gi:21531420.
 Draft sequence produced by Genome Therapeutics Corp, 100 Beaver
 Street, Waltham, MA 02453, USA
 http://www.genomecorp.com

----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWISSPROT; Tr: TrEMBL; Mp: MOPREP; Information on the MOPREP
 database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
 RPl1-298J20 is from the library RPl1-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBac3.6.

FEATURES
 source
 1..91516
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RPl1-298J20"
 /clone_1ib="RPl1-11.2"

Query Match 2.2%; Score 40; DB 9; Length 91516;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCAGACCTGTATCCGACACTT 1561
 Db 64519 AGACGAGGACAGTGGCTCAGACCTGTATCCGACACTT 64480

RESULT 77
 LOCUS AC092624 101158 bp DNA linear PRI 01-MAR-2002
 DEFINITION Homo sapiens BAC clone RPl1-261J9 from 2, complete sequence.
 ACCESSION AC092624 AC022787
 VERSION AC092624.2 GI:15668126
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 101158)
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 101158)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 98063792
 PUBMED 9847074
 2 (bases 1 to 101158)
 Haglund, K., Meyer, R. and Dixon, R.
 The sequence of Homo sapiens BAC clone RPl1-261J9
 Unpublished (2001)
 3 (bases 1 to 101158)


```

repeat_region      /rpt_family="MaLR"
                    27500..27528
                    /rpt_family="AT_rich"
repeat_region      27794..28092
                    /rpt_family="ERV1"
repeat_region      30883..30908
                    /rpt_family="(TTCA)n"
repeat_region      33747..34052
                    /rpt_family="Alu"
repeat_region      34031..34052
                    /rpt_family="(A)n"
repeat_region      34885..35300
                    /rpt_family="L1"
repeat_region      35068..35107
                    /rpt_family="L1"
repeat_region      35328..35582
                    /rpt_family="AT_rich"
repeat_region      35603..35642
                    /rpt_family="L1"
repeat_region      35667..36013
                    /rpt_family="AT_rich"
repeat_region      36019..38118
                    /rpt_family="L1"
repeat_region      36837..36865
                    /rpt_family="AT_rich"
repeat_region      37359..37394
                    /rpt_family="AT_rich"
repeat_region      37867..37898
                    /rpt_family="AT_rich"
repeat_region      38196..38270
                    /rpt_family="L1"
repeat_region      38264..38293
                    /rpt_family="AT_rich"
repeat_region      43827..44933

```

Query Match 2.2%; Score 40; DB 9; Length 101158;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1522 AGACCGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
 DB 25303 AGACCGGACAGTGGCTCAGACCTGTATCCAGCACTT 25342

RESULT 78
 AC104084 109138 bp DNA linear PRI 29-MAY-2002
 LOCUS Homo sapiens BAC clone RP11-60118 from 2, complete sequence.
 DEFINITION AC104084
 ACCESSION AC104084.5 GI:20522218
 VERSION HTG.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITL Toward a complete human genome sequence
 AUTHORS Sulston, J.E. and Waterston, R.
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 109138)
 AUTHORS Daughin, S., Meyer, R. and Creason, K.
 TITLE The sequence of Homo sapiens BAC clone RP11-60118
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 109138)
 AUTHORS Waterston, R.H.
 TITLE Direct Submision
 JOURNAL Submitted (03-DEC-2001) Genome Sequencing Center, Washington
 MO 63108, USA
 REFERENCE 4 (bases 1 to 109138)
 AUTHORS Waterston, R.H.

TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE 5 (bases 1 to 109138)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On May 10, 2002 this sequence version replaced gi18370073.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: saplens@wuston.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0601108

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male
 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tateo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
 and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP13-5133; the clone sequenced
 to the right is RP11-35617, 2000 bp overlap. Actual start of this
 clone is at base position 14078 of RP13-5133; actual end is at
 base position 87559 of RP11-35617.

The region from 86808 to 86831 is covered only by a PCR product of
 clone DNA. Single plasmid region exists between 61091 and 61115.
 Polymorphisms exist between AC109343 and AC104084. Data from
 AC109343 was used to finish AC104084.

FEATURES

SOURCE
 1..109138
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="12"
 /map="2"
 /clone="RP11-60118"
 /clone_1lb="RPCT-11"
 865..889
 /rpt_family="(CA)n"
 repeat_region 1692..1926
 /rpt_family="Alu"
 2137..2573
 /rpt_family="L1"
 repeat_region


```

repeat_region      2596..2881
/rpt_family="MERL_type"
repeat_region      2889..3539
/rpt_family="L1"
repeat_region      3613..3861
/rpt_family="Alu"
repeat_region      4202..4242
/rpt_family="(TG)n"
repeat_region      4243..4400
/rpt_family="L1"
repeat_region      4405..4633
/rpt_family="Alu"
repeat_region      4634..5273
/rpt_family="L1"
repeat_region      5275..5767
/rpt_family="L1"
repeat_region      5768..6085
/rpt_family="Alu"
repeat_region      6086..6288
/rpt_family="L1"
repeat_region      6289..6432
/rpt_family="Alu"
repeat_region      6433..6849
/rpt_family="L1"
repeat_region      9267..9611
/rpt_family="ERV1"
repeat_region      9612..10771
/rpt_family="ERVX"
repeat_region      10772..11273
/rpt_family="ERV1"
repeat_region      12557..12713
/rpt_family="MIR"
repeat_region      12942..13125
/rpt_family="MERL_type"
repeat_region      13126..13254
/rpt_family="Alu"
repeat_region      13764..14032
/rpt_family="ERV1"
repeat_region      14704..14820
/rpt_family="MERL"
repeat_region      14861..14965
/rpt_family="Alu"
repeat_region      15905..16178
/rpt_family="Alu"
repeat_region      16433..16481
/rpt_family="L2"
repeat_region      16623..16822
/rpt_family="L2"
repeat_region      16885..17178
/rpt_family="L2"
repeat_region      17179..17575
/rpt_family="MERL"
repeat_region      17576..17667
/rpt_family="L2"
repeat_region      18029..18091
/rpt_family="L1"
repeat_region      18778..18432
/rpt_family="L1"
repeat_region      20792..20827
/rpt_family="MERL_type"
repeat_region      21815..21938
/rpt_family="MIR"
repeat_region      22409..22622
/rpt_family="MIR"
repeat_region      23208..23434
/rpt_family="MIR"
repeat_region      23910..24112
/rpt_family="MIR"
repeat_region      24578..24887
/rpt_family="MERL_type"
repeat_region      25249..25671
/rpt_family="MERL"
repeat_region      26117..26152

```

```

repeat_region      26160..26211
/rpt_family="MERL_type"
repeat_region      26257..26917
/rpt_family="L2"
repeat_region      26965..27022
/rpt_family="MERL"
repeat_region      27175..28772
/rpt_family="ERV1"
repeat_region      29314..29359
/rpt_family="L2"
repeat_region      29410..30108
/rpt_family="L2"
repeat_region      30123..30924
/rpt_family="L2"
misc_feature      31213..32175
/note="CPG island (%GC=71.8, c/e=0.80, #CPGs=93)"
repeat_region      32517..32545
/rpt_family="(TTCA)n"
repeat_region      33503..33590
/rpt_family="MIR"
repeat_region      33823..34086
/rpt_family="L2"
repeat_region      34153..34322
/rpt_family="MERL_type"
repeat_region      34471..34645
/rpt_family="MERL_type"

```

```

Query Match      2.2% Score 40; DB 9; Length 109138;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1522 AGACGAGGACAGTGGCTCAACCTGTATCCAGACTT 1561
Db      52987 AGACGAGGACAGTGGCTCAACCTGTATCCAGACTT 52948

```

```

RESULT 79
AL451052/c      109864 bp      DNA      linear      PRI 16-NOV-2001
LOCUS
DEFINITION
ACCESSION      AL451052 AC021354
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

On Nov 17, 2001 this sequence version replaced gi:16214713. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; information on the WormPeP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> Rpl1-24P14 is from the library RPl1-11.1 constructed by the group of Piter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RPl1-24P14 it may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RPl1-24P14 is at 109864 in this sequence. The true left end of clone RPl1-175N15 is at 3171 in this sequence. The true right end of clone RPl1-90H3 is at 2000 in this sequence.

FEATURES

source

1..109864
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RPl1-24P14"
/clone_lib="RPl1-11.1"

ORIGIN

Query Match 2.2%; Score 40; DB 9; Length 109864;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1522 AGACCAAGCAGCTGCTCACCCTGTATCCACACTT 1561

Db 75699 AGACCAAGCAGCTGCTCACCCTGTATCCACACTT 75660

RESULT 80

AC009801.0/c

WCOMMENT

Sequence split into 4 fragments LOCUS AC009801 Accession AC009801

Fragment Name

Begin

End

AC009801_0 1 110000

AC009801_1 100001 210000

AC009801_2 200001 310000

AC009801_3 300001 368200

LOCUS AC009801 368200 bp DNA linear HTG 25-JUN-2000
DEFINITION Homo sapiens chromosome 8 clone RPl1-399D24 map 8, *** SEQUENCING
IN PROGRESS ***; 123 unordered pieces.

AC009801

AC009801.4 GI:8671953

HTG; HTGS PHASE1.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 368200)

Biren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 8, clone RPl1-399D24

Unpublished

2 (bases 1 to 368200)

Biren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., Dearellano,K., Depayre,E., Devon,K., Dewar,K.,

Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,

Funker,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,

Hagos,B., Heford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,

Karatas,N., Lehotzky,J., Lieu,C., Locke,K., MacDonald,P.,

Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,

Meldrum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,

Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,

Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,

Stanger-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,

Teetate,S., Tornella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

TITLE

JOURNAL

COMMENT

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted 101-SEP-1999 Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 23, 2000 this sequence version replaced gi:7801426.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/XW/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 12435

Center clone name: 399_D_24

NOTE: This is a 'working draft' sequence. It currently
* consists of 123 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1178: contig of 1178 bp in length
1 1179 1278: gap of 100 bp
* 1279 2423: contig of 1145 bp in length
* 2424 2523: gap of 100 bp
* 2524 3593: contig of 1059 bp in length
* 3593 3793: gap of 100 bp
* 3793 4804: contig of 1012 bp in length
* 4805 4904: gap of 100 bp
* 4904 6052: contig of 1148 bp in length
* 6052 6152: gap of 100 bp
* 6153 7168: contig of 1016 bp in length
* 7168 7268: gap of 100 bp
* 7269 8399: contig of 1131 bp in length
* 8400 8499: gap of 100 bp
* 8500 9791: contig of 1252 bp in length
* 9792 9891: gap of 100 bp
* 9892 10910: contig of 1019 bp in length
* 10911 11010: gap of 100 bp
* 11011 12312: contig of 1302 bp in length
* 12313 12412: gap of 100 bp
* 12413 13687: contig of 1285 bp in length
* 13688 13797: gap of 100 bp
* 13798 14817: contig of 1020 bp in length
* 14818 14917: gap of 100 bp
* 14918 16124: contig of 1207 bp in length
* 16125 16224: gap of 100 bp
* 16225 17423: contig of 1199 bp in length
* 17424 17523: gap of 100 bp
* 17524 18770: contig of 1247 bp in length
* 18771 18870: gap of 100 bp
* 18871 19877: contig of 1007 bp in length
* 19878 19977: gap of 100 bp
* 19978 21287: contig of 1310 bp in length
* 21288 21387: gap of 100 bp
* 21388 22559: contig of 1172 bp in length
* 22560 22659: gap of 100 bp
* 22660 23731: contig of 1072 bp in length
* 23732 23831: gap of 100 bp
* 23832 25217: contig of 1366 bp in length
* 25218 25317: gap of 100 bp
* 25318 26468: contig of 1151 bp in length
* 26469 26568: gap of 100 bp
* 26569 27580: contig of 1012 bp in length
* 27581 27680: gap of 100 bp
* 27681 29050: contig of 1370 bp in length
* 29051 30753: gap of 100 bp
* 30754 30853: contig of 1603 bp in length

```

* 30854 32319: contig of 1466 bp in length
* 32320 32419: gap of 100 bp
* 32420 33749: contig of 1330 bp in length
* 33750 33849: gap of 100 bp
* 33850 35010: contig of 1161 bp in length
* 35011 35110: gap of 100 bp
* 35111 36366: contig of 1426 bp in length
* 36367 36637: gap of 100 bp
* 36638 37829: contig of 1193 bp in length
* 37830 37929: gap of 100 bp
* 37930 39114: contig of 1185 bp in length
* 39115 39214: gap of 100 bp
* 39215 40434: contig of 1220 bp in length
* 40435 40534: gap of 100 bp
* 40535 41859: contig of 1335 bp in length
* 41860 41959: gap of 100 bp
* 41960 43280: contig of 1331 bp in length
* 43281 43380: gap of 100 bp
* 43381 43991: contig of 1579 bp in length
* 43992 44069: gap of 100 bp
* 44070 46415: contig of 1346 bp in length
* 46416 46515: gap of 100 bp
* 46516 47677: contig of 1162 bp in length
* 47678 47777: gap of 100 bp
* 47778 49135: contig of 1358 bp in length
* 49136 49235: gap of 100 bp
* 49236 50982: contig of 1747 bp in length
* 50983 51082: gap of 100 bp
* 51083 52114: contig of 1032 bp in length
* 52115 52214: gap of 100 bp
* 52215 53308: contig of 1054 bp in length
* 53309 53408: gap of 100 bp
* 53409 55158: contig of 1750 bp in length
* 55159 55258: gap of 100 bp
* 55259 56265: contig of 1007 bp in length
* 56266 56365: gap of 100 bp
* 56366 57847: contig of 1482 bp in length
* 57848 57947: gap of 100 bp
* 57948 59763: contig of 1816 bp in length
* 59764 59863: gap of 100 bp
* 59864 61586: contig of 1723 bp in length
* 61587 61686: gap of 100 bp
* 61687 63543: contig of 1857 bp in length
* 63544 63643: gap of 100 bp
* 63644 65001: contig of 1358 bp in length
* 65002 65101: gap of 100 bp
* 65102 66998: contig of 1897 bp in length
* 66999 67098: gap of 100 bp
* 67099 69248: contig of 2150 bp in length
* 69249 69348: gap of 100 bp
* 69349 71062: contig of 1714 bp in length
* 71063 71162: gap of 100 bp
* 71163 73128: contig of 1966 bp in length
* 73129 73228: gap of 100 bp
* 73229 74568: contig of 1340 bp in length
* 74569 74668: gap of 100 bp
* 74669 76272: contig of 1604 bp in length
* 76273 76372: gap of 100 bp
* 76373 77895: contig of 1523 bp in length
* 77896 77995: gap of 100 bp
* 77996 79960: contig of 1966 bp in length
* 79961 80060: gap of 100 bp
* 80061 82011: contig of 1951 bp in length
* 82012 82111: gap of 100 bp
* 82112 83518: contig of 1407 bp in length
* 83519 83618: gap of 100 bp
* 83619 86404: contig of 2786 bp in length
* 86405 86504: gap of 100 bp
* 86505 88828: contig of 2324 bp in length
* 88829 88928: gap of 100 bp
* 88929 90109: contig of 1181 bp in length
* 90110 90209: gap of 100 bp
* 90210 91340: contig of 1131 bp in length

```

```

Query Match      2.2%; Score 40; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 5,7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1522 AGACGAGGACAGTGGCTCACCCTGTATCCGACACTT 1561
Db      23245 AGACGAGGACAGTGGCTCACCCTGTATCCGACACTT 23206

```

```

RESULT 81
AL354877/c
LOCUS
DEFINITION
Human DNA sequence from clone RP11-430K21 on chromosome 9, complete
sequence.
ACCESSION
AL354877
VERSION
AL354877.25 GI:15020885
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
Organism
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Corby,N.
TITLE
Direct Submission
JOURNAL
Submitted (21-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On Jul 25, 2001 this sequence version replaced gi:14529786.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Emu, EMBL; Swi,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-430K21 is from the library RPCT-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6

```

IMPORTANT: This sequence is not the entire insert of clone Rpl1-430K21. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone Rpl1-430K21 is at 1 in this sequence. The true left end of clone Rpl1-570D4 is at 114237 in this sequence. The true right end of clone Rpl1-310C13 is at 66953 in this sequence.

FEATURES

```
Source      Location/Qualifiers
1..116236
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /chromosome="9"
  /clone="Rpl1-430K21"
  /clone_1fb="RPC1-11.2"
  70..363
    repeat_region repeat: matches 1..293 of consensus"
    repeat_region repeat: matches 1..381 of consensus"
    repeat_region repeat: matches 1..303 of consensus"
    repeat_region repeat: matches 1..691 of consensus"
    repeat_region repeat: matches 381..436 of consensus"
    repeat_region repeat: matches 2555..2750 of consensus"
    repeat_region repeat: matches 1..303 of consensus"
    repeat_region repeat: matches 1..2555 of consensus"
    repeat_region repeat: matches 5..299 of consensus"
    repeat_region repeat: matches 5814..5970 of consensus"
    repeat_region repeat: matches 9..98 of consensus"
    repeat_region repeat: matches 2315..2412 of consensus"
    repeat_region repeat: matches 9..189 of consensus"
    repeat_region repeat: matches 1..309 of consensus"
    repeat_region repeat: matches 61..122 of consensus"
    repeat_region repeat: matches 34..301 of consensus"
    repeat_region repeat: matches 12..218 of consensus"
    repeat_region repeat: matches 464..1694 of consensus"
    repeat_region repeat: matches 126..592 of consensus"
    repeat_region repeat: matches 1713..2156 of consensus"
    repeat_region repeat: matches 1..365 of consensus"
    repeat_region repeat: matches 1..2740 of consensus"
    repeat_region repeat: matches 26..303 of consensus"
    repeat_region repeat: matches 1..321 of consensus"
    repeat_region repeat: matches 983..2309 of consensus"
    repeat_region repeat: matches 195..298 of consensus"
    repeat_region repeat: matches 264..308 of consensus"
    repeat_region repeat: matches 39..201 of consensus"
    repeat_region repeat: matches 2300..2384 of consensus"
    repeat_region repeat: matches 2267..2488 of consensus"
```

```
repeat_region 15148..15288
  /note="MIR repeat: matches 45..202 of consensus"
repeat_region 15289..15377
  /note="MIR repeat: matches 2..80 of consensus"
repeat_region 15378..15441
  /note="MIR repeat: matches 202..261 of consensus"
repeat_region 15620..15911
  /note="MIR repeat: matches 1..289 of consensus"
repeat_region 15993..16016
  /note="MIR repeat: matches 145..112 of consensus"
repeat_region 16017..16368
  /note="MIR repeat: matches 1..2730 of consensus"
repeat_region 17367..17683
  /note="MIR repeat: matches 1..298 of consensus"
repeat_region 17954..18247
  /note="MIR repeat: matches 1..294 of consensus"
repeat_region 18931..19219
  /note="MIR repeat: matches 1..288 of consensus"
repeat_region 19369..19665
  /note="MIR repeat: matches 2..298 of consensus"
repeat_region 21002..21336
  /note="MIR repeat: matches 1..311 of consensus"
repeat_region 21549..22015
  /note="MIR repeat: matches 5340..5813 of consensus"
repeat_region 22024..22077
  /note="MIR repeat: matches 277..516 of consensus"
repeat_region 22885..23181
  /note="MIR repeat: matches 5494..5806 of consensus"
repeat_region 23222..23352
  /note="MIR repeat: matches 1..134 of consensus"
repeat_region 23383..23685
  /note="MIR repeat: matches 1..303 of consensus"
repeat_region 23686..23864
  /note="MIR repeat: matches 132..312 of consensus"
repeat_region 23877..23974
  /note="MIR repeat: matches 201..248 of consensus"
repeat_region 24533..24589
  /note="MIR repeat: matches 206..262 of consensus"
repeat_region 24533..24639
  /note="MIR repeat: matches 2634..2734 of consensus"
repeat_region 24655..24805
  /note="MIR repeat: matches 2084..2235 of consensus"
repeat_region 25061..25204
  /note="MIR repeat: matches 2548..2695 of consensus"
repeat_region 26754..27046
  /note="MIR repeat: matches 1..292 of consensus"
repeat_region 27639..27904
  /note="MIR repeat: matches 1..294 of consensus"
repeat_region 27955..28039
  /note="MIR repeat: matches 1..85 of consensus"
repeat_region 28660..28963
  /note="MIR repeat: matches 1..302 of consensus"
repeat_region 28966..29083
  /note="MIR repeat: matches 85..198 of consensus"
repeat_region 29801..29927
  /note="MIR repeat: matches 24..161 of consensus"
repeat_region 29941..30042
  /note="MIR repeat: matches 2197..2292 of consensus"
repeat_region 30125..30527
  /note="MIR repeat: matches 1..405 of consensus"
repeat_region 30856..30952
  /note="MIR repeat: matches 84..188 of consensus"
repeat_region 31857..32152
  /note="MIR repeat: matches 2..297 of consensus"
repeat_region 32159..32291
  /note="MIR repeat: matches 22..158 of consensus"
repeat_region 32564..32938
  /note="MIR repeat: matches 1..2454 of consensus"
repeat_region 32941..33045
  /note="MIR repeat: matches 2..114 of consensus"
```

```

repeat_region      33046..33093
                    /note="BC200 repeat: matches 1..172 of consensus"
repeat_region      33483..33952
                    /note="WER42 repeat: matches 1..504 of consensus"
repeat_region      34506..34661
                    /note="Alub repeat: matches 17..172 of consensus"
repeat_region      35309..36039
                    /note="LTR repeat: matches 1..691 of consensus"
repeat_region      36545..36676
                    /note="WER94 repeat: matches 1..134 of consensus"
repeat_region      36901..37201

Query Match      2.2%; Score 40; DB 9; Length 116236;
Best Local Similarity 100.0%; Pred.No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACGAGCAGCAGTGGCTCACACCTGTATCCAGCAGCTT 1561
        |||||
Db      61294 AGACGAGCAGCAGTGGCTCACACCTGTATCCAGCAGCTT 61255

RESULT 82
HS989H11/c      118831 bp      DNA      linear      PRI 04-MAR-2003
LOCUS      Human DNA sequence from clone CTA-989H11 on chromosome
DEFINITION      22q13.1-13.2, complete sequence.
ACCESSION      283851
VERSION      283851.17 GI:5441348
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 118831)
REFERENCE      Beasley/H.
AUTHORS      Direct Submission
TITLE      Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
JOURNAL      Cambridgehire, CB10 1SA, UK. E-mail enquiries:
              humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
              On Jul 10, 1999 this sequence version replaced gi:5419652.
              ----- Genome Center
              Center: Wellcome Trust Sanger Institute
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              -----
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              This sequence was finished as follows unless otherwise noted: all
              regions were either double-stranded or sequenced with an alternate
              chemistry or covered by high quality data (i.e., phred quality >=
              30); an attempt was made to resolve all sequencing problems, such
              as compressions and repeats; all regions were covered by at least
              one plasmid subclone or more than one M13 subclone; and the
              assembly was confirmed by restriction digest, except on the rare
              occasion of the clone being a YAC.
              The following abbreviations are used to associate primary accession
              numbers given in the feature table with their source databases:
              Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information
              on the WORMPEP database can be found at
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
              was generated from part of bacterial clone contigs of human
              chromosome 22, constructed by the Sanger Centre Chromosome 22
              Mapping Group. Further information can be found at
              http://www.sanger.ac.uk/HGP/Chr22
              CTA-989H11 is from the human BAC library described in U-J. Kim et
              al. (1996) Genomics 34, 213-218.
              VECTOR: pBelBAC11.
              Location/Qualifiers

```

```

source      1..118831
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="22"
            /map="q13.1-13.2"
            /clone="CTA-989H11"
            /clone_11b="CIT9788K-A2"

ORIGIN

Query Match      2.2%; Score 40; DB 9; Length 118831;
Best Local Similarity 100.0%; Pred.No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACGAGCAGCAGTGGCTCACACCTGTATCCAGCAGCTT 1561
        |||||
Db      108900 AGACGAGCAGCAGTGGCTCACACCTGTATCCAGCAGCTT 108661

RESULT 83
HSJ1077B9      126525 bp      DNA      linear      PRI 03-JAN-2001
LOCUS      Human DNA sequence from clone RP5-1077B9 on chromosome
DEFINITION      1p36.11-1p36.32 Contains the PLOD (procollagen-lysine,
              2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos
              syndrome type VI) gene, the gene for KIAA0214 protein, a pseudogene
              similar to IMPAI (inositol (myo)-1(or 4)-monophosphatase 1), ESTs,
              STSs, GSSs and CpG islands, complete sequence.
              AL096840
              AL096840.25 GI:9944243
              HTG; 2-oxoglutarate 5-dioxygenase; Cpg island;
              Ehlers-Danlos syndrome; IMPAI; inositol; KIAA0214; lysine
              hydroxylase; monophosphatase; PLOD; procollagen-lysine.
              Homo sapiens (human)
              Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 126525)
REFERENCE      Pearce/A.
AUTHORS      Direct Submission
TITLE      Submitted (03-JAN-2001) Sanger Centre, Hinxton, Cambridgehire,
JOURNAL      Cambridgehire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
              requests: clonerequests@sanger.ac.uk
              On Aug 29, 2000 this sequence version replaced gi:3844576.
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              The following abbreviations are used to associate primary accession
              numbers given in the feature table with their source databases:
              Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information
              on the WORMPEP database can be found at
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
              was generated from part of bacterial clone contigs of human
              chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
              Group. Further information can be found at
              http://www.sanger.ac.uk/HGP/Chr1
              IMPORTANT: This sequence is not the entire insert of clone
              RP5-1077B9. It may be shorter because we sequence overlapping
              sections only once, except for a 100 base overlap.
              The true right end of clone RP5-1077B9 is at 126525 in this
              sequence. The true left end of clone RP11-426M1 is at 103372 in
              this sequence. The true right end of clone RP5-949G17 is at 100 in
              this sequence. This sequence has been finished according to
              sequence map criteria as follows. An attempt is made to resolve
              all sequencing problems, such as compressions and repeats, but not
              necessarily within known annotated repeat sequence elements. Where
              the sequence is ambiguous, there is an annotation using the
              'unsure' feature key. RP5-1077B9 is from the library RP01-5
              constructed by the group of Pieter de Jong. For further details see
              http://www.choil.org/bacpac/home.htm

```

VECTOR: pcypac2.
FEATURES
source
location/Qualifiers
1..126525
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.11-p36.32"
/clone="RPS-1077B9"
/clone_1ib="Rpci-5"
2..158
/note="AluJo repeat: matches 1..157 of consensus"
repeat_region
164..185
/note="11 copies 2 mer tt 10% conserved"
repeat_region
189..365
/note="FRAM repeat: matches 0..176 of consensus
FRAM repeat: matches 0..176 of consensus"
623..787
/note="match: STS: Em:G27183"
1890..2051
/note="AluSx repeat: matches 132..294 of consensus"
2194..2263
/note="Alu repeat: matches 2..71 of consensus
Alu repeat: matches 2..71 of consensus"
2264..2400
/note="AluSx repeat: matches 1..139 of consensus"
2428..2583
/note="12 repeat: matches 2589..2745 of consensus"
2966..3143
/note="MIR repeat: matches 6..207 of consensus"
3598..4588
/note="CPG island"
/evidence=not_experimental
4288..4395
/note="54 copies 2 mer cc 60% conserved"
4300..4407
/note="9 copies 12 mer 66% conserved"
4794..5103
/note="AluSg repeat: matches 2..303 of consensus"
5230..5365
/note="AluSx repeat: matches 1..145 of consensus"
5366..5676
/note="AluJ repeat: matches 1..311 of consensus"
5677..5868
/note="AluSx repeat: matches 145..306 of consensus"
6352..6653
/note="AluSx repeat: matches 4..312 of consensus"
6656..6956
/note="AluSg repeat: matches 1..304 of consensus"
6960..7267
/note="AluJb repeat: matches 7..302 of consensus"
7289..7366
/note="L1PA16 repeat: matches 6080..6157 of consensus
L1PA16 repeat: matches 6080..6157 of consensus"
7369..7663
/note="AluSg repeat: matches 1..295 of consensus"
7671..7732
/note="Alu repeat: matches 242..303 of consensus
Alu repeat: matches 243..304 of consensus"
8083..8502
/note="match: GSS: Em:AQ132030"
8089..8463
/note="match: GSS: Em:B90723"
8261..8577
/note="AluJb repeat: matches 1..303 of consensus"
8553..8831
/note="MIR repeat: matches 48..232 of consensus"
8832..9133
/note="AluJb repeat: matches 1..296 of consensus"
9134..9160
/note="MIR repeat: matches 232..256 of consensus"
9320..9421
/note="MIR repeat: matches 47..148 of consensus"

repeat_region
9487..9621
/note="AluJo repeat: matches 6..134 of consensus"
repeat_region
9681..9969
/note="AluSg repeat: matches 1..290 of consensus"
10008..10069
/note="31 copies 2 mer aa 71% conserved"
repeat_region
10188..10484
/note="AluSg1 repeat: matches 1..297 of consensus
AluSg1 repeat: matches 1..297 of consensus"
10592..10903
/note="AluSg repeat: matches 1..310 of consensus"
11110..11414
/note="AluSg repeat: matches 1..306 of consensus"
11600..11894
/note="AluSg repeat: matches 5..301 of consensus"
11895..12071
/note="AluJb repeat: matches 132..310 of consensus"
12791..5358
/gene="PLOC"
mRNA
join(12791..12866,25987..26078,27784..27917,28368..28531,
30634..30746,32841..32904,34928..35025,35853..35954,
36527..36658,38657..38778,41543..41647,42186..42311,
42655..42796,43491..43604,44262..44327,44998..45102,
48681..48827,50883..51008,52664..52819)
/gene="PLOC"
/product="ddj1077B9.1 (procollagen-lysine, 2-oxoglutarate
5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
type VII))"
/note="match: CDNA: Em:L25331 Em:AF046782 Em:L06419
Em:M98252 Em:AF054274 Em:AF046888 Em:AF068229 Em:M59183
Em:AF046783 Em:AF080572 Em:AL049852 Em:U84573
match: ESTs: Em:AW373818 Em:AA475262 Em:AL047837
Em:AI040270 Em:AW658624 Em:AW632184 Em:AA636211
Em:AA636452 Em:R60388 Em:AA659535 Em:AA655395 Em:AW2637.1
Em:AW068674 Em:AW362993 Em:AA928936 Em:AI903986
Em:AW402215 Em:AW392531 Em:AW137529 Em:AA38675
Em:AW53923 Em:AA411291"
/evidence=not_experimental
join(12791..12866,25987..26078,27784..27917,28368..28531,
30634..30746,32841..32904,34928..35025,35853..35954,
36527..36658,38657..38778,41543..41647,42186..42311,
42655..42796,43491..43604,44262..44327,44998..45102,
48681..48827,50883..51008,52664..52819)
/gene="PLOC"
/note="match: Protein: Sw:Q07588 Sw:Q00469 Tr:Q9R0E2
Sw:Q63321 Sw:Q02809 Sw:P24802 Tr:Q9R0B9 Sw:Q06056
Tr:Q9R0E1 Tr:Q9VTH0 Sw:Q20679"
/codon_start=1
/evidence=not_experimental
/product="ddj1077B9.1 (procollagen-lysine, 2-oxoglutarate
5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
type VII))"
/protein_id="CAC19722.1"
/db_xref="GI:12038976"
/db_xref="GOA:Q02809"
/translation="MRPILILALIGLWLLAIPAKGDKAPRDNLVLTVAKEFGPRF
KRSQFNRYKIDALGIDPMYVEKGSAGGQVRLTKALBKHAEDKLDLITAFASY
DVLPAQSPRELLKFRQAKSQQVFSAEELIPRRLKTRPVASDKRFLGSGGFLGY
LKPMLKLVANWEGQSDSDQLPYTKFLDPEKREKQVNLIDHRCRIFQNDGALDLY
LKGIDGALPTVAVGVLEQPTPEVSLFQRLRLRLYPOKMHMLFLHNHOKHQAQVE
EFLAAGSEKSVKLVGPVRANADAGADLCQDSCTFYFVDADVLTAEENS
LRLIIONKNVLAPLMTBGRPLMSNFWGLSDAGYARSDYVDIYQGRGVNANPY
LSVILIKGSLRGLGSSDLPHSKLDLMDACANIROODVMPFLNHTLGLHLSD
DSYRTHHNDLMEVSNPDWKEKYLHONYTALAKGVETPCPVYVMPFLTEYAC
DELVEEMERQMSLGNKNKDNRIQGGYENFTPIDIMKQIGFERMHEKELIETIAMT
EKLYPGYTRAQFDLAFVVRYPEDQPSLMPHDAFTITINLANKVGVADYBGCGCRF
LRNCSIRAPRKMTLMHPGRLLTHHEGLPTTGRTYIAVSFDP"
12972..13074
/note="MIR repeat: matches 50..151 of consensus"
13123..13357
/note="MIR repeat: matches 15..262 of consensus"

repeat_region 13523..13636
/note="AlusX repeat: matches 194..310 of consensus"

Query Match 2.2%; Score 40; DB 9; Length 126525;
Best Local Similarity 100.0%; Pred.No.5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACCTTAGG 1564
|||||
Db 54193 CCAGGACAGTGGCTCACACCTGTATCCAGACCTTAGG 54232

RESULT 84
HS436M1 134403 bp DNA linear PRI 05-MAR-2003
LOCUS Human DNA sequence from clone RP3-436M1 on chromosome
DEFINITION Xp22.11-22.2, complete sequence.
ACCESSION Z94056.1 GI:2326510
VERSION Z94056.1 GI:2326510
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 134403)
AUTHORS Grafham D.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Aug 14, 1997 this sequence version replaced gi:1944548.

COMMENT
-----Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the rare
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
EM, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP3-436M1 is from the library RPCI-3 constructed by the group of
Pierer de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.

FEATURES
source
Location/Qualifiers
1..134403

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="RZPD:RZPD:P04M11436"
/db_xref="taxon:9606"
/chromosome="X"
/map="p22.11-22.2"
/clone="RP3-436M1"

ORIGIN
/clone_lib="RPCI-3"

Query Match 2.2%; Score 40; DB 9; Length 134403;
Best Local Similarity 100.0%; Pred.No.5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCGACAGTGGCTCACACCTGTATCCAGACCTT 1561
|||||
Db 50293 AGACCGACAGTGGCTCACACCTGTATCCAGACCTT 50332

RESULT 85
AC137504 138539 bp DNA linear HTG 20-NOV-2002
LOCUS Homo sapiens chromosome 16 clone RP11-915F13, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
ACCESSION AC137504.1 GI:25139898
VERSION AC137504.1 GI:25139898
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 138539)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
2 (bases 1 to 138539)
DOE Joint Genome Institute.

REFERENCE 2 (bases 1 to 138539)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1645997
Center clone name: RPCI-11_915F13

Summary Statistics
Consensus quality: 138093 bases at least Q40
Consensus quality: 138272 bases at least Q30
Consensus quality: 138302 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 138339; sum-of-contigs estimation
Quality coverage: 5.51 in Q20 bases; agarose-fp estimation
Quality coverage: 6.38 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2113: contig of 2113 bp in length
* 2114 21213: gap of unknown length
* 21214 62292: contig of 41079 bp in length
* 62293 62392: gap of unknown length
* 62393 138539: contig of 76147 bp in length.

FEATURES
source
Location/Qualifiers
1..138539

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-915F13"
/clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 138539;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACGAGGACAGTGGCTGACACCTGTATCCGACACTT 1561
DB 115949 AGACGAGGACAGTGGCTGACACCTGTATCCGACACTT 115988

source 1..142000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-102F8"
/clone_11b="RPc1 human BAC library 11"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 142000;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTGACACCTGTATCCGACACTT 1561
DB 129153 AGACGAGGACAGTGGCTGACACCTGTATCCGACACTT 129114

RESULT 87

AL353637
LOCUS AL353637 146466 bp DNA linear PRI 27-JUL-2002
DEFINITION Human DNA sequence from clone RP11-159H20 on chromosome
9q21.12-21.32, complete sequence.
ACCESSION AL353637
VERSION AL353637.21 GI:22003095
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 142000)
AUTHORS Doe Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
2 (bases 1 to 142000)
DOE Joint Genome Institute.
Direct Submission
Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 445661
Center clone name: RPC1-11_102F8

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; SW:
SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information on the WormPeP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/RGP/Chr9>

RP11-159H20 is from the library RPC1-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES

source

1..146466
/organism="Homo sapiens"
/mol_type="genomic DNA"

FEATURES

Location/Qualifiers

Summary Statistics
Consensus quality: 138021 bases at least Q40
Consensus quality: 139286 bases at least Q20
Consensus quality: 140039 bases at least Q20
Estimated insert size: 175000; agarose-1p estimation
Estimated insert size: 141200; sum-of-contigs estimation
Quality coverage: 5.25 in Q20 bases; agarose-1p estimation
Quality coverage: 6.51 in Q20 bases; sum-of-contigs estimation.
* NOTE: this is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1375 1474: gap of 1374 bp in length
1475 2626: contig of 1152 bp in length
2627 2726: gap of unknown length
2727 4125: contig of 1399 bp in length
4126 4225: gap of unknown length
4226 5287: contig of 1062 bp in length
5288 5387: gap of unknown length
5388 9562: contig of 4175 bp in length
9563 9662: gap of unknown length
9663 15412: contig of 5750 bp in length
15413 20643: contig of 5131 bp in length
20644 20743: gap of unknown length
20744 40765: contig of 20022 bp in length
40766 40865: gap of unknown length
40866 142000: contig of 101135 bp in length.
Location/Qualifiers

/db_xref="taxon:9606"
/chromosome="9"
/map="q21.12-21.32"
/clone="RP11-159H20"
/clone_lib="RPCT-11.1"

ORIGIN

Query Match 2.2%; Score 40; DB 9; Length 146466;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1522 AGACGAGCAGACGTGCTCACACCTGTATCCAGCACTT 1561
11468 AGACGAGCAGACGTGCTCACACCTGTATCCAGCACTT 114727

Db AC135778 147184 bp DNA linear HTG 22-OCT-2002
AC135778 Homo sapiens chromosome 16 clone CTD-2306D9, WORKING DRAFT
AC135778 AC135778.1 GI:24211098
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFTN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 147184)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 147184)
DOE Joint Genome Institute.
Direct Submission
Submitted (22-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 745134
Center clone name: CITB-H1_2306D9

Summary Statistics
Consensus quality: 126150 bases at least Q40
Consensus quality: 129675 bases at least Q30
Consensus quality: 132648 bases at least Q20
Estimated insert size: 160000; agarose-ef estimation
Estimated insert size: 145184; sum-of-ctigs estimation
Quality coverage: 13.94 in Q20 bases; agarose-ef estimation
Quality coverage: 15.36 in Q20 bases; sum-of-ctigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1171: contig of 1171 bp in length
* 1172 1271: gap of unknown length
* 1272 2422: contig of 1151 bp in length
* 1273 2522: gap of unknown length
* 2523 3721: contig of 1199 bp in length
* 3722 3821: gap of unknown length
* 3822 4986: contig of 1165 bp in length
* 4987 5087: gap of unknown length
* 5088 6524: contig of 1538 bp in length
* 6525 6725: gap of unknown length
* 6726 8465: contig of 1741 bp in length

8466 8565: gap of unknown length
* 8566 10400: contig of 1835 bp in length
* 10401 10500: gap of unknown length
* 10501 11679: contig of 1179 bp in length
* 11680 11779: gap of unknown length
* 11780 13096: contig of 1317 bp in length
* 13097 13196: gap of unknown length
* 13197 14303: contig of 1107 bp in length
* 14304 14403: gap of unknown length
* 14404 16154: contig of 1751 bp in length
* 16155 16254: gap of unknown length
* 16255 17677: contig of 1423 bp in length
* 17678 17777: gap of unknown length
* 17778 20438: contig of 2661 bp in length
* 20439 20538: gap of unknown length
* 20539 24172: contig of 3634 bp in length
* 24173 24272: gap of unknown length
* 24273 35459: contig of 11187 bp in length
* 35460 35559: gap of unknown length
* 35560 50735: contig of 15176 bp in length
* 50736 50835: gap of unknown length
* 50836 64001: contig of 13166 bp in length
* 64002 64101: gap of unknown length
* 64102 78843: contig of 14742 bp in length
* 78844 78943: gap of unknown length
* 78944 94158: contig of 15215 bp in length
* 94159 94258: gap of unknown length
* 94259 113028: contig of 18770 bp in length
* 113029 113128: gap of unknown length
* 113129 147184: contig of 34056 bp in length.
Location/Qualifiers
1.147184
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTD-2306D9"
/clone_lib="Caltech human BAC library D"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 147184;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1521 GAGACGAGCAGACGTGCTCACACCTGTATCCAGCACTT 1560
17401 GAGACGAGCAGACGTGCTCACACCTGTATCCAGCACTT 17440

Db AC093011 148548 bp DNA linear PRI 28-NOV-2002
AC093011 AC093011.3 GI:20334503
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 148548)
Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,
Albrooke,S.L., Amaralungu,H.C., Are,J.R., Banks,T., Barbarella,J.,
Benton,T., Binsge,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brileya,M., Brown,E., Brown,M., Bryant,N.P., Buhey,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F.,
Carter,M., Cavasoe,S.R., Chacko,J., Chaver,D., Chen,G., Chen,R.,
Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Day-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douhwalte,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falle,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Huiyk,S., Hune,D., Jackson,L.B., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korah,J., Kovar,C., Kratovic,D., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,C., Liu,W., Louised,H., Loraado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Nagua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Moabadat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokhekwo,S., Oguh,M., Okomou,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Prit,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., RojudoKan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoochattari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Swatek,A., Tabor,P., Tameris,A., Tameris,K., Tang,H., Tansey,J., Taylor,C., Taylor,C., Telford,B., Thomas,N., Thomas,S., Umami,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Worley,K.C.
2 (bases 1 to 148548)
Direct Submission
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 148548)
Worley,K.C.
Direct Submission
Submitted (26-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 148548)
Worley,K.C.
Direct Submission
Submitted (27-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 148548)
Worley,K.C.
Direct Submission
Submitted (28-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Apr 27, 2002 this sequence version replaced gi:18674204.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the

EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

source

QUALSTAT-REPORT.

Location/Qualifiers
1. 148548
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-40P7"

misc_feature

1. 2004
/notes="overlaps bases 174118..176121 of clone AC131011"
/function="clone overlap"
complement(398..700)
/rpt_family="AluSg"
complement(783..1250)
/rpt_family="LMC4"
complement(1251..1564)
/rpt_family="AluSp"
complement(1565..1642)
/rpt_family="LMC4"
1939..1966
/rpt_family="AT-rich"
2042..2072
/rpt_family="TTG)n"
complement(2073..2354)
/rpt_family="AluSc"
complement(2485..2796)
/rpt_family="AluJo"
complement(3231..3533)
/rpt_family="AluSp"
complement(3534..3828)
/rpt_family="AluSx"
5332..5644
/rpt_family="AluY"
5850..6022
/standard name="75404"
6194..6471
/rpt_family="AluSg"
6472..6495
/rpt_family="TTAA)n"
complement(6904..7168)
/rpt_family="MIR"
7261..7560
/rpt_family="AluSg1"
7720..7739
/rpt_family="(TG)n"
complement(7740..8019)
/rpt_family="AluSx"
8051..8317
/rpt_family="AluJo"
8377..9123
/rpt_family="AluJo"
complement(9130..9251)
/rpt_family="LTR25"
9252..9532

```

repeat_region /rpt_family="AluSp"
complement(9533..10199)
/rpt_family="L1R25"
repeat_region 10200..10339
/rpt_family="Aluoc"
repeat_region 10639..10928
/rpt_family="AluSx"
repeat_region complement(11562..11866)
/rpt_family="AluSx"
repeat_region complement(11891..12194)
/rpt_family="AluSg"
repeat_region 12395..12672
/rpt_family="Aluoc"
repeat_region 12681..12785
/rpt_family="AluSg/x"
repeat_region 12786..13068
/rpt_family="AluSg/x"
repeat_region complement(13105..13283)
/rpt_family="MIR"
repeat_region complement(13500..13802)
/rpt_family="AluSx"
repeat_region 13894..14183
/rpt_family="AluSx"
repeat_region 14202..14479
/rpt_family="AluSg"
repeat_region 14482..14594
/rpt_family="TA)n"
repeat_region complement(14651..14799)
/rpt_family="MER112"
repeat_region 14987..15032
/rpt_family="CCCCCA)n"
repeat_region complement(15210..15516)

```

Query Match 2.2%; Score 40; DB 9; Length 148548;
 Best Local Similarity 100.0%; Pred. No. 5.8e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGTGGCTCAGACCTGATATCCAGCACTT 1561
 DB 127258 AGACGAGCAGTGGCTCAGACCTGATATCCAGCACTT 127219

RESULT 90
 AC084815 148624 bp DNA linear HTG 15-JAN-2001
 LOCUS Homo sapiens clone RP11-788A9, WORKING DRAFT SEQUENCE, 34 unordered
 DEFINITION pieces:
 AC084815
 AC084815.2 GI:12229388
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 148624) Nussbaum, C. and Lander, E.
 Homo sapiens, clone RP11-788A9
 Unpublished
 2 (bases 1 to 148624)
 Birren, B., Linton, L., Nussbaum, C., Lander, E., Adnan, H., Allen, N.,
 Anderson, S., Barta, N., Bastien, V., Bede, F., Boguslavsky, L.,
 Boukhalil, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 Deaellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
 Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
 Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
 Iliiev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Labocque, K.,
 Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Lieu, C., Liu, G.,
 Macdonald, P., Marguis, N., McCarthy, M., McEwan, P., McKernan, K.,
 McPherson, R., Meidert, U., Menus, L., Mihova, T., Mlenga, V.,
 Morrow, J., Murphy, T., Naylor, U., Norman, C.H., O'Connor, T.,
 O'Donnell, P., O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K.,
 Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,

TITLE JOURNAL COMMENT

Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
 Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J.,
 Tirrell, A., Travers, M., Trigglio, J., Vasilev, H., Viel, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, W.O., Young, G., Zainoun, J.,
 Zimmer, A., and Zody, N.
 Direct Submission
 Submitted (19-NOV-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 15, 2001 this sequence version replaced gi:11225647.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L1509

Center clone name: 788_A9

Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 13438 bases at least Q40
 Consensus quality: 13853 bases at least Q20
 Consensus quality: 13853 bases at least Q20
 Insert size: 164000; agarose-IP
 Insert size: 145324; sum-of-contrigs
 Quality coverage: 3.6 in Q20 bases; agarose-IP
 Quality coverage: 4.0 in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 34 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1163: contig of 1163 bp in length
 1164 1263: gap of 100 bp
 1264 1977: contig of 714 bp in length
 1978 2077: gap of 100 bp
 2078 3067: contig of 990 bp in length
 3068 3167: gap of 100 bp
 3168 4340: contig of 1173 bp in length
 4341 4440: gap of 100 bp
 4441 5361: contig of 921 bp in length
 5362 5461: gap of 100 bp
 5462 6605: contig of 1144 bp in length
 6606 6705: gap of 100 bp
 6706 7814: contig of 1109 bp in length
 7815 7914: gap of 100 bp
 7915 9497: contig of 1583 bp in length
 9498 9597: gap of 100 bp
 9598 11117: contig of 1520 bp in length
 11118 11217: gap of 100 bp
 11218 12816: contig of 1599 bp in length
 12817 12916: gap of 100 bp
 12917 14048: contig of 1132 bp in length
 14049 14148: gap of 100 bp
 14149 16423: contig of 2274 bp in length
 16424 16522: gap of 100 bp
 16523 17466: contig of 944 bp in length
 17467 17566: gap of 100 bp
 17567 19094: contig of 1528 bp in length
 19095 19194: gap of 100 bp
 19195 20931: contig of 1737 bp in length
 20932 21031: gap of 100 bp
 21032 22724: contig of 1693 bp in length
 22725 22824: gap of 100 bp

```

* 22825 24816: contig of 1992 bp in length
* 24817 24916: gap of 100 bp
* 24917 27863: contig of 2947 bp in length
* 27864 27963: gap of 100 bp
* 27964 30929: contig of 2966 bp in length
* 30930 31029: gap of 100 bp
* 31030 34191: contig of 3162 bp in length
* 34192 34292: gap of 100 bp
* 34292 36523: contig of 2231 bp in length
* 36523 36622: gap of 100 bp
* 36622 38549: contig of 1927 bp in length
* 38550 38649: gap of 100 bp
* 38650 41768: contig of 3119 bp in length
* 41769 41868: gap of 100 bp
* 41869 44626: contig of 2758 bp in length
* 44627 44726: gap of 100 bp
* 44727 49894: contig of 5168 bp in length
* 49895 49994: gap of 100 bp
* 49995 55860: contig of 5866 bp in length
* 55861 55960: gap of 100 bp
* 55961 61473: contig of 5513 bp in length
* 61474 61573: gap of 100 bp
* 61574 67234: contig of 5661 bp in length
* 67235 67334: gap of 100 bp
* 67335 74758: contig of 7424 bp in length
* 74759 74858: gap of 100 bp
* 74859 83919: contig of 9061 bp in length
* 83920 84019: gap of 100 bp
* 84020 94760: contig of 10741 bp in length
* 94761 94860: gap of 100 bp
* 94861 113489: contig of 18629 bp in length
* 113490 133716: contig of 100 bp
* 133717 133816: gap of 100 bp
* 13817 148624: contig of 14808 bp in length.

```

FEATURES

SOURCE

```

/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-788A9"
/clone_lib="RP11 Human Male BAC"
1. .1163
/note="assembly_fragment"
1264. .1977
/note="assembly_fragment"
2078. .3067
/note="assembly_fragment"
3188. .4340
/note="assembly_fragment"
4441. .5361
/note="assembly_fragment"
5462. .6605
/note="assembly_fragment"
6706. .7814
/note="assembly_fragment"
7915. .9497
/note="assembly_fragment"
9598. .11117
/note="assembly_fragment"
11218. .12816
/note="assembly_fragment"
12917. .14048
/note="assembly_fragment"
14149. .16422
/note="assembly_fragment"
16523. .17466
/note="assembly_fragment"
17567. .19094
/note="assembly_fragment"
19195. .20931
/note="assembly_fragment"
21032. .22724

```

```

misc_feature /note="assembly_fragment"
22825. .24816
/note="assembly_fragment"
24917. .27863
misc_feature /note="assembly_fragment"
27964. .30929
/note="assembly_fragment"
31030. .34191
misc_feature /note="assembly_fragment"
34292. .36522
/note="assembly_fragment"
36623. .38549
misc_feature /note="assembly_fragment"
38650. .41768
misc_feature /note="assembly_fragment"
41869. .44626
misc_feature /note="assembly_fragment"
44727. .49894
misc_feature /note="assembly_fragment"
49995. .55860
misc_feature /note="assembly_fragment"
55961. .61473
misc_feature /note="assembly_fragment"
61574. .67234
misc_feature /note="assembly_fragment"

```

Query Match 2.2%: Score 40; DB 2; Length 148624;
 Best Local Similarity 100.0%; Fred. No. 5.8e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1521 GAGACCGGACAGTGGCTCACACCTGTATCCAGCACT 1560
 Db 23828 GAGACCGGACAGTGGCTCACACCTGTATCCAGCACT 23867

```

RESULT 91
AC114799/c 152709 bp DNA linear HTG 11-MAR-2002
LOCUS Homo sapiens chromosome UNK clone RP11-741115, *** SEQUENCING IN
DEFINITION PROGRESS ***; 48 unordered pieces.
ACCESSION AC114799
VERSION AC114799.1 GI:19339261
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 152709)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 152709)
REFERENCE Waterston,R.H.
AUTHORS Waterston,R.H.
TITLE Direct Substitution
JOURNAL Submitted (11-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: H_NH0741115
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

```

* be preferred.	1316: contig of 1316 bp in length
* 1317	1416: gap of unknown length
* 1417	3034: contig of 1618 bp in length
* 3035	3134: gap of unknown length
* 4163	4162: contig of 1028 bp in length
* 4263	4262: gap of unknown length
* 5330	6339: contig of 2077 bp in length
* 5440	6439: gap of unknown length
* 7650	7694: contig of 1255 bp in length
* 7795	7794: gap of unknown length
* 7955	8988: contig of 1194 bp in length
* 8959	9088: gap of unknown length
* 9089	10970: contig of 1882 bp in length
* 10971	11070: gap of unknown length
* 12771	12770: contig of 1700 bp in length
* 12871	12870: gap of unknown length
* 14824	14823: contig of 1953 bp in length
* 14924	14923: gap of unknown length
* 19264	17205: contig of 2282 bp in length
* 17206	17305: gap of unknown length
* 17306	18998: contig of 1653 bp in length
* 18999	19098: gap of unknown length
* 19099	20450: contig of 1352 bp in length
* 20451	20450: gap of unknown length
* 20551	22670: contig of 2120 bp in length
* 22671	22770: gap of unknown length
* 22771	22770: contig of 2005 bp in length
* 24776	24775: gap of unknown length
* 24876	26515: contig of 1640 bp in length
* 26516	26515: gap of unknown length
* 26616	28281: contig of 1666 bp in length
* 28282	28381: gap of unknown length
* 28382	29472: contig of 1091 bp in length
* 29473	29572: gap of unknown length
* 29573	31009: contig of 2237 bp in length
* 31810	31809: gap of unknown length
* 31910	33408: contig of 1499 bp in length
* 33409	33508: gap of unknown length
* 33509	36363: contig of 2855 bp in length
* 36364	36463: gap of unknown length
* 36464	38458: contig of 1995 bp in length
* 38459	38558: gap of unknown length
* 38559	40473: contig of 1915 bp in length
* 40474	40573: gap of unknown length
* 40574	43866: contig of 3253 bp in length
* 43867	43966: gap of unknown length
* 43967	46754: contig of 2788 bp in length
* 46755	46854: gap of unknown length
* 46855	50422: contig of 3568 bp in length
* 50423	50522: gap of unknown length
* 50523	53495: contig of 2883 bp in length
* 53406	53505: gap of unknown length
* 53506	56376: contig of 2871 bp in length
* 56377	56476: gap of unknown length
* 56477	59167: contig of 2691 bp in length
* 59168	59267: gap of unknown length
* 59268	62501: contig of 3234 bp in length
* 62502	62601: gap of unknown length
* 62602	67094: contig of 4493 bp in length
* 67095	67194: gap of unknown length
* 67195	70289: contig of 3095 bp in length
* 70290	70389: gap of unknown length
* 70390	74074: contig of 3685 bp in length
* 74075	74174: gap of unknown length
* 74175	77998: contig of 3764 bp in length
* 77939	78038: gap of unknown length
* 78039	82522: contig of 4484 bp in length
* 82523	82622: gap of unknown length
* 82623	86319: contig of 3697 bp in length
* 86320	86419: gap of unknown length
* 86420	91243: contig of 4824 bp in length
* 91244	91343: gap of unknown length

	*	95344	95641	contig of 4298 bp in length
	*	95742	95741	gap of unknown length
	*	95742	100088	contig of 4447 bp in length
	*	100089	100188	gap of unknown length
	*	100188	104088	contig of 3900 bp in length
	*	104089	104188	gap of unknown length
	*	104189	107218	contig of 3030 bp in length
	*	107219	107318	gap of unknown length
	*	111889	111888	contig of 4570 bp in length
	*	111889	111988	gap of unknown length
	*	116335	116635	contig of 4447 bp in length
	*	116336	116735	gap of unknown length
	*	116736	122217	contig of 5442 bp in length
	*	122178	122217	gap of unknown length
	*	126738	126738	contig of 4461 bp in length
	*	126739	126838	gap of unknown length
	*	132078	132077	contig of 5239 bp in length
	*	132078	132177	gap of unknown length
	*	132178	138632	contig of 6455 bp in length
	*	138633	138732	gap of unknown length
	*	138733	144136	contig of 5404 bp in length
	*	144137	144236	gap of unknown length
	*	144237	152709	contig of 8473 bp in length
FEATURES				
SOURCE				Location/Qualifiers
				1..152709
		/organism="Homo sapiens"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:9606"		
		/chromosome="UNK"		
		/clone="RP11-741115"		
misc_feature		1..1316		
		/note="assembly_name:Contig25"		
misc_feature		1417..3034		
		/note="assembly_name:Contig36"		
misc_feature		3135..4162		
		/note="assembly_name:Contig28"		
misc_feature		4263..6339		
		/note="assembly_name:Contig32"		
misc_feature		6440..7694		
		/note="assembly_name:Contig35"		
misc_feature		7795..8988		
		/note="assembly_name:Contig36"		
misc_feature		9089..10970		
		/note="assembly_name:Contig38"		
misc_feature		11071..12770		
		/note="assembly_name:Contig40"		
misc_feature		12871..14823		
		/note="assembly_name:Contig41"		
misc_feature		14924..17205		
		/note="assembly_name:Contig43"		
misc_feature		17306..18998		
		/note="assembly_name:Contig44"		
misc_feature		19099..20450		
		/note="assembly_name:Contig45"		
misc_feature		20511..22670		
		/note="assembly_name:Contig46"		
misc_feature		22771..24775		
		/note="assembly_name:Contig47"		
misc_feature		24876..26515		
		/note="assembly_name:Contig48"		
misc_feature		26516..28281		
		/note="assembly_name:Contig49"		
misc_feature		28382..29472		
		/note="assembly_name:Contigs"		
misc_feature		29573..31809		
		/note="assembly_name:Contig50"		
misc_feature		31910..33408		
		/note="assembly_name:Contig51"		
misc_feature		33509..36363		
		/note="assembly_name:Contig52"		
misc_feature		36464..38458		
		/note="assembly_name:Contig53"		
misc_feature		38559..40473		

misc_feature	/note="assembly_name:Config54"
misc_feature	40574. .43866
misc_feature	/note="assembly_name:Config55"
misc_feature	43967. .46754
misc_feature	/note="assembly_name:Config56"
misc_feature	46855. 50422
misc_feature	/note="assembly_name:Config57"
misc_feature	50523. .53405
misc_feature	/note="assembly_name:Config58"
misc_feature	53506. .56376
misc_feature	/note="assembly_name:Config59"
misc_feature	56477. .59167
misc_feature	/note="assembly_name:Config60"
misc_feature	59268. .62501
misc_feature	/note="assembly_name:Config61"
misc_feature	62602. 67094
misc_feature	/note="assembly_name:Config62"
misc_feature	67195. .70289

Query Match	2.2%;	Score 40;	DB 2;	Length 152709;
Best Local Similarity	100.0%;	Pred. No. 5.8e-10;		
Matches	40;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	1322	AGACCAAGGCACTGGCTCACACCTGTATCCAGCACTT	1561
Db	104986	AGACCAGGCACTGGCTCACACCTGTATCCAGCACTT	104947

AC013533/c	AC013533	153289 bp	DNA	linear	HTG 26-MAY-2000
LOCUS					
DEFINITION	Homo sapiens clone RP11-114N8, WORKING DRAFT SEQUENCE, 8 unordered				

ACCESSION	AC013553
VERSION	AC013553.3
KEYWORDS	GI:7107783
SOURCE	Httg: HNGS_PHASE1; HNGS_DRAFT
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Eukaryota, Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 153289)
Biren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone Rp11-114n8
Unpublished
2 (bases 1 to 153289)
Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, N.

TITLE Direct Submission
JOURNAL Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Feb 28, 2000 this sequence version replaced gi:6649485.

```
-----
Center clone name: 114 N 8
Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.96073
Consensus quality: 147505 bases at least Q40
Consensus quality: 151078 bases at least Q30
Consensus quality: 152040 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 12589; sum-of-ctrls
Quality coverage: 5.1 in Q20 bases; agarose-fp
Quality coverage: 5.6 in Q20 bases; sum-of-ctrls
```

```
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

*	1065	gap of 100 bp
*	1161	contig of 2318 bp in length
*	1162	gap of 100 bp
*	3579	gap of 100 bp
*	3480	contig of 2283 bp in length
*	5862	gap of 100 bp
*	5863	gap of 100 bp
*	12427	contig of 6465 bp in length
*	12527	gap of 100 bp
*	14248	contig of 13895 bp in length
*	15528	contig of 100 bp
*	26522	gap of 100 bp
*	25523	contig of 22307 bp in length
*	48825	gap of 100 bp
*	48830	contig of 28693 bp in length
*	48930	gap of 100 bp
*	77623	gap of 100 bp
*	77723	contig of 75567 bp in length

FEATURES	Location/Qualifiers
source	1. .153289

```
misc_feature      1..1061  
                  /note="assembly_fragment"  
misc_feature      1162..3479  
                  /note="assembly_fragment"  
misc_feature      3580..5862  
                  /note="assembly_fragment"  
                  clone_end="r7"  
                  vector_side="right"  
misc_feature      5963..12427  
                  /note="assembly_fragment"  
misc_feature      12528..26422  
                  /note="assembly_fragment"  
misc_feature      26523..48829  
                  /note="assembly_fragment"  
misc_feature      48930..77622  
                  /note="assembly_fragment"  
                  clone_end="SP6"  
                  vector_side="right"  
misc_feature      77723..153289  
                  /note="assembly_fragment"
```

ORI

Query Match	2.2%	Score 40;	DB 2;	Length 153289;
Best Local Similarity	100.0%	Pred. No. 5.8e-10;		
Matches 40;	Conservative 0;	Mismatches 0;	Gaps 0	

Qy		1522 AGACGAGCACGTGGCTCACCCTGTATCCAGCACTT	1561
Db		21967 AGACCAGGCACAGTGCTCACACTGTATCCCAGCACTT	21928

```

RESULT 93
AC092726/c 159264 bp DNA linear HTG 21-JUL-2001
LOCUS Homo sapiens chromosome 16 clone RP11-77K21, WORKING DRAFT
DEFINITION AC092726, 9 unordered pieces.
ACCESSION AC092726 AC016686
VERSION AC092726.1 GI:14993713
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 159264)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 159264)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:7230858.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 436194
Center clone name: RPCT-11_77K21
-----
Summary Statistics
Consensus quality: 147604 bases at least Q40
Consensus quality: 155121 bases at least Q30
Consensus quality: 156628 bases at least Q20
Estimated insert size: 16000; agarose-fp estimation
Estimated insert size: 158464; sum-of-contigs estimation
Quality coverage: 6.34 in Q20 bases; agarose-fp estimation
Quality coverage: 6.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1026: contig of 1026 bp in length
1027 1126: gap of unknown length
1127 2248: contig of 1122 bp in length
2249 2348: gap of unknown length
2349 9903: contig of 7555 bp in length
9904 10003: gap of unknown length
10004 21613: contig of 11610 bp in length
21614 37840: contig of 16127 bp in length
37841 37940: gap of unknown length
37941 56393: contig of 18453 bp in length
56394 56494: gap of unknown length
56494 88962: contig of 32469 bp in length
88962 89062: gap of unknown length
89063 119384: contig of 30322 bp in length
119385 119484: gap of unknown length
119485 159264: contig of 39780 bp in length.
Location/Qualifiers
1. 159264
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-77K21"
/clone_1b="RPCT human BAC library 11"

```

```

ORIGIN
Query Match 2.2% Score 40; DB 2; Length 159264;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1521 GAGACCGACGACAGTGCGCTCACACCTGTATCCGACACT 1560
2986 GAGACCGACGACAGTGCGCTCACACCTGTATCCGACACT 2947

Db

RESULT 94
AC021454 159849 bp DNA linear HTG 13-MAY-2001
LOCUS Homo sapiens chromosome 11 clone RP11-135C4 map 11, WORKING DRAFT
DEFINITION AC021454, 10 unordered pieces.
ACCESSION AC021454
VERSION AC021454.6 GI:14030020
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 159849)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-135C4
Unpublished
2 (bases 1 to 159849)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckert,L.R., Beda,F.,
Boguslavsky,I., Bouckhalter,B., Brown,A., Burkett,G., Casale,A.,
Choquel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeRubeis,K., Dewar,K., Domino,M., Doyle,M., Fenger,J.,
Ferrante,P., Fitzhugh,M., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heath,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karas,A., Klein,J.,
Lander,T., Lechoczek,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Margis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheters,R., Meidum,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivier,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vasiliou,H., Vail,R., Vo,A., Wu,X., Wyman,D., Ye,W.,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 13, 2001 this sequence version replaced gi:13164154.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center Code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----Project Information
Center Project Name: 135_C4
Center clone name: 135_C4
-----Summary Statistics
Sequencing vector: M13; M77815; 43% of reads
Sequencing vector: Plasmid; n/a; 57% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157951 bases at least Q40
Consensus quality: 158500 bases at least Q30
Consensus quality: 158500 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 158949; sum-of-contigs
Quality coverage: 8.5 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 bases;
* NOTE: This is a 'working draft' sequence. It currently

```

* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
823 822: contig of 822 bp in length
923 922: gap of 100 bp
2424 2423: contig of 1501 bp in length
2524 2523: gap of 100 bp
5822 5822: contig of 3299 bp in length
5923 5922: gap of 100 bp
8687 8687: contig of 2765 bp in length
8788 8787: gap of 100 bp
14999 14998: contig of 6211 bp in length
15099 15098: gap of 100 bp
24863 24862: contig of 9764 bp in length
24963 24962: gap of 100 bp
34327 34326: contig of 9364 bp in length
34427 34426: gap of 100 bp
86297 86297: contig of 51871 bp in length
86397 86397: gap of 100 bp
133112 133111: contig of 46914 bp in length
133412 133411: gap of 100 bp
133412 159849: contig of 26438 bp in length.

FEATURES
source

1.159849
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-135C4"
/clone_lib="RP11-11 Human Male BAC"
1.822
/note="assembly_fragment"
clone_end:8p6
vector_side:left"
923..2423
/note="assembly_fragment"
2524..5822
/note="assembly_fragment"
5923..8687
/note="assembly_fragment"
8788..14998
/note="assembly_fragment"
15099..24862
/note="assembly_fragment"
24963..34326
/note="assembly_fragment"
34427..86297
/note="assembly_fragment"
86398..133111
/note="assembly_fragment"
133412..159849
/note="assembly_fragment"
clone_end:17
vector_side:right"

ORIGIN

Query Match 2.2%: Score 40; DB 2; Length 159849;
Best Local Similarity 100.0%; Pred No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 10981 AGACGAGCAGTGGCTCACACCTGTATCCAGCACTT 11020

RESULT 95
AC051664
LOCUS

AC051664 160169 bp DNA linear HTG 01-SEP-2000

DEFINITION Homo sapiens chromosome 11 clone RP11-810P12, WORKING DRAFT
SEQUENCE, 24 unordered pieces.
AC051664
AC051664.2 GI:7637836
HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On Apr 23, 2000 this sequence version replaced gi:7574984.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H NH0810P12
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid, 0%
Chemistry: Dye-terminator Big Dye, 0% of reads
Chemistry: Dye-terminator Big Dye, 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147316 bases at least Q40
Consensus quality: 152875 bases at least Q30
Insert size: 16500; agarose-fp
Insert size: 157869; sum-of-contigs
Quality coverage: 3.91 in Q20 bases; agarose-fp
Quality coverage: 4.17 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1926: contig of 1926 bp in length
1927 2026: gap of unknown length
2027 4202: contig of 2176 bp in length
4203 4302: gap of unknown length
4303 7163: contig of 2861 bp in length
7164 7263: gap of unknown length
7264 9961: contig of 2698 bp in length
9962 10061: gap of unknown length
10062 12575: contig of 2514 bp in length
12576 12675: gap of unknown length
12676 15645: contig of 2870 bp in length
15646 15645: gap of unknown length
15646 20941: contig of 5296 bp in length
20942 21041: gap of unknown length
21042 23965: contig of 2925 bp in length
23967 24065: gap of unknown length
24066 27231: contig of 3165 bp in length
27232 27331: gap of unknown length
27332 30550: contig of 3219 bp in length
30551 30650: gap of unknown length
30651 35202: contig of 4552 bp in length
35203 35302: gap of unknown length
35303 40201: contig of 4899 bp in length
40202 40301: gap of unknown length


```
* 40302 45758: contig of 5457 bp in length
* 45759 45858: gap of unknown length
* 45859 51249: contig of 5391 bp in length
* 51250 51349: gap of unknown length
* 51350 58267: contig of 6818 bp in length
* 58268 58367: gap of unknown length
* 58368 66917: contig of 8549 bp in length
* 66917 77145: gap of unknown length
* 77145 77245: contig of 10129 bp in length
* 77245 86493: gap of unknown length
* 86493 86593: gap of unknown length
* 86594 96688: contig of 10095 bp in length
* 96689 96788: gap of unknown length
* 96789 107169: contig of 10381 bp in length
* 107170 107269: gap of unknown length
* 107270 117047: contig of 9778 bp in length
* 117048 117147: gap of unknown length
* 117148 127120: contig of 9973 bp in length
* 127121 127220: gap of unknown length
* 127221 142029: contig of 14809 bp in length
* 142030 142129: gap of unknown length
* 142130 160169: contig of 18040 bp in length.
* 142130 Location/Qualifiers
1. 160169
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-810P12"
1. 1926
/note="assembly_name:Contig18"
misc_feature 2027..4202
/note="assembly_name:Contig19"
misc_feature 4303..7163
/note="assembly_name:Contig20"
clone end:17
vector side:left"
7264..7961
/note="assembly_name:Contig21"
misc_feature 10062..12575
/note="assembly_name:Contig22"
misc_feature 12676..15345
/note="assembly_name:Contig23"
misc_feature 15646..20941
/note="assembly_name:Contig24"
misc_feature 21042..23966
/note="assembly_name:Contig25"
misc_feature 24067..27231
/note="assembly_name:Contig26"
misc_feature 27332..30550
/note="assembly_name:Contig27"
misc_feature 30651..35202
/note="assembly_name:Contig28"
misc_feature 35303..40201
/note="assembly_name:Contig29"
misc_feature 40302..45758
/note="assembly_name:Contig30"
misc_feature 45859..51249
/note="assembly_name:Contig31"
misc_feature 51350..58267
/note="assembly_name:Contig32"
misc_feature 58368..66916
/note="assembly_name:Contig33"
misc_feature 67017..77145
/note="assembly_name:Contig34"
misc_feature 77246..86493
/note="assembly_name:Contig35"
misc_feature 86594..96688
/note="assembly_name:Contig36"
misc_feature 96789..107169
/note="assembly_name:Contig37"
misc_feature 107270..117047
```

```
misc_feature /note="assembly_name:Contig38"
117148..127120
/note="assembly_name:Contig39"
clone end:SP6
vector side:right"
127221..142028
/note="assembly_name:Contig40"
142130..160169
/note="assembly_name:Contig41"
ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 160169;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 154494 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 154533
RESULT 96
LOCUS AL138815/c
DEFINITION Human DNA sequence from clone RP11-141F12 on chromosome 13 Contains the 3' end of a gene similar to chromaffin granule ATPase II, a pseudogene similar to a hypothetical protein, a Cpg island, ESTs, SNPs and GSSs, complete sequence.
ACCESSION AL138815
VERSION AL138815.6 GI:8248960
KEYWORDS HTG; ATPase II; CPG island.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160210)
Matthews,L.
Direct Submission
Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jun 5, 2000 this sequence version replaced gi:8217532.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations corresponding to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unseq' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elgans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/RGP/Chr13
RP11-141F12 is from the library RP01-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBac3.6
This sequence is the entire insert of clone RP11-141F12 The true left end of clone RP11-467D10 is at 7869 in this sequence. The true right end of clone RP11-398O19 is at 26919 in this sequence.
Location/Qualifiers
1. 160210
/organism="Homo sapiens"
/mol_type="genomic DNA"
```

```
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP1-141F12"
/clone_1ib="RP1-11.1"
15..557
/misc_feature
/note="match: GSS: Em:AQ389134"
39..582
/misc_feature
/note="match: GSS: Em:AQ324023
match: SIS: Em:G57102"
misc_feature
956..1422
/note="match: GSS: Em:AQ685826"
complement(join(2033..2436,9702..9793,53645..53749,
60661..60749,159916..160023))
/gene="BA141F12.1"
complement(join(2033..2436,9702..9793,53645..53749,
60661..60749,159916..160023))
/gene="BA141F12.1"
/product="BA141F12.1 (Similar to chromaffin granule ATPase
II)"
/note="match: cDNAs: Em:AF236871 Em:AL137256 Em:AF156550
Em:U75321
match: ESTs: Em:AA493861 Em:AA528117 Em:AI694347"
evidence=not_experimental
complement(2033)
/gene="BA141F12.1"
complement(2053..2058)
/gene="BA141F12.1"
complement(join(2339..2436,9702..9793,53645..53749,
60661..60749,159916..160023))
/gene="BA141F12.1"
/note="match: proteins: Tr:Q29449 Tr:Q9Y2Q0 Tr:P70704"
/codon_start=1
evidence=not_experimental
/product="BA141F12.1 (Similar to chromaffin granule ATPase
II)"
/protein_id="CAC12646.1"
/db_xref="GI:10638488"
/db_xref="GOA:Q9NT12"
/db_xref="SWISS-PROT:Q9NT12"
/translation="FSLHAWGSMILTWLVFGIVSTIWPPIPIADMGQATWLSA
HFWLGLFVPTACTLDEVAMRAKATKTLLEVEQELTSRVGLKVLDSGKSL
NERDRILKRGKRPPLPRSSSLQGVPHGAFSGEHNAGVSGEVLVAVDTTKKXS
PKK"
repeat_region
2917..3212
/note="AluX repeat: matches 1..293 of consensus"
complement(3230..3797)
/gene="BA141F12.1"
/note="match: GSS: Em:AQ537760"
3385..3603
repeat_region
/note="MIR repeat: matches 31..262 of consensus"
7556..7634
repeat_region
/note="MIR repeat: matches 201..262 of consensus"
7635..8093
repeat_region
/note="LOR1b repeat: matches 1..459 of consensus"
8094..8205
repeat_region
/note="MIR repeat: matches 31..201 of consensus"
8623..8931
repeat_region
/note="AluSg repeat: matches 1..310 of consensus"
9567..9690
/note="62 copies 2 mer cc 62% conserved"
9571..10174
/note="CPG island"
evidence=not_experimental
repeat_region
10377..10672
/note="AluJo repeat: matches 1..294 of consensus"
10806..11119
repeat_region
/note="MIR1B repeat: matches 3..390 of consensus"
11466..11864
/misc_feature
/note="match: GSS: Em:B38179"
12241..12540
repeat_region
/note="AluX repeat: matches 1..301 of consensus"
15396..16670
/note="LIM4 repeat: matches 3737..5016 of consensus"

repeat_region
16672..19745
/note="LIM43 repeat: matches 2930..6073 of consensus"
19763..20079
repeat_region
/note="LIP46 repeat: matches 5821..6138 of consensus"
20083..20313
repeat_region
/note="LIM47 repeat: matches 6047..6281 of consensus"
20329..21458
repeat_region
/note="LIMB5 repeat: matches 5009..6168 of consensus"
22578..22676
/note="L2 repeat: matches 2591..2707 of consensus"
complement(23016..23497)
/gene="BA141F12.1"
/note="match: GSS: Em:AQ215971"
23740..25209
repeat_region
/note="LIMB3 repeat: matches 240..1655 of consensus"
25210..25340
repeat_region
/note="AluSx repeat: matches 5..136 of consensus"
25341..25631
repeat_region
/note="AluSx repeat: matches 1..291 of consensus"
25632..25807
repeat_region
/note="AluSx repeat: matches 136..308 of consensus"
25808..28869
repeat_region
/note="LIMB3 repeat: matches 1655..5063 of consensus"
28830..29036
/note="LIP repeat: matches 4008..4232 of consensus"
29057..29627
/note="LIP2 repeat: matches 5576..6146 of consensus"
29643..30229
repeat_region
/note="LIMD1 repeat: matches 5023..5608 of consensus"
30230..30309
repeat_region
/note="LIMB6 repeat: matches 6083..6163 of consensus"
30328..30396
repeat_region
/note="MIR1H repeat: matches 424..493 of consensus"
30421..31070
repeat_region
/note="LIMD1 repeat: matches 5594..6224 of consensus"
31693..32138
repeat_region
/note="L2 repeat: matches 2252..2709 of consensus"
complement(34962..35338)
/gene="BA141F12.1"
/note="match: GSS: Em:AQ044136"
35489..36259
repeat_region
/note="LIM49 repeat: matches 5531..6308 of consensus"
37697..38002
repeat_region
/note="AluSx repeat: matches 1..312 of consensus"
38077..38371
repeat_region
/note="AluJo repeat: matches 3..293 of consensus"
41426..41599
repeat_region
/note="FAM repeat: matches 1..173 of consensus"
41686..41994
repeat_region
/note="L2 repeat: matches 2159..2495 of consensus"
42015..42063
repeat_region
/note="MIR39D repeat: matches 501..549 of consensus"
42113..42471
repeat_region
/note="MIR39 repeat: matches 4..743 of consensus"
42633..43138
/misc_feature
/note="match: GSS: Em:AQ664749"
43375..43664
repeat_region
/note="AluJo repeat: matches 1..291 of consensus"
44663..44692
repeat_region
/note="10 copies 3 mer aac 93% conserved"
45217..45544
repeat_region
/note="AluSg1 repeat: matches 1..306 of consensus"
46106..46237
repeat_region
/note="FLAM A repeat: matches 10..142 of consensus"
46510..46724
repeat_region
/note="LIMC5 repeat: matches 7712..7929 of consensus"
46727..47032
repeat_region
/note="AluJo repeat: matches 1..297 of consensus"
47189..47496
/misc_feature
/note="match: SIS: Em:G03395"
48135..48233
repeat_region
/note="MIR repeat: matches 22..133 of consensus"
complement(48526..48975)
```

/gene="BA141F12.1"
/note="match: GSS: Em:A0674520"
misc_feature 48983..49691

Query Match 2.2%; Score 40; DB 9; Length 160210;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGTCTACACCTGTATCCGACACTT 1561
Db 57447 AGACGAGGACAGTGTCTACACCTGTATCCGACACTT 57408

RESULT 97
AC109925/c 160855 bp DNA linear PRI 27-JAN-2003
DEFINITION Homo sapiens BAC clone RP11-398J16 from 4, complete sequence.
ACCESSION AC109925
VERSION AC109925.4 GI:27777623
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 160855)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE The sequence of Homo sapiens BAC clone RP11-398J16
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 160855)
AUTHORS Waterston, R.H.
TITLE Direct Submision
JOURNAL Submitted (08-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 160855)
AUTHORS Waterston, R.H.
TITLE Direct Submision
JOURNAL Submitted (11-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 160855)
AUTHORS Waterston, R.H.
TITLE Direct Submision
JOURNAL Submitted (17-JAN-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 160855)
AUTHORS Waterston, R.
TITLE Direct Submision
JOURNAL Submitted (27-JAN-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Jan 17, 2003 this sequence version replaced gi:20136966.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.edu
----- Summary Statistics
Center project name: H_NH0398J16

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Caranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

This sequence is not the entire insert of the clone. This clone is overlapped by AC110297 and AC093778.

FEATURES

source
1..160855
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-398J16"
/clone_11b="RP11-11"
3549..5998
/rpt_family="L1"
6246..6454
/rpt_family="L1"
6530..6685
/rpt_family="L2"
6787..7003
/rpt_family="L2"
6988..7370
/rpt_family="CR1"
7377..7790
/rpt_family="CR1"
8088..8224
/rpt_family="CR1"
8228..8472
/rpt_family="L1"
8473..8898
/rpt_family="ERV1"
8906..9475
/rpt_family="L1"
9476..10345
/rpt_family="ERV1"
10346..10684
/rpt_family="L1"
10823..11143
/rpt_family="L1"
11257..11294
/rpt_family="MALR"
11743..11893
/rpt_family="CR1"
13173..13284
/rpt_family="MIR"
13560..13869
/rpt_family="MIR"
14567..14906
/rpt_family="Alu"
15035..15326
/rpt_family="Alu"

```

repeat_region      15704..15777
                    /rpt_family="L1"
repeat_region      15778..16072
                    /rpt_family="Alu"
repeat_region      16073..16190
                    /rpt_family="L1"
repeat_region      16196..16404
                    /rpt_family="L1"
repeat_region      16495..16615
                    /rpt_family="L1"
repeat_region      17359..17653
                    /rpt_family="MaLR"
repeat_region      17634..17891
                    /rpt_family="Alu"
repeat_region      17897..17960
                    /rpt_family="(TTTC)n"
repeat_region      17963..18274
                    /rpt_family="Alu"
repeat_region      18287..18466
                    /rpt_family="Alu"
repeat_region      18470..18771
                    /rpt_family="Alu"
repeat_region      18778..18844
                    /rpt_family="MaLR"
repeat_region      19887..20007
                    /rpt_family="AT-rich"
repeat_region      20830..21032
                    /rpt_family="L2"
repeat_region      21693..21794
                    /rpt_family="MTR"
repeat_region      22315..22399
                    /rpt_family="MTR"
repeat_region      22396..22476
                    /rpt_family="L2"
repeat_region      22477..22764
                    /rpt_family="Alu"
repeat_region      22836..22935
                    /rpt_family="MTR"
repeat_region      23516..23745
                    /rpt_family="MTR"
repeat_region      24283..24373
                    /rpt_family="MTR"
repeat_region      24621..24754
                    /rpt_family="MTR"
repeat_region      25279..25366
                    /rpt_family="MTR"
repeat_region      25558..25841
                    /rpt_family="L1"
repeat_region      27220..27244
                    /rpt_family="AT-rich"
repeat_region      27468..27583
                    /rpt_family="L1"
repeat_region      27630..27926
                    /rpt_family="Alu"
repeat_region      28695..28848
                    /rpt_family="MTR"
repeat_region      30304..30605
                    /rpt_family="L1"
repeat_region      30767..30857
                    /rpt_family="MaLR"
repeat_region      30898..30983
                    /rpt_family="MaLR"
repeat_region      31278..31730
                    /rpt_family="ERVU"
repeat_region      31883..32541
                    /rpt_family="ERVU"
repeat_region      32549..32694
                    /rpt_family="ERVU"
repeat_region      32919..33213
                    /rpt_family="MERL_type"

```

Query Match 2.2%; Score 40; DB 9; Length 160855;
 Best Local Similarity 100.0%; Pred. No. 5,8e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy      1522 AGACGAGGACAGTGGCTCACACCTGTATCCAGACCTT 1561
Db      17892 AGACGAGGACAGTGGCTCACACCTGTATCCAGACCTT 17853

RESULT 98
AC021281
LOCUS   160984 bp      DNA      linear      HTG 16-MAR-2000
DEFINITION Homo sapiens clone RP11-21F13, WORKING DRAFT SEQUENCE, 22 unordered
           pieces
ACCESSION AC021281
VERSION   AC021281.3
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 160984)
           Birren,B., Linton,L., Nuebaum,C. and Lander,E.
           Homo sapiens chromosome, clone RP11-21F13
           Unpublished
           2 (bases 1 to 160984)
           Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
           Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bede,F.,
           Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,
           Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
           Daretellano,K., Dewar,K., Domino,M., Doyle,M., Fenesor,J.,
           Farrelira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
           Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
           Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
           Landers,T., Lepoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
           McDonaId,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K.,
           McPheters,R., Melgrim,J., Meneus,L., Morrow,J., Naylor,J.,
           Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
           Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Roehman,D.,
           Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
           Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
           Titrrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
           Zimmer,A. and Zody,M.
           Direct Submission
           Submitted (16-UN-2000) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
           On Feb 28, 2000 this sequence version replaced GI:6899768.
           All repeats were identified using RepeatMasker:
           Smit, A.F.A. & Green, P. (1996-1997)
           http://ftp.genome.washington.edu/RM/RepeatMasker.html
           ----- Genome Center
           Center: Whitehead Institute/ MIT Center for Genome Research
           Center code: WIR
           Web site: http://www-seq.wi.mit.edu
           Contact: sequence_submissions@genome.wi.mit.edu
           ----- Project Information
           Center project name: L3998
           ----- Summary Statistics
           Sequencing vector: M13; 877815, 100% of reads
           Chemistry: Dye-terminator Big Dye; 100% of reads
           Assembly program: Phrap; version 0.960731
           Consensus quality: 144959 bases at least Q40
           Consensus quality: 152120 bases at least Q30
           Consensus quality: 155461 bases at least Q20
           Insert size: 16500; agarose-fp
           Insert size: 15888; sum-of-contigs
           Quality coverage: 3.7 in Q20 bases; agarose-fp
           Quality coverage: 3.9 in Q20 bases; sum-of-contigs

```

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 22 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence

TITLE
JOURNAL
COMMENT

Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 4, 2001 this sequence version replaced gi:12039464.
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997) RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L11863
Center clone name: 810_P_12
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 162458 bases at least Q40
Consensus quality: 162916 bases at least Q20
Consensus quality: 163173 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 16315; sum-of-contigs
Quality coverage: 10.5 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 17285: contig of 17285 bp in length
* 17286 17385: gap of 100 bp
* 17386 19170: contig of 1785 bp in length
* 19171 19270: gap of 100 bp
* 19271 28600: contig of 9330 bp in length
* 28601 28700: gap of 100 bp
* 28701 47671: contig of 18871 bp in length
* 47672 47771: gap of 100 bp
* 47772 105063: contig of 57292 bp in length
* 105064 105163: gap of 100 bp
* 105164 142181: contig of 37018 bp in length
* 142182 142281: gap of 100 bp
* 142282 163915: contig of 21634 bp in length.

FEATURES

source

1.163915
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-810P12"
/clone_lib="RP11-11 Human Male BAC"
1.17285
/note="assembly_fragment"
clone_end:SP6
vector_side:left
17386..19170
/note="assembly_fragment"
19271..28600
/note="assembly_fragment"
28701..47671
/note="assembly_fragment"
47772..105063
/note="assembly_fragment"
105164..142181
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature

/note="assembly_fragment"
142282..163915
/note="assembly_fragment"
clone_end:T7
vector_side:right"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 163915;
Best local similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1522 AGACCGGACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 40267 AGACCGGACAGTGGCTCACACCTGTATCCGACACTT 40306

RESULT 100

AC123900 166485 bp DNA linear PRI 29-JUN-2002
LOCUS AC123900/c
DEFINITION Homo sapiens chromosome 3 clone RP11-640D6, complete sequence.
AC123900
AC123900.2 GI:21629387
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE

1 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Mammalia, Euteria, Primates, Catarrhini, Homnidae, Homo.
3 (bases 1 to 166485)
Saenphimachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission

REFERENCE

1 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
2 (bases 1 to 166485)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (04-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 166485)

REFERENCE

1 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission
Submitted (29-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 29, 2002 this sequence version replaced gi:21322810.

JOURNAL

On Jun 29, 2002 this sequence version replaced gi:21322810.

COMMENT

Center: University of Washington Genome Center
Center Code: UMG
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Project Information
Center project name: chr-3
Center clone name: RP11-640D6 (bc0506)
Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 10% of reads
Chemistry: Dye-terminator Big Dye; 81% of reads
Assembly program: Phrap; version 0.950319
Consensus quality: 166343 bases at least Q40
Consensus quality: 166451 bases at least Q30
Consensus quality: 166480 bases at least Q20
Insert size: 166485; sum-of-contigs
Quality coverage: 7.5x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-627J17 (UMGC:bc0502) AC112211 21818-bp overlap
3': RP11-294O18 (UMGC:bc0346) AC122176

Sequence Quality Assessment:

This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fingerprints with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

BglII

HindIII

SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt
8696	8737	2811	2816	1461	1410
6	<800	2067	2044	6382	6450
3530	3515	11749	11492	512	<800
5654	5722	4594	4513	449	<800
517	<800	4382	4513	8031	8087
3794	3785	4295	4513	4570	4537
8317	8204	2621	2816	274	<800
1659	1620	1611	1564	3606	3653
8141	8204	1043	1015	590	<800
646	<800	3299	3403	5372	5286
2223	2226	885	861	3079	3054
3811	3785	9258	9095	775	<800
3020	3008	282	<800	659	<800
2953	3008	2006	2044	1190	1170
3240	3226	11003	11492	1367	1328
3763	3785	8	<800	4836	4684
13647	13653	4619	4513	408	<800
3457	3515	449	<800	21	<800
379	<800	1955	2044	258	<800
10453	10224	2840	2816	4524	4537
5001	5031	1561	1564	3411	3436

388	<800	6877	6790	948	911
832	842	16065	15540	272	<800
165	<800	4076	3837	4359	4227
116	<800	15346	15540	210	<800
4232	4241	1520	1564	4666	4684
6490	6601	141	<800	854	911
3319	3327	83	<800	10084	10002
1081	1076	7283	7183	1420	1410
7379	7393	844	861	2040	2051
907	918	3456	3403	2972	3054
5434	5406	412	<800	4263	4227
14267	14476	4550	4513	4172	4227
7852	7869	439	<800	386	<800
2483	2526	12228	11492	3588	3653
1573	1533	525	<800	267	<800
2706	2706	2095	2044	10609	10500
5788	5722	533	<800	11893	11650
1413	1381	386	<800	645	<800
12127	11968	308	<800	1350	1328
901	918	2561	2598	1765	1742
2140	2117	3867	3837	1002	1007
430	<800	11514	11492	1619	1590
254	<800	743	731	4250	4227
		1621	1564	15992	16197
		720	731	5279	5286
		2767	2816	3965	4227
		144	<800	4595	4684
		542	<800	5928	5910
				900	911
				6373	6450
				1882	1867
				539	<800
				559	<800
				3763	3959

FEATURES

source

Location/Qualifiers
1..166485
/organism="Homo sapiens"
/mol_type="genomic DNA"

Mon Apr 19 12:46:05 2004

us-10-063-523-21.01g10.rge

Page 97

Query Match 2.2%; Score 40; DB 9; Length 16485;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACCGGCGACAGTGGCTCAGACCTGTATCCCGACTT 1561
DB 128469 AGACCGGCGACAGTGGCTCAGACCTGTATCCCGACTT 128430

Search completed: April 17, 2004, 21:04:26
Job time : 7293 secs

Mon Apr 19 12:46:09 2004

us-10-063-523-21.rmpb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 777 Seconds
(without alignments)

10648.005 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849
Sequence: 1 ctgagcgcgctagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2890132 seqs, 2237290423 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	1849	9	US-09-989-722-157 Sequence 157, App
2	1849	100.0	1849	9	US-09-989-723-157 Sequence 157, App
3	1849	100.0	1849	9	US-09-989-729-157 Sequence 157, App
4	1849	100.0	1849	9	US-09-989-727-157 Sequence 157, App
5	1849	100.0	1849	9	US-09-989-731-157 Sequence 157, App
6	1849	100.0	1849	9	US-09-989-732-157 Sequence 157, App
7	1849	100.0	1849	9	US-09-990-442-157 Sequence 157, App
8	1849	100.0	1849	9	US-09-991-163-157 Sequence 157, App
9	1849	100.0	1849	9	US-09-993-604-157 Sequence 157, App
10	1849	100.0	1849	9	US-09-990-456-157 Sequence 157, App
11	1849	100.0	1849	9	US-09-989-721-157 Sequence 157, App
12	1849	100.0	1849	9	US-09-992-598-157 Sequence 157, App
13	1849	100.0	1849	9	US-09-989-733A-157 Sequence 157, App
14	1849	100.0	1849	9	US-09-989-735-157 Sequence 157, App
15	1849	100.0	1849	9	US-09-989-735-157 Sequence 157, App

16	1849	100.0	1849	9	US-09-990-444-157 Sequence 157, App
17	1849	100.0	1849	9	US-09-991-181-157 Sequence 157, App
18	1849	100.0	1849	9	US-09-989-730-157 Sequence 157, App
19	1849	100.0	1849	9	US-09-990-436-157 Sequence 157, App
20	1849	100.0	1849	9	US-09-993-687-157 Sequence 157, App
21	1849	100.0	1849	10	US-09-989-734-157 Sequence 157, App
22	1849	100.0	1849	10	US-09-997-653-157 Sequence 157, App
23	1849	100.0	1849	10	US-09-993-663-157 Sequence 157, App
24	1849	100.0	1849	10	US-09-997-666-157 Sequence 157, App
25	1849	100.0	1849	10	US-09-990-438-157 Sequence 157, App
26	1849	100.0	1849	10	US-09-990-563-157 Sequence 157, App
27	1849	100.0	1849	10	US-09-990-711-157 Sequence 157, App
28	1849	100.0	1849	10	US-09-989-726-157 Sequence 157, App
29	1849	100.0	1849	10	US-09-988-158-157 Sequence 157, App
30	1849	100.0	1849	10	US-09-990-437-157 Sequence 157, App
31	1849	100.0	1849	10	US-09-991-157-157 Sequence 157, App
32	1849	100.0	1849	10	US-09-997-573-157 Sequence 157, App
33	1849	100.0	1849	10	US-09-997-573-157 Sequence 157, App
34	1849	100.0	1849	10	US-09-991-172-157 Sequence 157, App
35	1849	100.0	1849	10	US-09-997-573-157 Sequence 157, App
36	1849	100.0	1849	10	US-09-997-559-157 Sequence 157, App
37	1849	100.0	1849	10	US-09-997-601-157 Sequence 157, App
38	1849	100.0	1849	10	US-09-990-443-157 Sequence 157, App
39	1849	100.0	1849	10	US-09-991-854-157 Sequence 157, App
40	1849	100.0	1849	10	US-09-997-628-157 Sequence 157, App
41	1849	100.0	1849	10	US-09-997-683-157 Sequence 157, App
42	1849	100.0	1849	10	US-09-989-729A-157 Sequence 157, App
43	1849	100.0	1849	10	US-09-997-343-157 Sequence 157, App
44	1849	100.0	1849	10	US-09-997-440-157 Sequence 157, App
45	1849	100.0	1849	10	US-09-997-440-157 Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-989-722-157
Sequence 157, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyer, Luc
APPLICANT: Deonof, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C63
CURRENT APPLICATION NUMBER: US/09/989, 722
PRIORITY FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

1 PRIOR APPLICATION NUMBER: 60/091360
2 PRIOR FILING DATE: 1998-07-01
3 PRIOR APPLICATION NUMBER: 60/091478
4 PRIOR FILING DATE: 1998-07-02
5 PRIOR APPLICATION NUMBER: 60/091544
6 PRIOR FILING DATE: 1998-07-01
7 PRIOR APPLICATION NUMBER: 60/091519
8 PRIOR FILING DATE: 1998-07-02
9 PRIOR APPLICATION NUMBER: 60/091626
10 PRIOR FILING DATE: 1998-07-02
11 PRIOR APPLICATION NUMBER: 60/091633
12 PRIOR FILING DATE: 1998-07-02
13 PRIOR APPLICATION NUMBER: 60/091978
14 PRIOR FILING DATE: 1998-07-07
15 PRIOR APPLICATION NUMBER: 60/091982
16 PRIOR FILING DATE: 1998-07-07
17 PRIOR APPLICATION NUMBER: 60/092182
18 PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 1849;	DB 9;	Length 1849;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1849;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy		CTAGAGCGGCGGTAGCATGGAAGGGGAGAGTACGTCCGCGGTGCTCTCGGGCTTTGGTCT	60
Db	1	CTAGAGCGGCGGTAGCATGGAAGGGGAGAGTACGTCCGCGGTGCTCTCGGGCTTTGGTCT	60
Qy		CGGCGACATCGCTTCCAGCACTCAACAACGGACCTCGGACACGGAAAGTTTCTCTTGG	120
Db	61	CGGCGACATCGCTTCCAGCACTCAACAACGGACCTCGGACACGGAAAGTTTCTCTTGG	120
Qy		121 GGAAGTAAAGGTGAAGCCAGAACACGACTTACTGATTTCCAAATGATGATGTGAAGT	180
Db	121	GGAAGTAAAGGTGAAGCCAGAACACGACTTACTGATTTCCAAATGATGATGTGAAGT	180
Qy		181 TGTATTACATTTGACATTCAGAAATATATTCAGATGCTATGACCTTTTGGCTTTTAA	240
Db	181	TGTATTACATTTGACATTCAGAAATATATTCAGATGCTATGACCTTTTGGCTTTTAA	240
Qy		241 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAAAGAA	300
Db	241	TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAAAGAA	300
Qy		301 TGTGTAGAGTTGGTAAATAATTCGTCGATTCAGATGAGATCANTGAGCTTTAAGAGAG	360
Db	301	TGTGTAGAGTTGGTAAATAATTCGTCGATTCAGATGAGATCANTGAGCTTTAAGAGAG	360
Qy		361 GCTGCTTCACAAAACCTTCAGAGACATTTTCAACACCAAGACCTGTGTTTTCGCTATT	420
Db	361	GCTGCTTCACAAAACCTTCAGAGACATTTTCAACACCAAGACCTGTGTTTTCGCTATT	420
Qy		421 AACACCAAGTATATAACGAAGAACGTCCTCTCTCATGAGATGGAACATTCCTATATAA	480
Db	421	AACACCAAGTATATAACGAAGAACGTCCTCTCTCATGAGATGGAACATTCCTATATAA	480
Qy		481 ACCTCAAAAAGGACTTTTCAAGGGTACCTTTAGTGTGTGCATCTGGGACATGTCTGA	540
Db	481	ACCTCAAAAAGGACTTTTCAAGGGTACCTTTAGTGTGTGCATCTGGGACATGTCTGA	540
Qy		541 ACAACGTGGTATATAAACTGTATCAGGTTCCGTATATGTCACATGTTTAAACGAGAGT	600
Db	541	ACAACGTGGTATATAAACTGTATCAGGTTCCGTATATGTCACATGTTTAAACGAGAGT	600
Qy		601 ACAACGACACAGCTCAAAATTTTGTGAAGAGATGATGCTTTAAAGAGGTACTAAGAT	660
Db	601	ACAACGACACAGCTCAAAATTTTGTGAAGAGATGATGCTTTAAAGAGGTACTAAGAT	660
Qy		661 AAATGAAATGATGCTTCATTCACAGAGAAATTAAGAGTATAGCAAAAAGTGGAGAGA	720
Db	661	AAATGAAATGATGCTTCATTCACAGAGAAATTAAGAGTATAGCAAAAAGTGGAGAGA	720
Qy		721 CAGTGAACCAAGCATGTGATTAACCTAGTAAAGATGTAAACAGATTTAAACGAGAAATGA	780

Db	721	CAGTGAACAGACGATAGTATAAAGTAAAGATGTATAACGATTTAAACGAGAAATTTGA	780
Qy	781	GAAGAAGAGAGACACAGATTCAGGACAGACAGAGAAAGAACATCCAAAAAGACCTTCA	840
Db	781	GAAGAAGAGAGACACAGATTCAGGACAGACAGAGAAAGAACATCCAAAAAGACCTTCA	840
Qy	841	GGAGAACAATTTCTTTGTGACAGCATTAAGGACCTTTTCCAAATTCGAAATTCCTTCA	900
Db	841	GGAGAACAATTTCTTTGTGACAGCATTAAGGACCTTTTCCAAATTCGAAATTCCTTCA	900
Qy	901	TTCAATGTATATGTCTTTAAAAATAGACATGTCTTTAAAGTAGCTGTAACTAACCA	960
Db	901	TTCAATGTATATGTCTTTAAAAATAGACATGTCTTTAAAGTAGCTGTAACTAACCA	960
Qy	961	CCATCTCGATGTATAGACAAATCTGACCTTAAATGTGTAAACACACCTGACATCTCTGAAGC	1020
Db	961	CCATCTCGATGTATAGACAAATCTGACCTTAAATGTGTAAACACACCTGACATCTCTGAAGC	1020
Qy	1021	TAGTCCAGCTAGTACACACCAATCATTTAAGCATTAAGCCTTAGACTAGATGACAGATG	1080
Db	1021	TAGTCCAGCTAGTACACACCAATCATTTAAGCATTAAGCCTTAGACTAGATGACAGATG	1080
Qy	1081	GCAATTCAGAGAGATCTCGGTGTTAGATPACAAAGACAAAGATCTTAAAGCAATCTCG	1140
Db	1081	GCAATTCAGAGAGATCTCGGTGTTAGATPACAAAGACAAAGATCTTAAAGCAATCTCG	1140
Qy	1141	TAGTAGATACCAAGATTAAGATATCAAAATGAGAGGCCAGAAACAGATGAGAAATTTGA	1200
Db	1141	TAGTAGATACCAAGATTAAGATATCAAAATGAGAGGCCAGAAACAGATGAGAAATTTGA	1200
Qy	1201	AAAGATGAAAGGTTTGGTGAATATTCACGGTCTCTACATTTTGATCTTTTAACTTAA	1260
Db	1201	AAAGATGAAAGGTTTGGTGAATATTCACGGTCTCTACATTTTGATCTTTTAACTTAA	1260
Qy	1261	CAAAGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAATTCATTCATGTTTTTACTAT	1320
Db	1261	CAAAGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAATTCATTCATGTTTTTACTAT	1320
Qy	1321	GTTGAGCTACTGTCAGTAAAGTTCATTTGTTTTTACTATGTCACCTGTGTCAGTAATAC	1380
Db	1321	GTTGAGCTACTGTCAGTAAAGTTCATTTGTTTTTACTATGTCACCTGTGTCAGTAATAC	1380
Qy	1381	ACAGATTAATCTTAGTGCATTTACTTACCAAGATCTTTTCCAAACATCAGATGCTTTTA	1440
Db	1381	ACAGATTAATCTTAGTGCATTTACTTACCAAGATCTTTTCCAAACATCAGATGCTTTTA	1440
Qy	1441	TTTCCAAACCTTTTTTCACTTTCACCTTTCATTAAGTTTGTAGGGGAAGGCTTACACAGACA	1500
Db	1441	TTTCCAAACCTTTTTTCACTTTCACCTTTCATTAAGTTTGTAGGGGAAGGCTTACACAGACA	1500
Qy	1501	TTCTTTAGAAATTTGAAAAGTGAACCCAGGACAGTGCCTCACACCTGTAATCCACAGACT	1560
Db	1501	TTCTTTAGAAATTTGAAAAGTGAACCCAGGACAGTGCCTCACACCTGTAATCCACAGACT	1560
Qy	1561	TAGGGAAGACAGTCAGAGAGATTTGATTTGAAGCTAGAGTTAGAGACAGGCTGAGCAAC	1620
Db	1561	TAGGGAAGACAGTCAGAGAGATTTGATTTGAAGCTAGAGTTAGAGACAGGCTGAGCAAC	1620
Qy	1621	GTATTTGAGACCATGTATTAATAATTAATGGAAGACAGATAGCCTTAATTTTCAA	1680
Db	1621	GTATTTGAGACCATGTATTAATAATTAATGGAAGACAGATAGCCTTAATTTTCAA	1680
Qy	1681	AATTTGGAAGAAATTTTATATGAAATTTATCTGAGTCATTAATAATTCCTTAAGTGAT	1740
Db	1681	AATTTGGAAGAAATTTTATATGAAATTTATCTGAGTCATTAATAATTCCTTAAGTGAT	1740
Qy	1741	ACTTTTGTAGAGTACATTAATGCTGATAGTTGCCAGATTAATAATCTCGATATCATCAAT	1800
Db	1741	ACTTTTGTAGAGTACATTAATGCTGATAGTTGCCAGATTAATAATCTCGATATCATCAAT	1800
Qy	1801	AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTAAAAAATTTAAAAA	1845
Db	1801	AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTAAAAAATTTAAAAA	1845

RESULT 2
US-09-989-723-157
Sequence 157, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Nadler, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGAGGAGATACGTGCGGCTGCTCTCGGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGGTAGCATGAGGAGGAGATACGTGCGGCTGCTCTCGGGCTTTGTGCT 60

QY 61 CGGCGACTGCTTTCAGACCTCAACAGGACTCGGACACGGAAGTTTCTTCTTGG 120
DB 61 CGGCGACTGCTTTCAGACCTCAACAGGACTCGGACACGGAAGTTTCTTCTTGG 120

QY 121 GGAAGTAAAGGTGAAGCAAGAACAGCATTAAGTCCCAATGATGATGGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGAACAGCATTAAGTCCCAATGATGATGGAAGT 180

DB 121 GGAAGTAAAGGTGAAGCAAGAACAGCATTAAGTCCCAATGATGATGGAAGT 180
QY 181 TGTATTATCATTTGACATTTGGAATATATTTCCATGCTATATAGTTTTTTACTTTTATA 240
DB 181 TGTATTATCATTTGACATTTGGAATATATTTCCATGCTATATAGTTTTTTACTTTTATA 240

QY 241 TTCTTCAGGCGCAAGTAAATGAGCAAGCACTGGAAGAAATATTAATGATCAAAAAGAA 300
DB 241 TTCTTCAGGCGCAAGTAAATGAGCAAGCACTGGAAGAAATATTAATGATCAAAAAGAA 300

QY 301 TGTGTAGGTGTTGTCATTAATTCCTGCTCATTCAGATCAATCATGACGTTTAAAGAG 360
DB 301 TGTGTAGGTGTTGTCATTAATTCCTGCTCATTCAGATCAATCATGACGTTTAAAGAG 360

QY 361 GCTGCTTCAAAAACCTTGACAGACATTTTCAACCAAGACCTTGTTTCTGCTATT 420
DB 361 GCTGCTTCAAAAACCTTGACAGACATTTTCAACCAAGACCTTGTTTCTGCTATT 420

QY 421 AACACCAAGTATTAATTAACAGAACTGCTTACTCATGACTGGAACATTCCTTATATA 480
DB 421 AACACCAAGTATTAATTAACAGAACTGCTTACTCATGACTGGAACATTCCTTATATA 480

QY 481 ACCTCAAAAGACCTTTTTCACAGGTAACCTTAGTGTTGCCAATCTGGGCACTGTGTA 540
DB 481 ACCTCAAAAGACCTTTTTCACAGGTAACCTTAGTGTTGCCAATCTGGGCACTGTGTA 540

QY 541 ACAACTGGATTATAAACTGTATCAGGTCCTGTATGTCTCACTGTTTATAGCCGAGAGT 600
DB 541 ACAACTGGATTATAAACTGTATCAGGTCCTGTATGTCTCACTGTTTATAGCCGAGAGT 600

QY 601 ACAACACAGAGCTCTAATTTTGAAGAAAGATGATCCTTAAGAGGATCAATAAGAT 660
DB 601 ACAACACAGAGCTCTAATTTTGAAGAAAGATGATCCTTAAGAGGATCAATAAGAT 660

QY 661 AAATGAATGTATGCTTATTACAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720
DB 661 AAATGAATGTATGCTTATTACAGAGAAATTAAGATATATGCAAAAAGTGAAGA 720

QY 721 CAGTGAACAGCATTAATTAACATGTAAGAGATGTAACAGATTAATAAGAAATTTGA 780
DB 721 CAGTGAACAGCATTAATTAACATGTAAGAGATGTAACAGATTAATAAGAAATTTGA 780

QY 781 GAAAGGAGAGAGACACAGATTCAGGACAGAGAGAGAGAACATCCAAAAAGACCTCA 840
DB 781 GAAAGGAGAGAGACACAGATTCAGGACAGAGAGAGAGAACATCCAAAAAGACCTCA 840

QY 841 GGAAGACATTTTCTTTGTCAGGCACTTACGACCTTTTCCAAATCTGAAATTTCTCA 900
DB 841 GGAAGACATTTTCTTTGTCAGGCACTTACGACCTTTTCCAAATCTGAAATTTCTCA 900

QY 901 TTCAATGTTATGCTTTTAAATAATAGACATGTTCTTAAAGTGTGTAATCAACCA 960
DB 901 TTCAATGTTATGCTTTTAAATAATAGACATGTTCTTAAAGTGTGTAATCAACCA 960

QY 961 CCATCTGATATGATGACAACTGACCTTATGTTGAACACACTGACATTCCTGAAGC 1020
DB 961 CCATCTGATATGATGACAACTGACCTTATGTTGAACACACTGACATTCCTGAAGC 1020

QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAAGCATTAAGACCTTAGCTAGTGAAGATG 1080
DB 1021 TAGTCCAGCTAGTACACCAAAATCATTAAAGCATTAAGACCTTAGCTAGTGAAGATG 1080

QY 1081 GCAATTCAGAGATCTCGGTTTATGATACCAAGAACAAAGATCTTAAAGCAATCTG 1140
DB 1081 GCAATTCAGAGATCTCGGTTTATGATACCAAGAACAAAGATCTTAAAGCAATCTG 1140

QY 1141 TAGTAGTAACCAAGATTAAGATCCAAATGAGAGCCCAAGAAACATGAGAAATTTGA 1200
DB 1141 TAGTAGTAACCAAGATTAAGATCCAAATGAGAGCCCAAGAAACATGAGAAATTTGA 1200

QY 1201 AAGATGAAGGTTTGGTGAATATTAACAGGCTCTCTCAATTTGATCTTTTAACTTTA 1260
DB 1201 AAGATGAAGGTTTGGTGAATATTAACAGGCTCTCTCAATTTGATCTTTTAACTTTA 1260

УВ-10-063-523-21.гггг

Page 6

```

RESULT 3
US-09-989-279-157
; Sequence 157, Application US/09999279
; Patent No. US20020072496A1
;
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, U. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjaavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

```

```

1 FILEREFERENCE: P27301C56
2 CURRENT APPLICATION NUMBER: US/09/989,279
3 CURRENT FILING DATE: 2001-11-19
4 PRIOR APPLICATION NUMBER: 60/0495787
5 PRIOR FILING DATE: 1997-06-16
6 PRIOR APPLICATION NUMBER: 60/062250
7 PRIOR FILING DATE: 1997-10-17
8 PRIOR APPLICATION NUMBER: 60/065186
9 PRIOR FILING DATE: 1997-11-12
10 PRIOR APPLICATION NUMBER: 60/065311
11 PRIOR FILING DATE: 1997-11-13
12 PRIOR APPLICATION NUMBER: 60/066770
13 PRIOR FILING DATE: 1997-11-24
14 PRIOR APPLICATION NUMBER: 60/075945
15 PRIOR FILING DATE: 1998-02-25
16 PRIOR APPLICATION NUMBER: 60/078910
17 PRIOR FILING DATE: 1998-03-20
18 PRIOR APPLICATION NUMBER: 60/083322
19 PRIOR FILING DATE: 1998-04-28
20 PRIOR APPLICATION NUMBER: 60/084600
21 PRIOR FILING DATE: 1998-05-07
22 PRIOR APPLICATION NUMBER: 60/087106
23 PRIOR FILING DATE: 1998-05-28
24 PRIOR APPLICATION NUMBER: 60/087607
25 PRIOR FILING DATE: 1998-06-02
26 PRIOR APPLICATION NUMBER: 60/087609
27 PRIOR FILING DATE: 1998-06-02
28 PRIOR APPLICATION NUMBER: 60/087759
29 PRIOR FILING DATE: 1998-06-02
30 PRIOR APPLICATION NUMBER: 60/087827
31 PRIOR FILING DATE: 1998-06-03
32 PRIOR APPLICATION NUMBER: 60/088021
33 PRIOR FILING DATE: 1998-06-04
34 PRIOR APPLICATION NUMBER: 60/088025
35 PRIOR FILING DATE: 1998-06-04
36 PRIOR APPLICATION NUMBER: 60/088026
37 PRIOR FILING DATE: 1998-06-04
38 PRIOR APPLICATION NUMBER: 60/088028
39 PRIOR FILING DATE: 1998-06-04
40 PRIOR APPLICATION NUMBER: 60/088029
41 PRIOR FILING DATE: 1998-06-04
42 PRIOR APPLICATION NUMBER: 60/088030
43 PRIOR FILING DATE: 1998-06-04
44 PRIOR APPLICATION NUMBER: 60/088033
45 PRIOR FILING DATE: 1998-06-04
46 PRIOR APPLICATION NUMBER: 60/088326
47 PRIOR FILING DATE: 1998-06-04
48 PRIOR APPLICATION NUMBER: 60/088167
49 PRIOR FILING DATE: 1998-06-05
50 PRIOR APPLICATION NUMBER: 60/088202
51 PRIOR FILING DATE: 1998-06-05
52 PRIOR APPLICATION NUMBER: 60/088212
53 PRIOR FILING DATE: 1998-06-05
54 PRIOR APPLICATION NUMBER: 60/088217
55 PRIOR FILING DATE: 1998-06-05
56 PRIOR APPLICATION NUMBER: 60/088655
57 PRIOR FILING DATE: 1998-06-09
58 PRIOR APPLICATION NUMBER: 60/088734
59 PRIOR FILING DATE: 1998-06-10
60 PRIOR APPLICATION NUMBER: 60/088738
61 PRIOR FILING DATE: 1998-06-10
62 PRIOR APPLICATION NUMBER: 60/088742
63 PRIOR FILING DATE: 1998-06-10
64 PRIOR APPLICATION NUMBER: 60/088810
65 PRIOR FILING DATE: 1998-06-10
66 PRIOR APPLICATION NUMBER: 60/088824
67 PRIOR FILING DATE: 1998-06-10
68 PRIOR APPLICATION NUMBER: 60/088826
69 PRIOR FILING DATE: 1998-06-10
70 PRIOR APPLICATION NUMBER: 60/088858
71 PRIOR FILING DATE: 1998-06-11
72 PRIOR APPLICATION NUMBER: 60/088861
73 PRIOR FILING DATE: 1998-06-11

```

PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGGCGGCGGTGATGAGGAGAGAGTCTCGCGGTCTTCGCGCTTTGCT 60
1 CTGAGGCGGCGGTGATGAGGAGAGAGTCTCGCGGTCTTCGCGCTTTGCT 60
CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGAGCAAGAGTTCCTTCTGG 120
CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGAGCAAGAGTTCCTTCTGG 120
61 CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGAGCAAGAGTTCCTTCTGG 120
121 GGAAGTAAAGGTAGAGCAAGAAAGCACTTACTGATTCGCAATGATATGTTGAGT 180
121 GGAAGTAAAGGTAGAGCAAGAAAGCACTTACTGATTCGCAATGATATGTTGAGT 180
121 GGAAGTAAAGGTAGAGCAAGAAAGCACTTACTGATTCGCAATGATATGTTGAGT 180
181 TGTATTATACATTAACATTCAGAAATATATTCATGATAGCTTTTACCTTTTAA 240
181 TGTATTATACATTAACATTCAGAAATATATTCATGATAGCTTTTACCTTTTAA 240
181 TGTATTATACATTAACATTCAGAAATATATTCATGATAGCTTTTACCTTTTAA 240
241 TTCTTCAGGCGAATATATGAGCAAGCACTGAGAAATATATTCATATGCAAAAAGAA 300
241 TTCTTCAGGCGAATATATGAGCAAGCACTGAGAAATATATTCATATGCAAAAAGAA 300
301 TGTGTAGGTGATGACAAATTCGCTCATTCAGATCAGATGACGTTTAGAGAGAG 360
301 TGTGTAGGTGATGACAAATTCGCTCATTCAGATCAGATGACGTTTAGAGAGAG 360
301 TGTGTAGGTGATGACAAATTCGCTCATTCAGATCAGATGACGTTTAGAGAGAG 360
361 GCTGCTTCACAAAACCTTGACAGAGCACTTTTCAACCAAGACCTTGTTCGTATT 420
361 GCTGCTTCACAAAACCTTGACAGAGCACTTTTCAACCAAGACCTTGTTCGTATT 420
361 GCTGCTTCACAAAACCTTGACAGAGCACTTTTCAACCAAGACCTTGTTCGTATT 420
421 AACACCAAGTATATTAACAGAAAGCTGCTGATCATGAGCTGAAACATTCCTTATTA 480
421 AACACCAAGTATATTAACAGAAAGCTGCTGATCATGAGCTGAAACATTCCTTATTA 480
421 AACACCAAGTATATTAACAGAAAGCTGCTGATCATGAGCTGAAACATTCCTTATTA 480
481 ACCTCAAAAAGCACTTTTTCACAGGTAACCTTATGATGTTGCGCAATCGGGCATGTCTGA 540
481 ACCTCAAAAAGCACTTTTTCACAGGTAACCTTATGATGTTGCGCAATCGGGCATGTCTGA 540
541 ACAACTGGATTATTAACCTGATATAGGTTCTGATATGCACTGTTTAGCGAGAGAGT 600
541 ACAACTGGATTATTAACCTGATATAGGTTCTGATATGCACTGTTTAGCGAGAGAGT 600
601 ACAAAACAGACAGCTTAATTTTGAAGAAGATGATCCCTTAAGAAGAGTACATAAGAT 660
601 ACAAAACAGACAGCTTAATTTTGAAGAAGATGATCCCTTAAGAAGAGTACATAAGAT 660

QY	66	AAATGAAATGATAGCTTCATTACAGAGGAAATTAAGAGTAATATGCAAAAAAGTGAAGA	720
Db	661	AAATGAAATGATAGCTTCATTACAGAGGAAATTAAGAGTAATATGCAAAAAAGTGAAGA	720
QY	721	CAGTGAACAGACGATAGATTAACCTAGTAAGATGTATTAACAGATTAAAAACGAAATTGA	780
Db	721	CAGTGAACAGACGATAGATTAACCTAGTAAGATGTATTAACAGATTAAAAACGAAATTGA	780
QY	781	GAAAGAGAGAGAGCAACAGATTCAGGAGCAAGAGAGAAAGAAATCCCAAAAAGCCCTCA	840
Db	781	GAAAGAGAGAGAGCAACAGATTCAGGAGCAAGAGAGAAAGAAATCCCAAAAAGCCCTCA	840
QY	841	GGAGAACATTTTCTTTGTCAAGGATTAAGGACCTTTTCCAAATTCGATTTCTTCA	900
Db	841	GGAGAACATTTTCTTTGTCAAGGATTAAGGACCTTTTCCAAATTCGATTTCTTCA	900
QY	901	TTCAATGTATGTCTTTAAAAATAGACATGTCTTAAAAAGTAGCTGTAACTACACACA	960
Db	901	TTCAATGTATGTCTTTAAAAATAGACATGTCTTAAAAAGTAGCTGTAACTACACACA	960
QY	961	CCATTCGATGTAGTAGACAAATCGACCTTAATGTATGAACAACATGACATTCCTGAAGC	1020
Db	961	CCATTCGATGTAGTAGACAAATCGACCTTAATGTATGAACAACATGACATTCCTGAAGC	1020
QY	1021	TAGTCCAGCTAGTACACACAAATCATTTAAGCATTTAAAGCCTTAGCTAGATGACGATG	1080
Db	1021	TAGTCCAGCTAGTACACACAAATCATTTAAGCATTTAAAGCCTTAGCTAGATGACGATG	1080
QY	1081	GCAATTCAGAGATCTCGGTTGTATGATACAGAGCAAAAGCATTAAGCAAAATCTG	1140
Db	1081	GCAATTCAGAGATCTCGGTTGTATGATACAGAGCAAAAGCATTAAGCAAAATCTG	1140
QY	1141	TAGTAGTACCAAGATTAAGAGCATCCAAATGAGCAGCCAGAAACAGATGAGAGAAATTGA	1200
Db	1141	TAGTAGTACCAAGATTAAGAGCATCCAAATGAGCAGCCAGAAACAGATGAGAGAAATTGA	1200
QY	1201	AAAGATGAAGGTTTGGTGAATATTCACGGTCTCCATCAATTTGATCCCTTAACCTTA	1260
Db	1201	AAAGATGAAGGTTTGGTGAATATTCACGGTCTCCATCAATTTGATCCCTTAACCTTA	1260
QY	1261	CAAGAGATTTTATTATTGGCTGATGGGTAAAGCCAAACATTTCTATGTGTTTACTAT	1320
Db	1261	CAAGAGATTTTATTATTGGCTGATGGGTAAAGCCAAACATTTCTATGTGTTTACTAT	1320
QY	1321	GTTGAGCTACTTGCGTAGTTCATTTGTTTACATAGTCACTGTTTGCAGTAATAC	1380
Db	1321	GTTGAGCTACTTGCGTAGTTCATTTGTTTACATAGTCACTGTTTGCAGTAATAC	1380
QY	1381	ACAGATTAACCTCTAGTGCATTTACTTCCAAAGTACCTTTTCCAAACATCGATGCTTTTA	1440
Db	1381	ACAGATTAACCTCTAGTGCATTTACTTCCAAAGTACCTTTTCCAAACATCGATGCTTTTA	1440
QY	1441	TTTTCCAAACCTTTTTCACCTTACATAAGTGTGAGGGGAAAGGCTTACACAGACACA	1500
Db	1441	TTTTCCAAACCTTTTTCACCTTACATAAGTGTGAGGGGAAAGGCTTACACAGACACA	1500
QY	1501	TTCTTTAGATTTGAAAAGTAGAGCCAGGACAGTGCGCTCACACCTGTATTCACAGCACT	1560
Db	1501	TTCTTTAGATTTGAAAAGTAGAGCCAGGACAGTGCGCTCACACCTGTATTCACAGCACT	1560
QY	1561	TAGGGAAGCAAGTGCAGAGAGATTGATTGAAGCTGAGAGTTAGAGACACAGGCTGGGCAAC	1620
Db	1561	TAGGGAAGCAAGTGCAGAGAGATTGATTGAAGCTGAGAGTTAGAGACACAGGCTGGGCAAC	1620
QY	1621	GTAATTGAGCAATGTCTATTTAAAAATTAATGAAATGCAAGAAATAGCCTTAATTTTCA	1680
Db	1621	GTAATTGAGCAATGTCTATTTAAAAATTAATGAAATGCAAGAAATAGCCTTAATTTTCA	1680
QY	1681	AAATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATTCCTTTAAGTAT	1740
Db	1681	AAATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATTCCTTTAAGTAT	1740

QY	1741	ACTTTTTTAAGACGACATCTTATGGCTAGAGTTGCCAGATPAAAAGCTGATCTCATGCAAT	1800
Db	1741	ACTTTTTTAAGAGTACATCTATGCTTAAGAGTTGCCAGATPAAAATCTGATCTCATGCAAT	1800
QY	1801	AAATTGGCAAAACATCATCTPAAATTTTAAAAA	1849
Db	1801	AAATTGGCAAAACATCATCTPAAATTTTAAAAA	1849

PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952

PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092162
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CTGAGCGCGGTGATGAGGAGAGAGTACGTGCGGCGGTGCTCGGCGTTTGTCT 60
DB 1 CTGAGCGCGGTGATGAGGAGAGAGTACGTGCGGCGGTGCTCGGCGTTTGTCT 60

QY	61	GGGGGCACTGGCTTTCAGAGACTCAACACGGACTGGGACCGAGAAAGCTTTCCTTGG	120
Db	61	CGGGGCACTGGCTTTCAGAGACTCTCAACACGGACTGGGACCGAAAGCTTTCCTTGG	120
QY	121	GGAAGTAAAGGTGAAGCCAAAGAACAGCACTTACTGATTCGCCAATGATGATGGAAGT	180
Db	121	GGAAGTAAAGGTGAAGCCAAAGAACAGCACTTACTGATTCGCCAATGATGATGGAAGT	180
QY	181	TGATTATACAAATGACATTCAGAAATATATTCATGATCATCAGCTTTTAGCTTTATAA	240
Db	181	TGATTATACAAATGACATTCAGAAATATATTCATGATCATCAGCTTTTAGCTTTATAA	240
QY	241	TTCTTCAGCGAAGTAAATGACAGACCTGAAGAAATTTATCAAAATGTCAAAAAGAA	300
Db	241	TTCTTCAGCGAAGTAAATGACAGACCTGAAGAAATTTATCAAAATGTCAAAAAGAA	300
QY	301	TGTGTGAGGTGGTACAAATTCGCTCGTCAATCAGATCAGATCAGTACCTTTAGAGAG	360
Db	301	TGTGTGAGGTGGTACAAATTCGCTCGTCAATCAGATCAGATCAGTACCTTTAGAGAG	360
QY	361	GCTGCTTCACAAAACCTTGCAGAGACATTTTTCAAACAGACACTGTTTTCTGCTATT	420
Db	361	GCTGCTTCACAAAACCTTGCAGAGACATTTTTCAAACAGACACTGTTTTCTGCTATT	420
QY	421	AACACCAAGTATTAATACAGAAAGCTCTCTACTCATCGACTGGAAATTCTTTATTA	480
Db	421	AACACCAAGTATTAATACAGAAAGCTCTCTACTCATCGACTGGAAATTCTTTATTA	480
QY	481	ACCTCAAAAAGACATTTTTCACAGGGTACCTTTAGTGGTTGGCAATCTGGGCAATGTCTA	540
Db	481	ACCTCAAAAAGACATTTTTCACAGGGTACCTTTAGTGGTTGGCAATCTGGGCAATGTCTA	540
QY	541	ACAACCTGGGTATATAAACTGTATCAGGTTCTCTGATTCACATGTTTTAGCCGACAGT	600
Db	541	ACAACCTGGGTATATAAACTGTATCAGGTTCTCTGATTCACATGTTTTAGCCGACAGT	600
QY	601	ACAAAACACACGCTCTAAATTTTGTGAAGAAATGATCCTTTAAGAGAGTACATAAGAT	660
Db	601	ACAAAACACACGCTCTAAATTTTGTGAAGAAATGATCCTTTAAGAGAGTACATAAGAT	660
QY	661	AAATGAATGTATGCTTCATTACAAAGGAATTAAGAGTATATGCAAAAAAGTGAAGA	720
Db	661	AAATGAATGTATGCTTCATTACAAAGGAATTAAGAGTATATGCAAAAAAGTGAAGA	720
QY	721	CAGTGAACAAGCAGTAACTAACTAGTAAAGAGTGAACAGATTAACAGAGAAATTTGA	780
Db	721	CAGTGAACAAGCAGTAACTAACTAGTAAAGAGTGAACAGATTAACAGAGAAATTTGA	780
QY	781	GAAAAGAGAGAGACACAGATTCAGGCGACGAAGAGAAAGAACATCCAAAAAGCCTCA	840
Db	781	GAAAAGAGAGAGACACAGATTCAGGCGACGAAGAGAAAGAACATCCAAAAAGCCTCA	840
QY	841	GGAAGAACTTTTCTTTGTGACGGCATTAAGACCTTTTCCAAATCTGAATTTCTCA	900
Db	841	GGAAGAACTTTTCTTTGTGACGGCATTAAGACCTTTTCCAAATCTGAATTTCTCA	900
QY	901	TTCATGTGTATGTCTTTAAAAAATAGAATGTTCTTAAGATGCTGAATCTCAACCA	960
Db	901	TTCATGTGTATGTCTTTAAAAAATAGAATGTTCTTAAGATGCTGAATCTCAACCA	960
QY	961	GCATCTCGATGTAGTAAAGCAATCTGACCTTAAATGTTATGTTAAGCTGTAACTCAACCA	1020
Db	961	GCATCTCGATGTAGTAAAGCAATCTGACCTTAAATGTTATGTTAAGCTGTAACTCAACCA	1020
QY	1021	TAGTCCAGCTAGTACCAACAATCAATTAAGCATTAAGCTTTAGACTTAAGTGAAGT	1080
Db	1021	TAGTCCAGCTAGTACCAACAATCAATTAAGCATTAAGCTTTAGACTTAAGTGAAGT	1080
QY	1081	GCAATTCAGAGAGTCTGGTTGTTGAATCAACAAGCAAAACGATCTAAAGCAAAATATCG	1140
Db	1081	GCAATTCAGAGAGTCTGGTTGTTGAATCAACAAGCAAAACGATCTAAAGCAAAATATCG	1140

QY	1141	TAGTAGTACCAGATTAAGCATCCAAATGAGAGGCCAGAAACATAGTAAAGAAATTGA	1200
Db	1141	TAGTAGTACCAGATTAAGCATCCAAATGAGAGGCCAGAAACATAGTAAAGAAATTGA	1200
QY	1201	AAAGATGAAGGGTTTGGTGAATATTCAGAGGCTCCTTACATTTTGATCCTTTAACTTTA	1260
Db	1201	AAAGATGAAGGGTTTGGTGAATATTCAGAGGCTCCTTACATTTTGATCCTTTAACTTTA	1260
QY	1261	CAGAGATATTTTCTTAATTGGCTGATGCGTAAAGCCAAACATTCCTAATGTTTACTAT	1320
Db	1261	CAGAGATATTTTCTTAATTGGCTGATGCGTAAAGCCAAACATTCCTAATGTTTACTAT	1320
QY	1321	GTTGAGCTACTTCGAGTAAGTCAATTTGTTTTCATATGTTCACTGCTTTGCAAGTAATAC	1380
Db	1321	GTTGAGCTACTTCGAGTAAGTCAATTTGTTTTCATATGTTCACTGCTTTGCAAGTAATAC	1380
QY	1381	ACAGATTAACCTTTGATGATTTACTTACATCAAAAGATCTTTTCAAAACATCAGATGCTTTTA	1440
Db	1381	ACAGATTAACCTTTGATGATTTACTTACATCAAAAGATCTTTTCAAAACATCAGATGCTTTTA	1440
QY	1441	TTTCCAAACCTTTTTCACCTTTCACCTTAAGTTGTTGAAGGGAAGGCTTACACAGACACA	1500
Db	1441	TTTCCAAACCTTTTTCACCTTTCACCTTAAGTTGTTGAAGGGAAGGCTTACACAGACACA	1500
QY	1501	TTCTTTGAATTTGGAAAAGTGAAGACCAAGGAGGCTCACACCTGTAATCCAGCACT	1560
Db	1501	TTCTTTGAATTTGGAAAAGTGAAGACCAAGGAGGCTCACACCTGTAATCCAGCACT	1560
QY	1561	TAGGAGACACAAGTCAGAGAGATTTGATGAAGCTTAGAGATTAGAGACCAAGCTCGGGCAAC	1620
Db	1561	TAGGAGACACAAGTCAGAGAGATTTGATGAAGCTTAGAGATTAGAGACCAAGCTCGGGCAAC	1620
QY	1621	GTAATTGAGACCATGCTTATTAATAAATAAATGAAAGCAAGATAGCCTTATTTTCAA	1680
Db	1621	GTAATTGAGACCATGCTTATTAATAAATAAATGAAAGCAAGATAGCCTTATTTTCAA	1680
QY	1681	AATATGAAAGAAATTTATATGAATAATTTATCTGAGATTTAAATTTCTCCTTAGTGAT	1740
Db	1681	AATATGAAAGAAATTTATATGAATAATTTATCTGAGATTTAAATTTCTCCTTAGTGAT	1740
QY	1741	ACTTTTATGAAAGTATCATTTATGGCTAGAGTTGCCAGATTAATATGCTGTATATCATGCAAT	1800
Db	1741	ACTTTTATGAAAGTATCATTTATGGCTAGAGTTGCCAGATTAATATGCTGTATATCATGCAAT	1800
QY	1801	AAATTGGCAAAACATCATCTTAAATTTTAAAAAAAAAAAAAAAAAAAAAA 1849	1849
Db	1801	AAATTGGCAAAACATCATCTTAAATTTTAAAAAAAAAAAAAAAAAAAAAA 1849	1849
RESULT 5			
US-09-989-731-157			
Sequence 157, Application US/09989731			
Patent No. US20020103125A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eaton, Dan L.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gerber, Hanspeter			
APPLICANT: Gerlitsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, J. Christopher			
APPLICANT: Gurney, Austin L.			
APPLICANT: Kljavin, Ivar J.			
APPLICANT: Napier, Mary A.			
APPLICANT: Pan, James			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Stewart, Timothy A.			

APPLICANT: Tumas, Daniel
 APPLICANT: Matas, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C70
 CURRENT APPLICATION NUMBER: US/09/989,731
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088555
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824

PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGGCGGCGTAGCATGAGGCGGAGAGTACGTCGCGGTCCTCGGGCTTTGTGCT 60
 1 CTGAGGCGGCGTAGCATGAGGCGGAGAGTACGTCGCGGTCCTCGGGCTTTGTGCT 60
 61 CGGCGCATGCTGCTTCCAGACCTCAACGCGACTCGGACGAGAGTTTCTTCTG 120
 61 CGGCGCATGCTGCTTCCAGACCTCAACGCGACTCGGACGAGAGTTTCTTCTG 120
 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTCCCAATGGAATGTTGAAGT 180
 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTCCCAATGGAATGTTGAAGT 180
 181 TGTTTATACATTAACATTTCAAAATATTATTCATGCTATCAAGTTTATGCTTATTA 240
 181 TGTTTATACATTAACATTTCAAAATATTATTCATGCTATCAAGTTTATGCTTATTA 240
 241 TTTCTTCAGGCGAAGTAAATGAGCAAGCATGGAAGAAATTTATCAATGTCAAAAAGAA 300
 241 TTTCTTCAGGCGAAGTAAATGAGCAAGCATGGAAGAAATTTATCAATGTCAAAAAGAA 300
 301 TGTGTGAGGTTGTGACAAATTCCTGCTCATTCAGATGATCATGAGCTTTGAGAGAG 360
 301 TGTGTGAGGTTGTGACAAATTCCTGCTCATTCAGATGATCATGAGCTTTGAGAGAG 360
 361 GCTGCTTCACAAAAGCTTGCAGAGCATTTTTCACCAAGACCTTTGTTTCTGCTATT 420
 361 GCTGCTTCACAAAAGCTTGCAGAGCATTTTTCACCAAGACCTTTGTTTCTGCTATT 420
 421 AACACCAAGTATTAATTAACAGAAAGCTGCTCACTCACTGAGCTGGAATCTTATTA 480
 421 AACACCAAGTATTAATTAACAGAAAGCTGCTCACTCACTGAGCTGGAATCTTATTA 480
 481 ACCCTCAAAAAGAGCTTTTTCACAGGCTACCTTTAGTGTGCAATCTGGGCATGTCTGA 540
 481 ACCCTCAAAAAGAGCTTTTTCACAGGCTACCTTTAGTGTGCAATCTGGGCATGTCTGA 540

541 ACAACTGGGTTATTAACATGATCAGGTTCTGTATGCTCACTGGTTTATGCGGACAGT 600
 541 ACAACTGGGTTATTAACATGATCAGGTTCTGTATGCTCACTGGTTTATGCGGACAGT 600
 601 ACAACACACAGCTTAAATTTTGAAGAGATGATCTTTAAAGAGGTACATTAAGT 660
 601 ACAACACACAGCTTAAATTTTGAAGAGATGATCTTTAAAGAGGTACATTAAGT 660
 661 AAATGAATGATAGCTTCACTTCAAGAGAAATTAAGATATGCAAAAAGTGAGAGA 720
 661 AAATGAATGATAGCTTCACTTCAAGAGAAATTAAGATATGCAAAAAGTGAGAGA 720
 721 CAGTGAACAGCAGTATTAACATTAAGATGTAACAGATTAAACGAGAAATTGA 780
 721 CAGTGAACAGCAGTATTAACATTAAGATGTAACAGATTAAACGAGAAATTGA 780
 781 GAAAGAGAGAGGACACAGATTGAGCAGAGAGAGAGAGAGATCCAAAAGACCTGA 840
 781 GAAAGAGAGAGGACACAGATTGAGCAGAGAGAGAGAGAGATCCAAAAGACCTGA 840
 841 GGAAGACATTTTCTTTGTCAGGCAATTAAGACCTTTTCCAAATTTGAAATTTCTCA 900
 841 GGAAGACATTTTCTTTGTCAGGCAATTAAGACCTTTTCCAAATTTGAAATTTCTCA 900
 901 TTTCAATGTTATGCTTTTAAATTAAGATGATGTTTAAAGAGGTGATCAACCA 960
 901 TTTCAATGTTATGCTTTTAAATTAAGATGATGTTTAAAGAGGTGATCAACCA 960
 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 1021 TAGTCCAGCTATGACACCAATTAAGATGATGATGATGATGATGATGATGATGATG 1080
 1021 TAGTCCAGCTATGACACCAATTAAGATGATGATGATGATGATGATGATGATGATG 1080
 1081 GCAATTCAGAGATCTCGGTTGTAGATACACAGAACAAAGATCTTAAGCAAAATCTGG 1140
 1081 GCAATTCAGAGATCTCGGTTGTAGATACACAGAACAAAGATCTTAAGCAAAATCTGG 1140
 1141 TAGTATGATCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1200
 1141 TAGTATGATCAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1200
 1201 AAAGATGAAGGTTTGTGTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
 1201 AAAGATGAAGGTTTGTGTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
 1261 CAAGAGATTTTATTTATTTGCTATGAGTAAAGCCAAACATTTCTATGTTTATCTAT 1320
 1261 CAAGAGATTTTATTTATTTGCTATGAGTAAAGCCAAACATTTCTATGTTTATCTAT 1320
 1321 GTTAGGCTACTGAGATTAAGTCAATTTGTTTCTATGTTTCACTGTTTGAAGTATAC 1380
 1321 GTTAGGCTACTGAGATTAAGTCAATTTGTTTCTATGTTTCACTGTTTGAAGTATAC 1380
 1381 ACAGATTAACCTTAAGTCAATTTCTCAAAAGTATTTTCAAAACATCAAGATGCTTTTA 1440
 1381 ACAGATTAACCTTAAGTCAATTTCTCAAAAGTATTTTCAAAACATCAAGATGCTTTTA 1440
 1441 TTTCAAAACCTTTTATTTTCACTTCACTTAAGTGTGAGGGAAGGCTTACACAGACCA 1500
 1441 TTTCAAAACCTTTTATTTTCACTTCACTTAAGTGTGAGGGAAGGCTTACACAGACCA 1500
 1501 TTTCTTAAGATTTGAGAAAGTGAACAGAGCTGACAGCTGATTAATCCAGACCT 1560
 1501 TTTCTTAAGATTTGAGAAAGTGAACAGAGCTGACAGCTGATTAATCCAGACCT 1560
 1561 TAGGAGAGACAGTACAGAGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
 1561 TAGGAGAGACAGTACAGAGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
 1621 GTATTGAGACATGCTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1680

Db 1621 GATTGAGCCATGCTATTAAATAAATGAAAAAGCAAGATAGCTTATTTCGA 1680
 Qy 1681 AATATGGAAGAAATTTATATGAAAATTTATCTGAGTCTTAAATTCCTTAAGTAT 1740
 Db 1681 AATATGGAAGAAATTTATATGAAAATTTATCTGAGTCTTAAATTCCTTAAGTAT 1740
 Qy 1741 ACTTTTGAAGTACATATGCTAGAGTGCAGATATAATGCTGATATCATGCAAT 1800
 Db 1741 ACTTTTGAAGTACATATGCTAGAGTGCAGATATAATGCTGATATCATGCAAT 1800
 Qy 1801 AATTTGCAAAACATCATCTTAAATTTTAAAAAATTTAAAAAATTTAAAAA 1849
 Db 1801 AATTTGCAAAACATCATCTTAAATTTTAAAAAATTTAAAAAATTTAAAAA 1849
 RESULT 6
 US-09-989-733-157
 Sequence 157, Application US/09989732
 Patent No. US20020123453A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gutney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C57
 CURRENT APPLICATION NUMBER: US/09/989,732
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090682
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTGGGGGTCTCTCGGCTTTGTCT 60
 DB 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTGGGGGTCTCTCGGCTTTGTCT 60
 QY CGGGGCACTCGCTTTCAGACACTCAACGCGACTCGACACGGAAGTCTTCTCTG 120
 DB CGGGGCACTCGCTTTCAGACACTCAACGCGACTCGACACGGAAGTCTTCTCTG 120
 QY 61 CGGGGCACTCGCTTTCAGACACTCAACGCGACTCGACACGGAAGTCTTCTCTG 120
 DB 61 CGGGGCACTCGCTTTCAGACACTCAACGCGACTCGACACGGAAGTCTTCTCTG 120
 QY 121 GGAAGTAAAGGTGAAGCCCAAGACGACTTACTGATCCCAATGATGATGAGT 180
 DB 121 GGAAGTAAAGGTGAAGCCCAAGACGACTTACTGATCCCAATGATGATGAGT 180
 QY 181 TGTTATACAAATGACATTCAGAAATATTCATGCTATCAGCTTTTGTATATA 240
 DB 181 TGTTATACAAATGACATTCAGAAATATTCATGCTATCAGCTTTTGTATATA 240
 QY 241 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAA 300
 DB 241 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAA 300
 QY 301 TGTTGATGTTGTGATCAAAATTCGGTGTCTTCAATGATGATGATGATGATG 360
 DB 301 TGTTGATGTTGTGATCAAAATTCGGTGTCTTCAATGATGATGATGATGATG 360
 QY 361 GCTGCTTCACAAAACCTTTCAGAGAGCATTTTTCACCAAGACCTTGTCTGAT 420
 DB 361 GCTGCTTCACAAAACCTTTCAGAGAGCATTTTTCACCAAGACCTTGTCTGAT 420
 QY 421 AACACCAAGTAAATACAGAAAGCTCTTACTCATGCTGAAATCTTATATA 480
 DB 421 AACACCAAGTAAATACAGAAAGCTCTTACTCATGCTGAAATCTTATATA 480
 QY 481 ACTCAAAAAGACCTTTTTCAGAGAGCATTTTTCACCAAGACCTTGTCTG 540
 DB 481 ACTCAAAAAGACCTTTTTCAGAGAGCATTTTTCACCAAGACCTTGTCTG 540
 QY 541 ACAACCTGGTATTAACCTGATACAGTCTGATGCTGATGCTGATGCTGATG 600
 DB 541 ACAACCTGGTATTAACCTGATACAGTCTGATGCTGATGCTGATGCTGATG 600
 QY 601 ACAACCTGGTATTAACCTGATACAGTCTGATGCTGATGCTGATGCTGATG 660
 DB 601 ACAACCTGGTATTAACCTGATACAGTCTGATGCTGATGCTGATGCTGATG 660
 QY 661 AAATGAATGTATGCTTCAATTAAGAGATTAAGAGATTAAGAGATTAAGAG 720
 DB 661 AAATGAATGTATGCTTCAATTAAGAGATTAAGAGATTAAGAGATTAAGAG 720
 QY 721 CAGTGAACAAGCAGTATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTA 780
 DB 721 CAGTGAACAAGCAGTATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTA 780
 QY 781 GAAAG 840
 DB 781 GAAAG 840
 QY 841 GGAAGACATTTTCTTGTGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 DB 841 GGAAGACATTTTCTTGTGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 901 TTCAATGATGATGCTTAAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 901 TTCAATGATGATGCTTAAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGAGAGAGAGAGAGAGAGAGAG 1080

Db 1021 TAGCCAGTAGTACACCAAAATCATTAGCATTAAGCTTAGTATGATGACGATG 1080
Qy 1081 GCATTGAAGAGATCTGGTGTAGTATACAGAGCAAAACGATCTTAAGCAATCTG 1140
Db 1081 GCATTGAAGAGATCTGGTGTAGTATACAGAGCAAAACGATCTTAAGCAATCTG 1140
Qy 1141 TAGTAGTAAACCAAGATTAAGCATCCAAATGAGCAGCCAGAAACAGATGAGAAATGA 1200
Db 1141 TAGTAGTAAACCAAGATTAAGCATCCAAATGAGCAGCCAGAAACAGATGAGAAATGA 1200
Qy 1201 AAGATGAAGGTTTGGTGAATATTCACGGTCTCCATCTTTGATCCCTTTAACTTA 1260
Db 1201 AAGATGAAGGTTTGGTGAATATTCACGGTCTCCATCTTTGATCCCTTTAACTTA 1260
Qy 1261 CAAGAGATTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTACTAT 1320
Db 1261 CAAGAGATTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTACTAT 1320
Qy 1321 GTTAGAGTACTGAGTAAATTCATTTGTTTACTATGTTTCACTGTTTGCAGTAATAC 1380
Db 1321 GTTAGAGTACTGAGTAAATTCATTTGTTTACTATGTTTCACTGTTTGCAGTAATAC 1380
Qy 1381 ACAGATTAACCTTAGTGCATTTACTTCACAAAGTACTTTTCAAACATGAGATGCTTTA 1440
Db 1381 ACAGATTAACCTTAGTGCATTTACTTCACAAAGTACTTTTCAAACATGAGATGCTTTA 1440
Qy 1441 TTTCCAAACCTTTTTCACCTTTCATTAAGTTGTTGAGGGAGAGGCTTACACAGACACA 1500
Db 1441 TTTCCAAACCTTTTTCACCTTTCATTAAGTTGTTGAGGGAGAGGCTTACACAGACACA 1500
Qy 1501 TTCTTTAGAAATGGAAAAGTGAACACAGGACAGTGGCTCAACCTGTTATCCAGCACT 1560
Db 1501 TTCTTTAGAAATGGAAAAGTGAACACAGGACAGTGGCTCAACCTGTTATCCAGCACT 1560
Qy 1561 TAGGGAAGACCAAGTCAAGAGATTTGAAGCTAGAGTTGAGACACAGCTGGGCAAC 1620
Db 1561 TAGGGAAGACCAAGTCAAGAGATTTGAAGCTAGAGTTGAGACACAGCTGGGCAAC 1620
Qy 1621 GTATTAGAACCATGCTATTAATAAATTAAGAAACAGAAATGCTTATTTTCA 1680
Db 1621 GTATTAGAACCATGCTATTAATAAATTAAGAAACAGAAATGCTTATTTTCA 1680
Qy 1681 AATATGAAAAGAAATTTATATGAATTTATCTGACTCAATTAATTCCTTAAAGTAT 1740
Db 1681 AATATGAAAAGAAATTTATATGAATTTATCTGACTCAATTAATTCCTTAAAGTAT 1740
Qy 1741 ACTTTTGTAGAGTACATTAATGCTAGAGTTGCCAGATTAATAATGCTGATATCATGCAAT 1800
Db 1741 ACTTTTGTAGAGTACATTAATGCTAGAGTTGCCAGATTAATAATGCTGATATCATGCAAT 1800
Qy 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
Db 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849

RESULT 7
US-09-991-073-157
Sequence 157, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Aekkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kijavira, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540

PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
 Best Local Similarity 100.0%; Pired. No. 0; Mismatches 0; Gaps 0;
 Matches 1849; Conservative 0; Indels 0; Gaps 0;

1 CTGAGCGCGCGGTAGCATGAGGAGAGTACGTCGCGGTGCTCGGAGCTTGTGCT 60
 1 CTGAGCGCGCGGTAGCATGAGGAGAGTACGTCGCGGTGCTCGGAGCTTGTGCT 60

61 CGGCGCACTGCTTCCAGCACCTCACAAGGACTCGGACACGGAAGTTTCTTCTGG 120
 61 CGGCGCACTGCTTCCAGCACCTCACAAGGACTCGGACACGGAAGTTTCTTCTGG 120

121 GGAAGTAAAGGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
 121 GGAAGTAAAGGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180

181 TGTTTATACATTTACATTTACATTTACATTTACATTTACATTTACATTTACATTT 240
 181 TGTTTATACATTTACATTTACATTTACATTTACATTTACATTTACATTTACATTT 240

241 TTCTTCAGCGAATTAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
 241 TTCTTCAGCGAATTAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300

301 TGTGTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360
 301 TGTGTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360

361 GGTGCTTCACAAACTTGACAGAGCAATTTTCAACCAAGCAAGCAAGCAAGCAAGCA 420
 361 GGTGCTTCACAAACTTGACAGAGCAATTTTCAACCAAGCAAGCAAGCAAGCAAGCA 420

421 AACACCAAGTATTAATTAAGAAAGTGTCTACTCATCATGAGCAAGCAAGCAAGCA 480
 421 AACACCAAGTATTAATTAAGAAAGTGTCTACTCATCATGAGCAAGCAAGCAAGCA 480


```
Db 421 AACCAAGTAATTAACAGAAAGCTGCTACTCATGACGTGAACATTTCTTAATATA 480
Qy 481 ACCTCAAAAAGAGCTTTTTCACAGGGTACCTTTAGTGGTGGCAATCGGGCATGTCTGA 540
Db 481 ACCTCAAAAAGAGCTTTTTCACAGGGTACCTTTAGTGGTGGCAATCGGGCATGTCTGA 540
Qy 541 ACAATGGGTATATAAACTGTATCAAGTCTGTATGCTCACTGGTTTATGCCGAGCACT 600
Db 541 ACAATGGGTATATAAACTGTATCAAGTCTGTATGCTCACTGGTTTATGCCGAGCACT 600
Qy 601 ACAACACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGGTACATAAGAT 660
Db 601 ACAACACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGGTACATAAGAT 660
Qy 661 AAATGAATGTATGCTTCATTACAGAGGAATTAAGATATATGCAAAAAAGTGAGAGA 720
Db 661 AAATGAATGTATGCTTCATTACAGAGGAATTAAGATATATGCAAAAAAGTGAGAGA 720
Qy 721 CAGTGAACAGACAGTAACTAACTAAAGATGATTAAGATTAAGAGAAATTTGA 780
Db 721 CAGTGAACAGACAGTAACTAACTAAAGATGATTAAGATTAAGAGAAATTTGA 780
Qy 781 GAAAAGAGAGAGACAGATTCAGGACGACAGAGAGAGAGAGAAACATCCAAAAAGACCTCA 840
Db 781 GAAAAGAGAGAGACAGATTCAGGACGACAGAGAGAGAGAGAAACATCCAAAAAGACCTCA 840
Qy 841 GGAGAACATTTTCTTGTCTCAGGATTAACCGACCTTTTCCAAATCTGAATTTCTTCA 900
Db 841 GGAGAACATTTTCTTGTCTCAGGATTAACCGACCTTTTCCAAATCTGAATTTCTTCA 900
Qy 901 TTCAATGTATGTCTTTAAAAAATAGACATGTTCTTAAAGATGCTGAATCAACA 960
Db 901 TTCAATGTATGTCTTTAAAAAATAGACATGTTCTTAAAGATGCTGAATCAACA 960
Qy 961 CCATCTCGATGTATAGACATCTGACCTTAATGTGAGAACACACATCACTTCTGAGC 1020
Db 961 CCATCTCGATGTATAGACATCTGACCTTAATGTGAGAACACACATCACTTCTGAGC 1020
Qy 1021 TAGTCCAGCTAGTACACCACAAAATCATTAAAGCATAAAGCCTTAGACTTAGACAGAT 1080
Db 1021 TAGTCCAGCTAGTACACCACAAAATCATTAAAGCATAAAGCCTTAGACTTAGACAGAT 1080
Qy 1081 GCAATTCAGAGATCTCGTGTGTATGATACCAAGACAAACGATCTAAAGCAATCTGG 1140
Db 1081 GCAATTCAGAGATCTCGTGTGTATGATACCAAGACAAACGATCTAAAGCAATCTGG 1140
Qy 1141 TAGTAGTAAACAAGTAAAGATCCAAATGAGACGCCAGAAACAGATGAAGAAATGA 1200
Db 1141 TAGTAGTAAACAAGTAAAGATCCAAATGAGACGCCAGAAACAGATGAAGAAATGA 1200
Qy 1201 AAAGATGAAGGCTTTGTGTGAATATCAAGGCTCTCTACATTTTGTATCTTTTAACTTA 1260
Db 1201 AAAGATGAAGGCTTTGTGTGAATATCAAGGCTCTCTACATTTTGTATCTTTTAACTTA 1260
Qy 1261 CAAGGAGTTTTTTTATTTGGCTATGGGTAAAGCCAAACATTTCTATTTGTATTTACTAT 1320
Db 1261 CAAGGAGTTTTTTTATTTGGCTATGGGTAAAGCCAAACATTTCTATTTGTATTTACTAT 1320
Qy 1321 GTTAGGCTACTTGACGTAAAGTCAATTTGTTTTTACTATGTTCACTGTTTGAATAATAC 1380
Db 1321 GTTAGGCTACTTGACGTAAAGTCAATTTGTTTTTACTATGTTTACTATGTTTGAATAATAC 1380
Qy 1381 ACAATATCTCTTAGTGATTTACTTACAAAGATCTTTTGAACATTCAGATGCTTTTA 1440
Db 1381 ACAATATCTCTTAGTGATTTACTTACAAAGATCTTTTGAACATTCAGATGCTTTTA 1440
Qy 1441 TTTCACAAACCTTTTTCACCTTCACTAGTTGTGAGGGAGAGGCTTACACAGACACA 1500
Db 1441 TTTCACAAACCTTTTTCACCTTCACTAGTTGTGAGGGAGAGGCTTACACAGACACA 1500
Qy 1501 TTCTTTAGATTTGAAAAGTGAAGCCAGGACAGTGGCTCACACCTGTAACTCCAGACT 1560
Db 1501 TTCTTTAGATTTGAAAAGTGAAGCCAGGACAGTGGCTCACACCTGTAACTCCAGACT 1560
```

```
Db 1501 TTCTTTAGATTTGAAAAGTGAAGCCAGGACAGTGGCTCACACCTGTAACTCCAGACT 1560
Qy 1561 TAGGAGAACAAAGTCAGAGAGATTTGATTTGAAGCTTAGAGATTAGACACGCTTGGCAAC 1620
Db 1561 TAGGAGAACAAAGTCAGAGAGATTTGATTTGAAGCTTAGAGATTAGACACGCTTGGCAAC 1620
Qy 1621 GATATGAGACCATGTCTTTTAAAAAATPAAATGAAAAAGCAAGATAGCTTAATTTTCAA 1680
Db 1621 GATATGAGACCATGTCTTTTAAAAAATPAAATGAAAAAGCAAGATAGCTTAATTTTCAA 1680
Qy 1681 AATATGAAAAGAAATTTATATGAAAAATTTATCTGAGCTATTAATTCCTTTAAGTAT 1740
Db 1681 AATATGAAAAGAAATTTATATGAAAAATTTATCTGAGCTATTAATTCCTTTAAGTAT 1740
Qy 1741 ACTTTTTRAGATCATATTAAGCTAGAGTTCAGAGATTAATGCTGATATATCATGCAAT 1800
Db 1741 ACTTTTTRAGATCATATTAAGCTAGAGTTCAGAGATTAATGCTGATATATCATGCAAT 1800
Qy 1801 AATTTGCAAAACATCATCTAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849
Db 1801 AATTTGCAAAACATCATCTAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849

RESULT 8
US-09-990-442-157
; Sequence 157, Application US/09990442
; Patent No. US2002013252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjaevlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-26
```



```
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGCGGCTGAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGCTTTGTGCT 60
DB 1 CTAGGCGGCGGCTAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGCTTTGTGCT 60
QY 61 CGGCGCATCTGCTTCCAGACCTCAACAGGACTCGGACAGGAGGTTTCTTCTG 120
DB 61 CGGCGCATCTGCTTCCAGACCTCAACAGGACTCGGACAGGAGGTTTCTTCTG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAAACAGCATTAAGTATCCCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAGAAACAGCATTAAGTATCCCAATGATGATGTAAGT 180
QY 181 TGTTTATACATTAAGCATTAAGTATTAATTCATGATGATGATGATGATGATGAT 240
DB 181 TGTTTATACATTAAGCATTAAGTATTAATTCATGATGATGATGATGATGATGAT 240
QY 241 TTCTTCAGCGAAGTAAATGAGCAAGCATGAGAAATATTAATCAATGTCAGAAAGAA 300
DB 241 TTCTTCAGCGAAGTAAATGAGCAAGCATGAGAAATATTAATCAATGTCAGAAAGAA 300
QY 301 TGTGTGATGCTTGTGTACAAATTCGCTGCTCATGATGATGATGATGATGATGATG 360
DB 301 TGTGTGATGCTTGTGTACAAATTCGCTGCTCATGATGATGATGATGATGATGATG 360
QY 361 GCTGCTTCACAAAAACCTTGAGAGAGATTTTCAAAACCAAGACCTTGTCTGCTAT 420
DB 361 GCTGCTTCACAAAAACCTTGAGAGAGATTTTCAAAACCAAGACCTTGTCTGCTAT 420
QY 421 AACACCAAGTATTAATTAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTAATA 480
DB 421 AACACCAAGTATTAATTAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTAATA 480
QY 481 ACCTCAAAAAGAGACTTTTCAAGGTAACCTTAGTGTGCTGCAATCTGGGATGCTGA 540
DB 481 ACCTCAAAAAGAGACTTTTCAAGGTAACCTTAGTGTGCTGCAATCTGGGATGCTGA 540
QY 541 ACAACTGCGGTATTAACAGTATCAAGGTTCTGTATGTCACATGCTTTAGCCGAGCA 600
DB 541 ACAACTGCGGTATTAACAGTATCAAGGTTCTGTATGTCACATGCTTTAGCCGAGCA 600
QY 601 ACAAAACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGATCATTAAGT 660
DB 601 ACAAAACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGATCATTAAGT 660
QY 661 AAATGAATGTATGCTTCAATTAACAAGAAATTAAGATTAAGCAAAAAGTGAAGA 720
DB 661 AAATGAATGTATGCTTCAATTAACAAGAAATTAAGATTAAGCAAAAAGTGAAGA 720
QY 721 CAATGAACAAGAGTATGATTAAGTAAAGATTAAGCAAGTAAAGCAAGAAATTA 780
DB 721 CAATGAACAAGAGTATGATTAAGTAAAGATTAAGCAAGTAAAGCAAGAAATTA 780
QY 781 GAAAGAGAGAGAGACAGATTCAGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 GAAAGAGAGAGAGAGACAGATTCAGGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTGATGTATGATGCTTAAAGAAATAGACATGTTTCAAAAGTGTGTAACCAACA 960
DB 901 TTGATGTATGATGCTTAAAGAAATAGACATGTTTCAAAAGTGTGTAACCAACA 960
```

```
DB 901 TTGATGTATGATGCTTAAAGAAATAGACATGTTTCAAAAGTGTGTAACCAACA 960
QY 961 CCATCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CCATCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TAGTCCAGCTAGTACACCAACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1080
DB 1021 TAGTCCAGCTAGTACACCAACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1080
QY 1081 GCAATTCAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 GCAATTCAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TAGTATGATACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1200
DB 1141 TAGTATGATACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1200
QY 1201 AAAGTGAAGGCTTTTGTGTAATTTACCGGTCTCTCAATTTTGAATCTTTTAACTTA 1260
DB 1201 AAAGTGAAGGCTTTTGTGTAATTTACCGGTCTCTCAATTTTGAATCTTTTAACTTA 1260
QY 1261 CAAGAGATTTTATTTTGTGCTGATGAGTAAAGCCAAACATTTCTATTTGTTTACTAT 1320
DB 1261 CAAGAGATTTTATTTTGTGCTGATGAGTAAAGCCAAACATTTCTATTTGTTTACTAT 1320
QY 1321 GTTGAAGTACTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GTTGAAGTACTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ACAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 ACAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 TTTCCTTGAATTTGAGAAAGTGAAGCAAGGACAGTGGCTCAACCTGTAATCCAGCACT 1500
DB 1441 TTTCCTTGAATTTGAGAAAGTGAAGCAAGGACAGTGGCTCAACCTGTAATCCAGCACT 1500
QY 1501 TTTCCAAACCTTTTTCACCTTCACTAAGTGTGTAAGGAGGAGGCTTACACAGACACA 1560
DB 1501 TTTCCAAACCTTTTTCACCTTCACTAAGTGTGTAAGGAGGAGGCTTACACAGACACA 1560
QY 1561 TAGGAGAGACAGTCAAGAGATTAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
DB 1561 TAGGAGAGACAGTCAAGAGATTAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
QY 1621 GTATTTGAGACATGCTATTAATAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1680
DB 1621 GTATTTGAGACATGCTATTAATAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1680
QY 1681 AATATGAGAAAGATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
DB 1681 AATATGAGAAAGATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
QY 1741 ACTTTTGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 ACTTTTGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1849
DB 1801 AAATTTGCAAAACATCATCTAAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1849
```

RESULT 9

```
US-09-991-163-157
; Sequence 157, Application US/09991163
; Patent No. US2002012253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
```

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212

PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;

Best Local Similarity 100.0%; Fred. No. 0;

Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGCGGCGGTAGATGAGGAGAGAGTACGTCGGCGGTCTCTCGGGCTTTTGCT 60
1 CTGAGCGGCGGTAGATGAGGAGAGAGTACGTCGGCGGTCTCTCGGGCTTTTGCT 60
61 CGGCGACTCGCTTCCAGACCTCAACAGGACTGGAGACAGGAGTTTCTTTG 120
61 CGGCGACTCGCTTCCAGACCTCAACAGGACTGGAGACAGGAGTTTCTTTG 120
121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGGATGATGAGT 180
121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGGATGATGAGT 180
121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGGATGATGAGT 180
181 TGTATTAACAATTACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTATTA 240
181 TGTATTAACAATTACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTATTA 240
241 TTCTTCAGGCGAATTAATGAGCAAGCACTGAGAAATATTAATCAAAATCAAAAAAG 300
241 TTCTTCAGGCGAATTAATGAGCAAGCACTGAGAAATATTAATCAAAATCAAAAAAG 300
301 TGTGATGTTGTGATCAAAATCCGTGCTATTCAGATCAATCATGAGCTTTAGAGAG 360

301 TGTGATGTTGTGATCAAAATCCGTGCTATTCAGATCAATCATGAGCTTTAGAGAG 360
361 GCTGCTTCACAAAACTTGAGAGAGATTTTTCAAACCAAGCTTTTCTGTAAT 420
361 GCTGCTTCACAAAACTTGAGAGAGATTTTTCAAACCAAGCTTTTCTGTAAT 420
421 AACACCAAGTATTAACAGAAAGCTGCTACCTACAGCACTGGAATTCCTATATA 480
421 AACACCAAGTATTAACAGAAAGCTGCTACCTACAGCACTGGAATTCCTATATA 480
481 AACTCAAAAGACTTTTTCACAGGATACCTTTAGTGTGCTGATCGCATGTCTGA 540
481 AACTCAAAAGACTTTTTCACAGGATACCTTTAGTGTGCTGATCGCATGTCTGA 540
541 ACAAAGTATTAATTAACCTGATAGCTTCTGATGCTGATGCTGATGCTGATGCTG 600
541 ACAAAGTATTAATTAACCTGATAGCTTCTGATGCTGATGCTGATGCTGATGCTG 600
601 ACAAAGTATTAATTAACCTGATAGCTTCTGATGCTGATGCTGATGCTGATGCTG 600
601 ACAAAGTATTAATTAACCTGATAGCTTCTGATGCTGATGCTGATGCTGATGCTG 600
661 AATGAAATGTATCTTCATTAACAGAGATTAAGATTAAGATTAAGATTAAGATTA 720
661 AATGAAATGTATCTTCATTAACAGAGATTAAGATTAAGATTAAGATTAAGATTA 720
721 CAGTGAACAGCAGTATTAACCTGATTAAGATTAAGATTAAGATTAAGATTAAGAT 780
721 CAGTGAACAGCAGTATTAACCTGATTAAGATTAAGATTAAGATTAAGATTAAGAT 780
781 GAAAAGAGAGAGACAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 GAAAAGAGAGAGAGACAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 GAGAGAGAGAGAGAGAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 GAGAGAGAGAGAGAGAGATTCAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
901 TTGATGTTATGCTTTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 960
901 TTGATGTTATGCTTTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 960
961 CCATCTGATGATGAGCAATCTGACCTTAAGTATGAGTGAACAGCTGATCTGAGAG 1020
961 CCATCTGATGATGAGCAATCTGACCTTAAGTATGAGTGAACAGCTGATCTGAGAG 1020
1021 TAGTCAGCTAGTACACCAAAATCATTAAGCATTAAGCTTTAGATTAAGTGAAGATG 1080
1021 TAGTCAGCTAGTACACCAAAATCATTAAGCATTAAGCTTTAGATTAAGTGAAGATG 1080
1081 GCAATTCAGAGATCTGCTGTTGATGATCAAGAGCAAGAGATTAAGATTAAGATTA 1140
1081 GCAATTCAGAGATCTGCTGTTGATGATCAAGAGCAAGAGATTAAGATTAAGATTA 1140
1141 TAGTATTAACAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200
1141 TAGTATTAACAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200
1201 AAGATTAAGATTTGTTGATTAATTCAGGCTTCTGATTAATTTGATTTTAACTTA 1260
1201 AAGATTAAGATTTGTTGATTAATTCAGGCTTCTGATTAATTTGATTTTAACTTA 1260
1201 AAGATTAAGATTTGTTGATTAATTCAGGCTTCTGATTAATTTGATTTTAACTTA 1260
1261 CAAGAGATTTTATTTATTTGCTGATGAGTGAAGCAAAATCTTATTTTAACTAT 1320
1261 CAAGAGATTTTATTTATTTGCTGATGAGTGAAGCAAAATCTTATTTTAACTAT 1320
1321 GTTGAAGTATTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1380
1321 GTTGAAGTATTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1380
1321 GTTGAAGTATTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1380
1381 AAGATTAAGATTTGTTGATTAATTCAGGCTTCTGATTAATTTGATTTTAACTTA 1440
1381 AAGATTAAGATTTGTTGATTAATTCAGGCTTCTGATTAATTTGATTTTAACTTA 1440

QY 1441 TTTCACAACTTTTTCACCTTTCACCTAGTTGTTAGAGGAGGCTTACACAGACACA 1500
DB 1441 TTTCACAACTTTTTCACCTTTCACCTAGTTGTTAGAGGAGGCTTACACAGACACA 1500
QY 1501 TTCTTGAATTTGAAAAGTTGAGACAGGACAGGCTTCACTGTAATCCAGCACT 1560
DB 1501 TTCTTGAATTTGAAAAGTTGAGACAGGACAGGCTTCACTGTAATCCAGCACT 1560
QY 1561 TAGGGAAGACAGTCAAGGAGATTTGATTTAGAGCTTGAAGACAGCTGGGCAAC 1620
DB 1561 TAGGGAAGACAGTCAAGGAGATTTGATTTAGAGCTTGAAGACAGCTGGGCAAC 1620
QY 1621 GTATTGAGACATGCTTATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 1680
DB 1621 GTATTGAGACATGCTTATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 1680
QY 1681 AATATGAAAAGAAATTTATATGAAAATTTATCTGAGTCAATTTAAATTTCTCTTAAGTAT 1740
DB 1681 AATATGAAAAGAAATTTATATGAAAATTTATCTGAGTCAATTTAAATTTCTCTTAAGTAT 1740
QY 1741 ACTTTTGAAGTACATTATGCTGAGTTCAGATTTAAATGCTGATATCATGCAAT 1800
DB 1741 ACTTTTGAAGTACATTATGCTGAGTTCAGATTTAAATGCTGATATCATGCAAT 1800
QY 1801 AAATTGCAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849
DB 1801 AAATTGCAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849

RESULT 10
US-09-993-604-157
; Sequence 157, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-15
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089338
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544

PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTGCTCGGGCTTTGCT 60
1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTGCTCGGGCTTTGCT 60
61 CGGCGCACTGCTTTCCAGCACTCCACAGGACTCGGACACGGAAGTTTCTCTTG 120
61 CGGCGCACTGCTTTCCAGCACTCCACAGGACTCGGACACGGAAGTTTCTCTTG 120
121 GGAAGTAAAGGTAGCAAGCAAGACGATTACTGATTTCCCAATGATGATTTGAAGT 180
121 GGAAGTAAAGGTAGCAAGCAAGACGATTACTGATTTCCCAATGATGATTTGAAGT 180
181 TGTTTATACATTCATTCAGAAATATATTCATGCTATCAGTTTACCTTTATTA 240
181 TGTTTATACATTCATTCAGAAATATATTCATGCTATCAGTTTACCTTTATTA 240
241 TTCTTCAGCGCAATTAATGAGCAAGCACTGAGAAATATTAATGATGATTTAA 300
241 TTCTTCAGCGCAATTAATGAGCAAGCACTGAGAAATATTAATGATGATTTAA 300
301 TGTGTAGTGTGTGACAAATTCGCTGTCATTCAGATCAGTCAAGCTTTAGAGAG 360
301 TGTGTAGTGTGTGACAAATTCGCTGTCATTCAGATCAGTCAAGCTTTAGAGAG 360
361 GCTGCTTCAAAAACCTTGAGGAGCACTTTTCAACCAAGCTTGTGTTTCTGATT 420
361 GCTGCTTCAAAAACCTTGAGGAGCACTTTTCAACCAAGCTTGTGTTTCTGATT 420
421 AACACCAAGTATTAATACAGAAAGCTGCTACTCATCGACTGGAACATTCCTATATA 480
421 AACACCAAGTATTAATACAGAAAGCTGCTACTCATCGACTGGAACATTCCTATATA 480
481 ACCCTCAAAAAGACTTTTTCACAGGTAACCTTGTGTTGCGCATGCGGCTGCTGA 540
481 ACCCTCAAAAAGACTTTTTCACAGGTAACCTTGTGTTGCGCATGCGGCTGCTGA 540
541 ACAACTGGGTTATTAACCTGATCAGGTTCTGATGCTGATGCTGTTTACCCAGCAGT 600
541 ACAACTGGGTTATTAACCTGATCAGGTTCTGATGCTGATGCTGTTTACCCAGCAGT 600
601 ACAAAACACAGCTCTTAATTTTGAAGAAAGATGATGCTTAAGAGGATGATTAAGT 660
601 ACAAAACACAGCTCTTAATTTTGAAGAAAGATGATGCTTAAGAGGATGATTAAGT 660
661 AAATGAATGTATGTTTATTATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 720
661 AAATGAATGTATGTTTATTATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 720
721 CAGTGAACACAGCTGATTAATCTGTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 780
721 CAGTGAACACAGCTGATTAATCTGTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 780
781 GAAAGGAGAGAGACAGATTCAGGACGACAGAGAGAGAGAGATTCGAAAAGACCTTCA 840
781 GAAAGGAGAGAGACAGATTCAGGACGACAGAGAGAGAGAGATTCGAAAAGACCTTCA 840

PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088555
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089558
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGGATGATGAGGAGGAGTACGTCCGCGGTCTCTCGGCTTGAGCT 60
DB 1 CTGAGCGCGCGGATGATGAGGAGGAGTACGTCCGCGGTCTCTCGGCTTGAGCT 60
QY 61 CGGCGCATCGCTTCCGACACTCAACACGAGCTCGACACGAGATTTCTTCTTG 120
DB 61 CGGCGCATCGCTTCCGACACTCAACACGAGCTCGACACGAGATTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCAAGAAAGCATTACTGATTTCCCAATGATGATTTGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGAAAGCATTACTGATTTCCCAATGATGATTTGAAGT 180
QY 181 TGTATTACAAATTGACATTGACATTGAAATATATTCATGCTATGAGCTTTTACCTTTATTA 240
DB 181 TGTATTACAAATTGACATTGACATTGAAATATATTCATGCTATGAGCTTTTACCTTTATTA 240

QY 241 TTCTTCAGGCGAAGTAATGAGACGACTGAAGAAATATTTGCAATGTCACAAAANA 300
 DB 241 TTCTTCAGGCGAAGTAATGAGACGACTGAAGAAATATTTGCAATGTCACAAAANA 300
 QY 301 TGTGTAGGTTGTGTAATTCCTGTCATTCAGATCGATCATGAGTTAGAGAG 360
 DB 301 TGTGTAGGTTGTGTAATTCCTGTCATTCAGATCGATCATGAGTTAGAGAG 360
 QY 361 GCTGCTTCAAAAACCTTCAGAGAGATTTTCAACCAAGCTTGTGTTTCTGCTAT 420
 DB 361 GCTGCTTCAAAAACCTTCAGAGAGATTTTCAACCAAGCTTGTGTTTCTGCTAT 420
 QY 421 AACCAAGATATATATACAGAAAGCTGCTATGATGATGATGATGATGATGATGAT 480
 DB 421 AACCAAGATATATATACAGAAAGCTGCTATGATGATGATGATGATGATGATGAT 480
 QY 481 ACCTCAAAAAGGACTTTTCAAGGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTG 540
 DB 481 ACCTCAAAAAGGACTTTTCAAGGCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 541 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 DB 541 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 QY 541 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 DB 541 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 QY 601 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 DB 601 ACAGCTGGGTTTAAAGCTGATCAAGTTCCTGATGCTGATGCTGATGCTGATGCTG 600
 QY 661 AAATGAAATGATGCTTCAATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 720
 DB 661 AAATGAAATGATGCTTCAATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 720
 QY 721 CAGTGAACAGAGATGATTAAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 780
 DB 721 CAGTGAACAGAGATGATTAAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 780
 QY 781 GAAAAG 840
 DB 781 GAAAAG 840
 QY 841 GAG 900
 DB 841 GAG 900
 QY 901 TTCAATGTTATGCTTTTAAAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 960
 DB 901 TTCAATGTTATGCTTTTAAAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 960
 QY 961 CCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 961 CCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 TAGTCCAGCTAGTACACCAACCAATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 1080
 DB 1021 TAGTCCAGCTAGTACACCAACCAATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAG 1080
 QY 1081 GCAATTCAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1081 GCAATTCAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 1141 TAGTGAAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1200
 DB 1141 TAGTGAAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1200
 QY 1201 AAAGAGAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1260
 DB 1201 AAAGAGAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1260
 QY 1261 CAAAGAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1320
 DB 1261 CAAAGAGAGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGAT 1320

QY 1321 GTTGAAGTACTGAGTAAAGTATGTTGTTTACTATGTTGACCTGTTGAGATATAC 1380
 DB 1321 GTTGAAGTACTGAGTAAAGTATGTTGTTTACTATGTTGACCTGTTGAGATATAC 1380
 QY 1381 ACAGATTAAGTATGATGATTAAGTATGATTAAGTATGATTAAGTATGATTAAGTAT 1440
 DB 1381 ACAGATTAAGTATGATGATTAAGTATGATTAAGTATGATTAAGTATGATTAAGTAT 1440
 QY 1441 TTTCGAAAGCTTTTTCACCTTCACTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAG 1500
 DB 1441 TTTCGAAAGCTTTTTCACCTTCACTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAG 1500
 QY 1501 TTCTTGAAGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 DB 1501 TTCTTGAAGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 TAGGAAAG 1620
 DB 1561 TAGGAAAG 1620
 QY 1621 GATTTGAAG 1680
 DB 1621 GATTTGAAG 1680
 QY 1681 AAATGGAAG 1740
 DB 1681 AAATGGAAG 1740
 QY 1741 ACTTTTGAAG 1800
 DB 1741 ACTTTTGAAG 1800
 QY 1801 AAATTTGAAG 1860
 DB 1801 AAATTTGAAG 1860

RESULT 12

US-09-989-721-157

; Sequence 157 Application US/09989721
 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijewski, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C55
 ; CURRENT APPLICATION NUMBER: US/09/989,721
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16

[illegible]

PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Mismatch 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGCGCGGTCTCTCGGCTTTGTCT 60
1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGCGCGGTCTCTCGGCTTTGTCT 60
61 CGGCGCATCGCTTTCCAGACCTCAACACGAGCTCGACACGGAAGTTTCTTTGG 120
61 CGGCGCATCGCTTTCCAGACCTCAACACGAGCTCGACACGGAAGTTTCTTTGG 120
121 GGAATGAAAGGTGAGCCAGAAACAGCATTAATCTGATCCCAATGATGATCTGAAT 180
121 GGAATGAAAGGTGAGCCAGAAACAGCATTAATCTGATCCCAATGATGATCTGAAT 180
181 TGTTATACATGACATGACAAATATATTCATGATCAGCTTTTAGCTTTATTA 240
181 TGTTATACATGACATGACAAATATATTCATGATCAGCTTTTAGCTTTATTA 240
181 TGTTATACATGACATGACAAATATATTCATGATCAGCTTTTAGCTTTATTA 240
241 TTCTTCAGCGAAGTAATGAGCAAGCACTGAAAGAAATTTATCAATCTCAAAAAGA 300
241 TTCTTCAGCGAAGTAATGAGCAAGCACTGAAAGAAATTTATCAATCTCAAAAAGA 300
301 TGTGTAGGTGTGACAAATTCCTGCTCATTCAGATCAGATCAGATCGTTTAGAGAG 360
301 TGTGTAGGTGTGACAAATTCCTGCTCATTCAGATCAGATCAGATCGTTTAGAGAG 360
361 GCTGCTTCACAAAACCTTGACAGGCAATTTTCAACCAAGACCTTGTCTGTATT 420
361 GCTGCTTCACAAAACCTTGACAGGCAATTTTCAACCAAGACCTTGTCTGTATT 420
421 AACCCAGATTAATACAGAAAGCTCTCTACATCGACTGGAACATCTCTTATTA 480
421 AACCCAGATTAATACAGAAAGCTCTCTACATCGACTGGAACATCTCTTATTA 480
421 AACCCAGATTAATACAGAAAGCTCTCTACATCGACTGGAACATCTCTTATTA 480
481 ACCTCAAAAAGCACTTTTTCACAGGCTACCTTAGTGTGCAATCTGAGCAATGCTGA 540
481 ACCTCAAAAAGCACTTTTTCACAGGCTACCTTAGTGTGCAATCTGAGCAATGCTGA 540
541 ACAACTGGGTATATAAAGCTGTATCAGGTTCTGTATCTCACTGTGTTTAGCCGAGCA 600
541 ACAACTGGGTATATAAAGCTGTATCAGGTTCTGTATCTCACTGTGTTTAGCCGAGCA 600
541 ACAACTGGGTATATAAAGCTGTATCAGGTTCTGTATCTCACTGTGTTTAGCCGAGCA 600
601 ACAATGCAAGCTCTTAATTTTGAAGAAAGATGATCTTAAAGAGGATCTAAGAT 660
601 ACAATGCAAGCTCTTAATTTTGAAGAAAGATGATCTTAAAGAGGATCTAAGAT 660
661 AATGAAATGTATGCTTCATTAACAAGGAAATTAAGATATATGCAAAAAAGTGAAGA 720
661 AATGAAATGTATGCTTCATTAACAAGGAAATTAAGATATATGCAAAAAAGTGAAGA 720
661 AATGAAATGTATGCTTCATTAACAAGGAAATTAAGATATATGCAAAAAAGTGAAGA 720

721 CAGTGAACAAGCATGATTAACCTAGTAAGATGTAAACAGATTAACAGAAATTGA 780
721 CAGTGAACAAGCATGATTAACCTAGTAAGATGTAAACAGATTAACAGAAATTGA 780
781 GAAAGAGAGGAGACAGATTCAGGACAGAGAGAGAGAAATCAATCAAAAAGCCTCA 840
781 GAAAGAGAGGAGACAGATTCAGGACAGAGAGAGAGAGAAATCAATCAAAAAGCCTCA 840
841 GGAGACATTTTCTTTGTGAGGCAATTCGAGCTTTTTCAAATCTGAATTTCTTCA 900
841 GGAGACATTTTCTTTGTGAGGCAATTCGAGCTTTTTCAAATCTGAATTTCTTCA 900
901 TTCAATGTTATGCTTTTAAATAATGACATGTTTCTAAAGAGCTGATCAACCA 960
901 TTCAATGTTATGCTTTTAAATAATGACATGTTTCTAAAGAGCTGATCAACCA 960
961 CCATCTGATGATGATGACATTCGACCTTAATGTTAGAAACACATGACATTCCTGAGC 1020
961 CCATCTGATGATGATGACATTCGACCTTAATGTTAGAAACACATGACATTCCTGAGC 1020
1021 TAGTCAGCTGATGACACCAAAATCATTAAGCATTAAGCCTTAGATGACATG 1080
1021 TAGTCAGCTGATGACACCAAAATCATTAAGCATTAAGCCTTAGATGACATG 1080
1081 GCAATTCAGAGATCTCGGTTGTTAGATACACAAGACAAACGATCTAAACCAATCTGG 1140
1081 GCAATTCAGAGATCTCGGTTGTTAGATACACAAGACAAACGATCTAAACCAATCTGG 1140
1141 TAGTATGACCAAGATTAAGCATTCAAATGAGAGCCGACCAAAACATGAAAGAAATGA 1200
1141 TAGTATGACCAAGATTAAGCATTCAAATGAGAGCCGACCAAAACATGAAAGAAATGA 1200
1201 AAGATGAGGTTTGTGTAATTCACGGTCTCTACATTTGATCTTTAACTTA 1260
1201 AAGATGAGGTTTGTGTAATTCACGGTCTCTACATTTGATCTTTAACTTA 1260
1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAAGCCAAACATTTCTTTTACTAT 1320
1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAAGCCAAACATTTCTTTTACTAT 1320
1321 GTGAGCTACTGAGATGATGATGATTTGTTTCTATGTTTCACTGCTTTGACATATAC 1380
1321 GTGAGCTACTGAGATGATGATGATTTGTTTCTATGTTTCACTGCTTTGACATATAC 1380
1381 AAGATTAACCTTATGATGATTTACTTCAAAAAGTAACTTTTCAAACTCAATGCTTTTA 1440
1381 AAGATTAACCTTATGATGATTTACTTCAAAAAGTAACTTTTCAAACTCAATGCTTTTA 1440
1441 TTTCGAACCTTTTTCACCTTCACTAATGTTTGAAGGAGGAGCTTACAGAGACA 1500
1441 TTTCGAACCTTTTTCACCTTCACTAATGTTTGAAGGAGGAGCTTACAGAGACA 1500
1501 TTCTTAAATTTGAAAAGTGAACAGGCAAGCTGCTCACACTGTAATCCAGACCT 1560
1501 TTCTTAAATTTGAAAAGTGAACAGGCAAGCTGCTCACACTGTAATCCAGACCT 1560
1561 TAGGAAACAGATCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1561 TAGGAAACAGATCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1621 GATATGAGCAATGCTATTAATAAATTAATAAGAAAGCAAGAAATGCTTAATTTTCA 1680
1621 GATATGAGCAATGCTATTAATAAATTAATAAGAAAGCAAGAAATGCTTAATTTTCA 1680
1681 AATATGAGAAAGAAATTTATGAAATTTATCTGATGATTAATTTCTTTAAGTAT 1740
1681 AATATGAGAAAGAAATTTATGAAATTTATCTGATGATTAATTTCTTTAAGTAT 1740
1741 ACTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1741 ACTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1801 AATTTGCAAAACATCATCTAATTAATTAATAAATAAATAAATAAATAAATAAATAA 1849

PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGGCGGTGAGTGAAGGAGAGTACGTGGCGCTGCTCTCGGCGCTTTTGCT 60
DB 1 CTGAGCGGCGGTGAGTGAAGGAGAGTACGTGGCGCTGCTCTCGGCGCTTTTGCT 60
QY CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGGAGAGGTTTCTTCTTG 120
DB 61 CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGGAGAGGTTTCTTCTTG 120

QY 121 GGAAGTAAAGTGAAGCCAGAGACGATTAAGTATCCAAATGATGATGAGT 180
DB 121 GGAAGTAAAGTGAAGCCAGAGACGATTAAGTATCCAAATGATGATGAGT 180
QY 181 TGTATTAACAATTGACATTCAGAAATATATTCATGCTATGACCTTTTAA 240
DB 181 TGTATTAACAATTGACATTCAGAAATATATTCATGCTATGACCTTTTAA 240
QY 241 TTCTTCAGCGGAGTAAATGAGACAGCAAGAAATTTTCAATGTCAAAAGAA 300
DB 241 TTCTTCAGCGGAGTAAATGAGACAGCAAGAAATTTTCAATGTCAAAAGAA 300
QY 301 TGTGTAGTGTGATCAAAATTCGCTGATTCAGATTCAGATCAACGTTTAA 360
DB 301 TGTGTAGTGTGATCAAAATTCGCTGATTCAGATTCAGATCAACGTTTAA 360
QY 361 GCTGCTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTTTCTGCA 420
DB 361 GCTGCTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTTTCTGCA 420
QY 421 AACCAAGTATATATACAGAAAGCTGCTACTCATGCACTGAAACATTCCTA 480
DB 421 AACCAAGTATATATACAGAAAGCTGCTACTCATGCACTGAAACATTCCTA 480
QY 481 ACCCTAAAAGACCTTTTCAAGGTAACCTTTAGTGTGCTCAATGTGGCAT 540
DB 481 ACCCTAAAAGACCTTTTCAAGGTAACCTTTAGTGTGCTCAATGTGGCAT 540
QY 541 ACAACCTGGTATATTAACCTGATCAGGTCCTGATTCAGATGTTTAAAG 600
DB 541 ACAACCTGGTATATTAACCTGATCAGGTCCTGATTCAGATGTTTAAAG 600
QY 601 ACAACCAACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGTACATA 660
DB 601 ACAACCAACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGTACATA 660
QY 661 AAATGAATGATGCTTATTAACAGAGAAATTAAGATGCAAAAGTGAAGA 720
DB 661 AAATGAATGATGCTTATTAACAGAGAAATTAAGATGCAAAAGTGAAGA 720
QY 721 CAGTGAACAAGCAGTATTAACCTGATTAAGATGTAACAGATTAACAGAA 780
DB 721 CAGTGAACAAGCAGTATTAACCTGATTAAGATGTAACAGATTAACAGAA 780
QY 781 GAAAGAGAGAGACACAGATTCAGGAGAGAGAGAGAGAGATCCAAAAG 840
DB 781 GAAAGAGAGAGACACAGATTCAGGAGAGAGAGAGAGAGATCCAAAAG 840
QY 841 GGAAGACATTTTCTTTGTGAGCATTAAGACCTTTTCCAAATTCGATTT 900
DB 841 GGAAGACATTTTCTTTGTGAGCATTAAGACCTTTTCCAAATTCGATTT 900
QY 901 TTCAATGTATATGCTTTTAAATTAACATGTTTCTTAAAGTGTGATCAACA 960
DB 901 TTCAATGTATATGCTTTTAAATTAACATGTTTCTTAAAGTGTGATCAACA 960
QY 961 CCATCTCGATGATGATCAATCTGACCTTAATGATGAACACACTGACATTC 1020
DB 961 CCATCTCGATGATGATCAATCTGACCTTAATGATGAACACACTGACATTC 1020
QY 1021 TAGTCCAGCTGTACACCAAAATCATTAAGCATTAAGCTTTAGTGAAGAT 1080
DB 1021 TAGTCCAGCTGTACACCAAAATCATTAAGCATTAAGCTTTAGTGAAGAT 1080
QY 1081 GCAATTTCAAGAGATCTCGTGTGATGATACAGAGCAAAAGATCTTAAAG 1140
DB 1081 GCAATTTCAAGAGATCTCGTGTGATGATACAGAGCAAAAGATCTTAAAG 1140
QY 1141 TAGTGTACCAAGATTAAGATTCAGAAATGAGAGCCGAGAAACAGATGA 1200
DB 1141 TAGTGTACCAAGATTAAGATTCAGAAATGAGAGCCGAGAAACAGATGA 1200
QY 1201 AAAGATGAAGGTTTGTGATATTCACGGTCTCTCAATTTGATCTTTTAA 1260

Db 1201 AAAATATAGAGGTTTGGTGAATATTCACGGTCTCCACATTTTGATTCCTTTTAACTTA 1260
Qy 1261 CAAGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTACTAT 1320
Db 1261 CAAAGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTACTAT 1320
Qy 1321 GTTAGCTACTTGCAGTAAGTTCATTTGTTTTCATATGTTTCACTGTTTGCAGTAATAC 1380
Db 1321 GTTAGCTACTTGCAGTAAGTTCATTTGTTTTCATATGTTTCACTGTTTGCAGTAATAC 1380
Qy 1381 ACAGATACCTCTTGTGATTTACTTACAAAGACTTTTCAACATCGATGCTTTTA 1440
Db 1381 ACAGATACCTCTTGTGATTTACTTACAAAGACTTTTCAACATCGATGCTTTTA 1440
Qy 1441 TTTCAAACCTTTTTCACCTTTCACTAAAGTTGAGGGGAAGGCTTACACAGACACA 1500
Db 1441 TTTCAAACCTTTTTCACCTTTCACTAAAGTTGAGGGGAAGGCTTACACAGACACA 1500
Qy 1501 TTCTTTGAATTTGGAAAAGTGAGACACAGGCAAGTGGCTCACACCTGTATCCACAGCT 1560
Db 1501 TTCTTTGAATTTGGAAAAGTGAGACACAGGCAAGTGGCTCACACCTGTATCCACAGCT 1560
Qy 1561 TAGGAAAGACAGTCAAGAGATGATTGAAGCTAGAGATTAGACACAGCTGGGCAAC 1620
Db 1561 TAGGAAAGACAGTCAAGAGATGATTGAAGCTAGAGATTAGACACAGCTGGGCAAC 1620
Qy 1621 GTATTGACCATCTCTTATTAATAATGAATAATGAATAATGAATAATGAATAATGAATA 1680
Db 1621 GTATTGACCATCTCTTATTAATAATGAATAATGAATAATGAATAATGAATAATGAATA 1680
Qy 1681 AATATGAAAGAAATTTATATGAATAATTTATCTGAGTCATTAATTTCTTAACTGAT 1740
Db 1681 AATATGAAAGAAATTTATATGAATAATTTATCTGAGTCATTAATTTCTTAACTGAT 1740
Qy 1741 ACTTTTTAGAGTACATTTATGCTTAGAGTTGCCAGATTAATAAGCTGAGATATGCAAT 1800
Db 1741 ACTTTTTAGAGTACATTTATGCTTAGAGTTGCCAGATTAATAAGCTGAGATATGCAAT 1800
Qy 1801 AAATTCGAAACATCATCTAAATTTAATAAAAAAAAAAAAAAAAAAAAA 1849
Db 1801 AAATTCGAAACATCATCTAAATTTAATAAAAAAAAAAAAAAAAAAAAA 1849

RESULT 14
US-09-989-293A-157
Sequence 157, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11

;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948

;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db      1 CTGAGGCGGGGATGAGTGGGGGAGGTAGTGGGGGCTCTCGGGGCTTTGTGT 60
Qy      61 CGGCGACTCGCTTCCAGACCTCAACAGAGACTCGGACAGGAAAGTTCCTTCTTGG 120
Db      61 CGGCGACTCGCTTCCAGACCTCAACAGAGACTCGGACAGGAAAGTTCCTTCTTGG 120
Qy      121 GGAAGTAAAGGTGAAGCCAGAAACAGCATTAAGTATCTCCAAATGATGATGTAAGT 180
Db      121 GGAAGTAAAGGTGAAGCCAGAAACAGCATTAAGTATCTCCAAATGATGATGTAAGT 180
Qy      181 TGTATACATTAATGACATTAATATATATCTCATCTAGCTTATAGCTTTTATATTA 240
Db      181 TGTATACATTAATGACATTAATATATATCTCATCTAGCTTATAGCTTTTATATTA 240
Qy      241 TTCTTCAAGGGAATGAAATGAGCAAGCACTGAAGAAATATATATCAATGTCAAAAAGA 300
Db      241 TTCTTCAAGGGAATGAAATGAGCAAGCACTGAAGAAATATATATCAATGTCAAAAAGA 300
Qy      301 TGTGTAGGTGTGTAGCAAAATCCGTGTGATTCAGATCAGATCAGATCAGATCAGAT 360
Db      301 TGTGTAGGTGTGTAGCAAAATCCGTGTGATTCAGATCAGATCAGATCAGATCAGAT 360
Qy      361 GCTGCTTCAAAAACCTTGGAGAGCATTTTCAAAACAAAGACCTTGTCTGTAT 420
Db      361 GCTGCTTCAAAAACCTTGGAGAGCATTTTCAAAACAAAGACCTTGTCTGTAT 420
Qy      421 AATACCAAGTATATTAACAAAGAGCTGTCTATCTATCGATGGAACATTCCTTATATA 480
Db      421 AATACCAAGTATATTAACAAAGAGCTGTCTATCTATCGATGGAACATTCCTTATATA 480
Qy      481 ACCTCAAAAAGGACCTTTTCAAGGATCTTATAGTGTGCAATCTGGCATGCTGA 540
Db      481 ACCTCAAAAAGGACCTTTTCAAGGATCTTATAGTGTGCAATCTGGCATGCTGA 540
Qy      541 ACAACTGGGTATATAAAGTATACAGGATCTGTATGTCACATGCTTTTGGCGAGCAT 600
Db      541 ACAACTGGGTATATAAAGTATACAGGATCTGTATGTCACATGCTTTTGGCGAGCAT 600
Qy      601 ACAACACACAGCTCAATATTTTGAAGAGATGATCTTAAAGAGATGATCAATAGAT 660
Db      601 ACAACACACAGCTCAATATTTTGAAGAGATGATCTTAAAGAGATGATCAATAGAT 660
Qy      661 AAATGAATGTATGCTTCAATTAAGAGAAATTAAGAGATTAAGAGAAATGAGAGA 720
Db      661 AAATGAATGTATGCTTCAATTAAGAGAAATTAAGAGATTAAGAGAAATGAGAGA 720
Qy      721 CAGTGAACAGAGCTGATTAATTAAGTAAAGATGTAACAGATTAAGAGAAATGTA 780
Db      721 CAGTGAACAGAGCTGATTAATTAAGTAAAGATGTAACAGATTAAGAGAAATGTA 780
Qy      781 GAAAGAGAGAGAGCAAGATTCAGAGCAAGAGAGAAAGATCAATCAAAAAGACCTCA 840
Db      781 GAAAGAGAGAGAGCAAGATTCAGAGCAAGAGAGAAAGATCAATCAAAAAGACCTCA 840
Qy      841 GGAAGACATTTTCTTTGTGACGATTAAGGACCTTTTCAAAATCTGAATTCCTTCA 900
Db      841 GGAAGACATTTTCTTTGTGACGATTAAGGACCTTTTCAAAATCTGAATTCCTTCA 900
Qy      901 TTCAATGTATGTCTTTTAAATATAGACATGTTCTAAAGATGCTGATCAACCA 960
Db      901 TTCAATGTATGTCTTTTAAATATAGACATGTTCTAAAGATGCTGATCAACCA 960
Qy      961 CCATCTCGATGTAGTACAACTGACCTTAATGATGAACACATGACATTCCTGAAGC 1020
Db      961 CCATCTCGATGTAGTACAACTGACCTTAATGATGAACACATGACATTCCTGAAGC 1020
Qy      1021 TAGTCAGCTAGTACACAAATCAATTAAGCATTAAGCTTAAGCTTATAGATGACAGATG 1080
Db      1021 TAGTCAGCTAGTACACAAATCAATTAAGCATTAAGCTTATAGATGACAGATG 1080
Qy      1081 GCATTCAGAGATCTGGTGTGATTAACAAAGCAACGATCTAAAGCAATCTGG 1140

```

```

Db      1081 GCATTCAGAGATCTGGTGTGATTAACAAAGCAACGATCTAAAGCAATCTGG 1140
Qy      1141 TAGTATGTAACCAAGATTAAGATCCAAATATGAGAGCCAGAAACAGATGAAGAAATGA 1200
Db      1141 TAGTATGTAACCAAGATTAAGATCCAAATATGAGAGCCAGAAACAGATGAAGAAATGA 1200
Qy      1201 AAAGTGAAGGCTTTTGTGAAATTTACCGGTCTCTCAATTTTGAATCTTTAACTTGA 1260
Db      1201 AAAGTGAAGGCTTTTGTGAAATTTACCGGTCTCTCAATTTTGAATCTTTAACTTGA 1260
Qy      1261 CAAGAGATTTTATTTATTTGAGTGAAGGATTAAGCAAACTTCTATGTTTATACAT 1320
Db      1261 CAAGAGATTTTATTTATTTGAGTGAAGGATTAAGCAAACTTCTATGTTTATACAT 1320
Qy      1321 GTTATGCTACTGAGTGAAGTCAATTTGTTTATATGTTCACTGCTGTTGCAATATAC 1380
Db      1321 GTTATGCTACTGAGTGAAGTCAATTTGTTTATATGTTCACTGCTGTTGCAATATAC 1380
Qy      1381 ACAGATACCTGATGATTAATTAATCAAAAGTATTTTCAAAATCAATCAATCTTTTA 1440
Db      1381 ACAGATACCTGATGATTAATTAATCAAAAGTATTTTCAAAATCAATCAATCTTTTA 1440
Qy      1441 TTTCAAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTT 1500
Db      1441 TTTCAAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTT 1500
Qy      1501 TTTCTTGAATTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db      1501 TTTCTTGAATTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy      1561 TAGGAGAGACAGATCAAGAGATTAAGTGAAGCTGAAGATTAAGAGAGAGAGAGAG 1620
Db      1561 TAGGAGAGACAGATCAAGAGATTAAGTGAAGCTGAAGATTAAGAGAGAGAGAGAG 1620
Qy      1621 GTATTTGAGACCATCTCTATTAATAAATTAATAAATTAATAAATTAATAAATTAATA 1680
Db      1621 GTATTTGAGACCATCTCTATTAATAAATTAATAAATTAATAAATTAATAAATTAATA 1680
Qy      1681 AATATGAAAGAAATTTATATGAATAATTTATCTGAGTCATTAATAATTCCTTAAGTAT 1740
Db      1681 AATATGAAAGAAATTTATATGAATAATTTATCTGAGTCATTAATAATTCCTTAAGTAT 1740
Qy      1741 ACTTTTGAAGATCAATTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 1800
Db      1741 ACTTTTGAAGATCAATTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 1800
Qy      1801 AAATTTGCAAAACATCATCTTAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTT 1849
Db      1801 AAATTTGCAAAACATCATCTTAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTT 1849

```

Search completed: April 17, 2004, 19:00:05
Job time : 791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 760 seconds

(without alignments)
10335.419 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849
Sequence: 1 cctgagcgcgccgctagcatgys.....aaaaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY NTC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124098041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*
1: geneseqn1800s:*
2: geneseqn1900s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1849	100.0	1849	3	AAZ64999 Membrane-
2	1849	100.0	1849	3	AAZ64999 Membrane-
3	1849	100.0	1849	5	AAZ64999 Membrane-
4	1849	100.0	1849	5	AAZ64999 Membrane-
5	1849	100.0	1849	6	ABX74388 Human CDN
6	1849	100.0	1849	7	ABX78594 Human PRO
7	1849	100.0	1849	7	ACA75566 Novel hum
8	1849	100.0	1849	7	ACA71046 Human sec
9	1849	100.0	1849	7	ACCA7574 Human sec
10	1849	100.0	1849	7	ACCA6960 Human sec
11	1849	100.0	1849	7	ACCD04133 Human sec
12	1849	100.0	1849	7	ABX77815 Human PRO
13	1849	100.0	1849	7	ABX80227 Novel hum
14	1849	100.0	1849	7	ACA69133 Human CDN
15	1849	100.0	1849	7	ACA69464 CDNA enco
16	1849	100.0	1849	7	ACA90309 Novel hum
17	1849	100.0	1849	7	ACCA89416 Human sec
18	1849	100.0	1849	7	ABX90204 Human sec
19	1849	100.0	1849	7	ACA98207 Novel hum
20	1849	100.0	1849	7	ACA93849 Human sec
21	1849	100.0	1849	7	ACD15242 Human sec
22	1849	100.0	1849	7	ACCD08829 Human sec
23	1849	100.0	1849	7	ACC96749 Human sec

24	1849	100.0	1849	7	ACFI5470 Human sec
25	1849	100.0	1849	7	ABX64050 CDNA enco
26	1849	100.0	1849	7	ACA72837 Human PRO
27	1849	100.0	1849	7	ACD03009 Novel hum
28	1849	100.0	1849	7	ACD01824 Novel hum
29	1849	100.0	1849	7	ACA92016 Novel hum
30	1849	100.0	1849	7	ACA89441 CDNA enco
31	1849	100.0	1849	7	ACA73451 Human sec
32	1849	100.0	1849	7	ACA05766 Human sec
33	1849	100.0	1849	7	ACA66600 CDNA enco
34	1849	100.0	1849	7	ACA64272 Novel hum
35	1849	100.0	1849	7	ACA91174 Novel hum
36	1849	100.0	1849	7	ACD81551 Human CDN
37	1849	100.0	1849	7	ACF20175 Human sec
38	1849	100.0	1849	7	ACF19561 Human sec
39	1849	100.0	1849	7	ACD21849 Human sec
40	1849	100.0	1849	7	ACF13014 Human sec
41	1849	100.0	1849	7	ACD25117 Human sec
42	1849	100.0	1849	7	ACF00166 Human sec
43	1849	100.0	1849	7	ACA60373 Novel hum
44	1849	100.0	1849	7	ACA72223 Novel hum
45	1849	100.0	1849	7	ACD04747 Novel hum

ALIGNMENTS

RESULT 1	AAZ64999	standard; CDNA; 1849 BP.
ID	AAZ64999	standard; CDNA; 1849 BP.
AC	AAZ64999;	
XX		
DT	05-APR-2000	(first entry)
DE		Membrane-bound protein PRO1013 encoding CDNA.
XX		
KX		Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW		pharmaceutical; receptor immunoadhesin; gene mapping; ss.
OS	Homo sapiens.	
XX		
PN	W09963088-A2.	
XX		
PD	09-DEC-1999.	
XX		
PF	02-JUN-1999;	99WO-US012252.
XX		
PR	02-JUN-1998;	98US-0087607P.
XX		
PR	02-JUN-1998;	98US-0087609P.
XX		
PR	02-JUN-1998;	98US-0087759P.
XX		
PR	04-JUN-1998;	98US-0088021P.
XX		
PR	04-JUN-1998;	98US-0088025P.
XX		
PR	04-JUN-1998;	98US-0088028P.
XX		
PR	04-JUN-1998;	98US-0088029P.
XX		
PR	04-JUN-1998;	98US-0088030P.
XX		
PR	04-JUN-1998;	98US-0088033P.
XX		
PR	05-JUN-1998;	98US-0088167P.
XX		
PR	05-JUN-1998;	98US-0088202P.
XX		
PR	05-JUN-1998;	98US-0088212P.
XX		
PR	05-JUN-1998;	98US-0088217P.
XX		
PR	05-JUN-1998;	98US-0088655P.
XX		
PR	09-JUN-1998;	98US-0088722P.
XX		
PR	10-JUN-1998;	98US-0088730P.
XX		
PR	10-JUN-1998;	98US-0088734P.
XX		
PR	10-JUN-1998;	98US-0088738P.
XX		
PR	10-JUN-1998;	98US-0088740P.
XX		
PR	10-JUN-1998;	98US-0088741P.
XX		
PR	10-JUN-1998;	98US-0088742P.
XX		
PR	10-JUN-1998;	98US-0088810P.
XX		
PR	10-JUN-1998;	98US-0088811P.

[illegible]

04-AUG-1998; 98US-0095335P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096339P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096881P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 18-AUG-1998; 98US-0096937P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0087971P.
PR 26-AUG-1998; 98US-0087974P.
PR 26-AUG-1998; 98US-0087978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098852P.
PR 15-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
PI Wood WI, Yuan J;
XX MPI: 2000-072883/06.
DR P-PSEB; MAY66666.

Membrane-bound proteins and related nucleotide sequences.

Claim 2; Fig 94; 822pp; English.

The invention provides membrane-bound PRO polypeptides and
polynucleotides encoding them. The PRO sequences of the invention were
identified based on extracellular domain homology screening. The PRO
sequences have homology with proteins including LDL receptors, TIR
ligands and various enzymes. The membrane-bound proteins and receptor
molecules are useful as pharmaceutical and diagnostic agents. Receptor
immunoadhesins, for instance, can be used as therapeutic agents to block
receptor-ligand interactions. The membrane-bound proteins can also be
employed for screening of potential peptide or small molecule inhibitors
of the relevant receptor/potent interaction. The PRO encoding sequences
are useful as hybridization probes, in chromosome and gene mapping and in
the generation of antisense RNA and DNA. PRO nucleic acid sequences will
also be useful for the preparation of PRO polypeptides, especially by
recombinant techniques

Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 3; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTAGAGCGCGGTACATGAGGGGAGAGACTCCGCCGTCTCTCAGGCTTTTGACT 60

```

Db      1 CTGAGCGCGGTAGATGAGGAGGAGTACGTGCGGTGCTCTCGGCGCTTTGTGCT
Qy      61 CGGCGACTCGCTTTCAGCACTCAACGCGACTCGGACAGGAGGTTTCTTCTTG
Db      61 CGGCGACTCGCTTTCAGCACTCAACGCGACTCGGACAGGAGGTTTCTTCTTG
Qy      121 GGAAGTAAAGGTGAAGCCAGAAAGCAGATTACTGATTCCTCAATGATGATGTTGAAGT
Db      121 GGAAGTAAAGGTGAAGCCAGAAAGCAGATTACTGATTCCTCAATGATGATGTTGAAGT
Qy      181 TGTATTATCAATTGACATTCAGAAATATATTCATGATCTGATCTTTTACGTTTATA
Db      181 TGTATTATCAATTGACATTCAGAAATATATTCATGATCTGATCTTTTACGTTTATA
Qy      241 TTCTTCAGCGAGTAAATGACAGACACTGAGAAATATATTCATGATCTGATCTTTA
Db      241 TTCTTCAGCGAGTAAATGACAGACACTGAGAAATATATTCATGATCTGATCTTTA
Qy      301 TGTGTAGTGTGTGATCAAAATTCGTGTCTCATTCAGATCAGATCATGACGTTTGAAGAG
Db      301 TGTGTAGTGTGTGATCAAAATTCGTGTCTCATTCAGATCAGATCATGACGTTTGAAGAG
Qy      361 GGTGCTTCACAAAAACCTGACAGAGCATTTTCAACCAAGACCTTGTGTTTCTGCTAT
Db      361 GGTGCTTCACAAAAACCTGACAGAGCATTTTCAACCAAGACCTTGTGTTTCTGCTAT
Qy      421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCTGAAACATTCCTTATATA
Db      421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCTGAAACATTCCTTATATA
Qy      481 ACCTCAAAAAGGACTTTTACAGGAGTCTTATAGTGGTCCAACTGGGCACTGCTGA
Db      481 ACCTCAAAAAGGACTTTTACAGGAGTCTTATAGTGGTCCAACTGGGCACTGCTGA
Qy      541 ACAAGTGGTATTAACCTGTATCAAGTCTGTATGTCATCGATGTTTACCGGACAGT
Db      541 ACAAGTGGTATTAACCTGTATCAAGTCTGTATGTCATCGATGTTTACCGGACAGT
Qy      601 ACAACACACAGCTCTTAAATTTTGAAGAGTGTATCTTAAAGAGTCACTAAGT
Db      601 ACAACACACAGCTCTTAAATTTTGAAGAGTGTATCTTAAAGAGTCACTAAGT
Qy      661 AAATGAATGTATGCTTCAATTAACAAGAGATTTAAAGATATATGCAAAAAGTGAAGA
Db      661 AAATGAATGTATGCTTCAATTAACAAGAGATTTAAAGATATATGCAAAAAGTGAAGA
Qy      721 CAGTGAACAGAGCTAGATTAACATGTAAGAGTGTAAACAGATTAAACGAGAAATGA
Db      721 CAGTGAACAGAGCTAGATTAACATGTAAGAGTGTAAACAGATTAAACGAGAAATGA
Qy      781 GAAAAGAGAGAGCAGATTCAGGACAGAGAGAGAGAAATCATCAAAAAGACCTCA
Db      781 GAAAAGAGAGAGCAGATTCAGGACAGAGAGAGAGAAATCATCAAAAAGACCTCA
Qy      841 GAGAAACATTTTCTTTGTGTCAGGACATTCGACCTTTTTCCTCAATTCCTGAATTTCTTA
Db      841 GAGAAACATTTTCTTTGTGTCAGGACATTCGACCTTTTTCCTCAATTCCTGAATTTCTTA
Qy      901 TTGATGTGATATGCTTTTAAATAATGACATGTTTCTTAAAGAGTGTAACTAACAACA
Db      901 TTGATGTGATATGCTTTTAAATAATGACATGTTTCTTAAAGAGTGTAACTAACAACA
Qy      961 CCATCTCGATGTAGTACAAATCTGACCTTAATGTATGAACAACACTGACATTCCTGAAGC
Db      961 CCATCTCGATGTAGTACAAATCTGACCTTAATGTATGAACAACACTGACATTCCTGAAGC
Qy      1021 TAGTCCAGCTAGTACCAACAATCATTAAGCATTAAGCTTGAAGCTTGAAGTACAGATG
Db      1021 TAGTCCAGCTAGTACCAACAATCATTAAGCATTAAGCTTGAAGTACAGATG
Qy      1081 GCAATTCAGAGATCTCGTGTGTAGATACAAAGACAAACGATCTTAAACAAATACCTGG

```

```

Db      1081 GCAATTCAGAGATCTCGTGTGTAGATACAAAGACAAACGATCTTAAACAAATACCTGG
Qy      1141 TAGTATGTAACCAAGATTAAGCATCCAAATATGACAGCCAGAAACAGATGAAGAAATGA
Db      1141 TAGTATGTAACCAAGATTAAGCATCCAAATATGACAGCCAGAAACAGATGAAGAAATGA
Qy      1201 AAAGATGAAGGTTTGTGTGAATTTCAAGGTCCTTCAATTTTGAATCTTTAAACCTTA
Db      1201 AAAGATGAAGGTTTGTGTGAATTTCAAGGTCCTTCAATTTTGAATCTTTAAACCTTA
Qy      1261 CAAGAGATTTTATTTATGCTGATGGGTAAAGCCAAACATTCCTAATGTTTACTAT
Db      1261 CAAGAGATTTTATTTATTTGCTGATGGGTAAAGCCAAACATTCCTAATGTTTACTAT
Qy      1321 GTTAGCTACTTGAAGTATTCATTTGTTTATCTAATGTTTACCTGTTGACGTAATAC
Db      1321 GTTAGCTACTTGAAGTATTCATTTGTTTATCTAATGTTTACCTGTTGACGTAATAC
Qy      1381 AAGATTAACCTGATGATTTACTTCAAAAGTACCTTTTCAACATCAGATGCTTTA
Db      1381 AAGATTAACCTGATGATTTACTTCAAAAGTACCTTTTCAACATCAGATGCTTTA
Qy      1441 TTCCAAACCTTTTTCACCTTCACTAAGTGTGAGGGGAAGCTTACACAGACACA
Db      1441 TTCCAAACCTTTTTCACCTTCACTAAGTGTGAGGGGAAGCTTACACAGACACA
Qy      1501 TTCTTTAAGATTTGAAAAAGTGAACCAAGCAACAGTGGCTCACCTGTAAATCCAGACACT
Db      1501 TTCTTTAAGATTTGAAAAAGTGAACCAAGCAACAGTGGCTCACCTGTAAATCCAGACACT
Qy      1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAGCTTGAAGAGTGAAGACCAAGCTGGGCAAC
Db      1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAGCTTGAAGAGTGAAGACCAAGCTGGGCAAC
Qy      1621 GTATTGAGACCAATGCTTATTAATAATAATGAAGAAAGCAAGATAGCTTATTTTCAA
Db      1621 GTATTGAGACCAATGCTTATTAATAATAATGAAGAAAGCAAGATAGCTTATTTTCAA
Qy      1681 AATATGAAAGAAATTTATATGAATAATTTATCTAGTCACTTAAATTCCTCTTAAGTAT
Db      1681 AATATGAAAGAAATTTATATGAATAATTTATCTAGTCACTTAAATTCCTCTTAAGTAT
Qy      1741 ACTTTTGAAGATCATTAATGCTTGAAGTTCAGATTAATGCTGATTCATGCAAT
Db      1741 ACTTTTGAAGATCATTAATGCTTGAAGTTCAGATTAATGCTGATTCATGCAAT
Qy      1801 AAATTTGCAAAACATCATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA
Db      1801 AAATTTGCAAAACATCATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA

```

RESULT 2
ID AA545991 standard; CDNA; 1849 BP.

AA545991;
18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #67.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
dog; cat; pig; goat; rabbit; tumor necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
PCR primer.

Homo sapiens.
WO200168848-A2.

20-SEP-2001.

PF 28-FEB-2001; 2001MO-US006520.
XX
XX 01-MAR-2000; 2000MO-US006501.
PR 02-MAR-2000; 2000MO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189330P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000MO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000MO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196680P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199357P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR P-PSDB; AAU29090.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 133; 774p; English.
XX
XX Sequences AA845925-AA846231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumor in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumor necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX

SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;
Query Match 100.0%; Score 1849; DB 4; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGCGGTAGCATGAGGAGAGAGTACGCGGCTCTCGGCTTTGTGCT 60
DB 1 CTGAGCGCGCGGTAGCATGAGGAGAGAGTACGCGGCTCTCGGCTTTGTGCT 60
QY 61 CGGCGCATTCGCTTTCCAGACCTTCAACAGGACTCGGACCGAAGCTTTCTTTGG 120
DB 61 CGGCGCATTCGCTTTCCAGACCTTCAACAGGACTCGGACCGAAGCTTTCTTTGG 120
QY 121 GGAAGTAAAGGTGAGGAGCAAGAACAGCATTAATCCCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAGGAGCAAGAACAGCATTAATCCCAATGATGATGTAAGT 180
QY 181 TGTTTATCAATTGACATTCAGAAATATATTCATGCTATGCTTTTACCTTTATTA 240
DB 181 TGTTTATCAATTGACATTCAGAAATATATTCATGCTATGCTTTTACCTTTATTA 240
QY 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATTTATCAATGTCAAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATTTATCAATGTCAAAAAGAA 300
QY 301 TGTGTAGGTTGTATCAAAATTCCTGCTCATTCAGATCAGATCAGCTTTAGAGAG 360
DB 301 TGTGTAGGTTGTATCAAAATTCCTGCTCATTCAGATCAGATCAGCTTTAGAGAG 360
QY 361 GGTGCTTCAAAAACCTTGACAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
DB 361 GGTGCTTCAAAAACCTTGACAGAGCATTTTTCACCAAGACCTGTTTCTGCTATT 420
QY 421 AACACCAAGTATATTAACAGAAAGTGTCTACTCATGCTGAGCACTTCTTATATTA 480
DB 421 AACACCAAGTATATTAACAGAAAGTGTCTACTCATGCTGAGCACTTCTTATATTA 480
QY 481 ACCCTAAAAAGACTTTTTCACAGGATCTTTTGTGTTGCTTGTGCTGAGCTGCTGA 540
DB 481 ACCCTAAAAAGACTTTTTCACAGGATCTTTTGTGTTGCTTGTGCTGAGCTGCTGA 540
QY 541 ACAACTGGGTTATATAAATCTGATCAGGTTCTGTATGTCACCTGTTTACCGAGCAGT 600
DB 541 ACAACTGGGTTATATAAATCTGATCAGGTTCTGTATGTCACCTGTTTACCGAGCAGT 600
QY 601 ACAAAACACACAGCTTAATTTTGAAGAAATGATCCTTAAAGAGGATCAATTAAGAT 660
DB 601 ACAAAACACACAGCTTAATTTTGAAGAAATGATCCTTAAAGAGGATCAATTAAGAT 660
QY 661 AATATGAATGTATGCTTCAATTAACAAGAGATTAAGAGTATATGCAAAAAGTGAAGA 720
DB 661 AATATGAATGTATGCTTCAATTAACAAGAGATTAAGAGTATATGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAGCAGTATGATTAATCTATGTAAGATGTAACAGATTAACAGAAATTTGA 780
DB 721 CAGTGAACAGCAGTATGATTAATCTATGTAAGATGTAACAGATTAACAGAAATTTGA 780
QY 781 GAAAAGGAGGAGCAGATTCAGGACGACGACGACGACGACGACGACGACGACGAC 840
DB 781 GAAAAGGAGGAGCAGATTCAGGACGACGACGACGACGACGACGACGACGACGAC 840
QY 841 GGAGAACATTTTCTTTGTGACGACATTAAGGACCTTTTTCCAATTTGATTTCTTCA 900
DB 841 GGAGAACATTTTCTTTGTGACGACATTAAGGACCTTTTTCCAATTTGATTTCTTCA 900
QY 901 TTCATGTTATGTTATTTTAAATATGACATGTTTCTAAAGTACCTTAATCAACCA 960
DB 901 TTCATGTTATGTTATTTTAAATATGACATGTTTCTAAAGTACCTTAATCAACCA 960
QY 961 CCATCTGATGTAGTATGACATCTGATCTTAATGATGAAACACACTGACATTCCTGAAGC 1020
DB 961 CCATCTGATGTAGTATGACATCTGATCTTAATGATGAAACACACTGACATTCCTGAAGC 1020

QY	1021	TAGTCCAGCTGTGTACACCAAAATCATTTAGCATTAAGCCTTAGAGCTTAATGACAGATG	1080
Db	1021	TAGTCCAGCTGTGTACACCAAAATCATTTAGCATTAAGCCTTAGAGCTTAATGACAGATG	1080
QY	1081	GCAATTCAAGAGATCTCGTGTGTTAGATACCAAGACAAACGATCTTAAGCAAACTACTGG	1140
Db	1081	GCAATTCAAGAGATCTCGTGTGTTAGATACCAAGACAAACGATCTTAAGCAAACTACTGG	1140
QY	1141	TAGTAGTAAACAAGATAAGGATCCAAATATAGACAGCCACAGAAACAGATGAAGAAATTGA	1200
Db	1141	TAGTAGTAAACAAGATAAGGATCCAAATATAGACAGCCACAGAAACAGATGAAGAAATTGA	1200
QY	1201	AAAGATGAAGGCTTTTGGTGAATATTCACGGCTTCCTACATTTTGATCCTTTAAACCTTA	1260
Db	1201	AAAGATGAAGGCTTTTGGTGAATATTCACGGCTTCCTACATTTTGATCCTTTAAACCTTA	1260
QY	1261	CAAGAGATTTTTTTTATTTTGGCTGATGAGTAAAGCAAAACATTTCTATGTTTTTACAT	1320
Db	1261	CAAGAGATTTTTTTTATTTTGGCTGATGAGTAAAGCAAAACATTTCTATGTTTTTACAT	1320
QY	1321	GTTGAGCTACTTCGAGTAGTCAATTTGTGTTTACTATGTTACACCTGTTTGACGTAATAC	1380
Db	1321	GTTGAGCTACTTCGAGTAGTCAATTTGTGTTTACTATGTTACACCTGTTTGACGTAATAC	1380
QY	1381	ACAAGTAACCTTTAGTGTGATTTACTTCACAAAGTACTTTTCCAAACATCAGATGCTTTTA	1440
Db	1381	ACAAGTAACCTTTAGTGTGATTTACTTCACAAAGTACTTTTCCAAACATCAGATGCTTTTA	1440
QY	1441	TTTCCAAACCTTTTTCACCTTCACCTAAGTGTGTTGAGGGAAAGGCTTACACAGACACA	1500
Db	1441	TTTCCAAACCTTTTTCACCTTCACCTAAGTGTGTTGAGGGAAAGGCTTACACAGACACA	1500
QY	1501	TTCTTTAGAAATTTGGAAAAGTGAGACACAGGCTCTCACACCTGTAATCCAGACACT	1560
Db	1501	TTCTTTAGAAATTTGGAAAAGTGAGACACAGGCTCTCACACCTGTAATCCAGACACT	1560
QY	1561	TAGGGAAGACAAAGTCAGAGAGATTGATTGAAGCTPAGAGATTAGAGACAGGCTGGGCAAC	1620
Db	1561	TAGGGAAGACAAAGTCAGAGAGATTGATTGAAGCTPAGAGATTAGAGACAGGCTGGGCAAC	1620
QY	1621	GTAATGAGACCACTGCTAATTAATAAAATGAAAAAGCAAGATAGCCTTAATTTTCAA	1680
Db	1621	GTAATGAGACCACTGCTAATTAATAAAATGAAAAAGCAAGATAGCCTTAATTTTCAA	1680
QY	1681	AAATATGAAAGAAATTTATATGAAAAATTATCTGTCATTTAAATTCCTCTTAAGTAT	1740
Db	1681	AAATATGAAAGAAATTTATATGAAAAATTATCTGTCATTTAAATTCCTCTTAAGTAT	1740
QY	1741	ACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATTAATAATGCTGATATCATGCAAT	1800
Db	1741	ACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATTAATAATGCTGATATCATGCAAT	1800
QY	1801	AAATTTGAAAAACATCATCTTAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA	1849
Db	1801	AAATTTGAAAAACATCATCTTAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA	1849
RESULT 3			
AAFP92068			
ID	AAFP92068 standard; cDNA, 1849 BP.		
XX	AAFP92068;		
AC			
XX	15-MAY-2001 (first entry)		
DT			
XX	Human PRO1013 cDNA.		
DE			
XX	Human; PRO protein; mapping: ss.		
KW			
XX	Homo sapiens.		
XX			
XX	WO200116318-A2.		

XX	08-MAR-2001.
PD	
XX	
PF	24-AUG-2000; 2000CWO-US023328.
XX	
PR	01-SEP-1999; 99CWO-US020111.
PR	15-SEP-1999; 99CWO-US021080.
PR	07-DEC-1999; 99US-0168495P.
PR	09-DEC-1999; 99US-0170262P.
PR	11-JAN-2000; 2000US-0175481P.
PR	18-FEB-2000; 2000CWO-US004341.
PR	18-FEB-2000; 2000CWO-US004342.
PR	22-FEB-2000; 2000CWO-US005601.
PR	01-MAR-2000; 2000CWO-US005602.
PR	03-MAR-2000; 2000US-0187202P.
PR	21-MAR-2000; 2000US-0191007P.
PR	30-MAR-2000; 2000CWO-US008439.
PR	25-APR-2000; 2000US-0199397P.
PR	22-MAY-2000; 2000CWO-US014042.
PR	05-JUN-2000; 2000US-0205832P.

P1 Eacron DL, Filvarsoff E, Gerritsen MB, Goddard A, Godowski PJ,
 P1 Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,
 XX
 DR WPI: 2001-183260/18.
 DR P-PSDB: AAB87536.
 XX
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 P1 biology, including use as hybridization probes, and in chromosome and
 P1 gene mapping.

Claim 2; Fig 21; 278pp; English.

The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1849;	DB 4;	Length 1849;
-------------	---------	-------------	-------	--------------

```
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CTGAGCGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTCTCTCGGGCTTTGTGCT 60

Db
1 CTGAGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT 60

61 CGCGCACTCGCTTCCAGCACTCAACACGACTCGGACACGGAAGTTTCTTCTTG 120

Db 61 CGGCGACTCGCTTCCAGCACTCAACAGGACTCGACACGGAAGTTTCTTCTTGG 120

121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGT 180

Dp 121 GGAAGTAAAGGTGACGCCAGACAGCATTA CTGATTC CCAATGGATGATGTTGAAGT 180

181 TGTTTATACAATTGACATTCAGAAATATATATTCATGCTATCAGCTTTTAGCTTTATTA 240

Db 181 TGTATACCAATTGACATTGAGAATATATTCCATGCTATCAGCTTTTAA 240

241 TTCTTCAGCGAAGTAAATGAGCAAGCACTGAGAGAAATATTTATCAATGTCAAAAGAA 300

Db 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAGAAATATTATCAATGTCAAAAGAA 300

301 TGTGGTAGGTTGGTACAAATTCGGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAG 360

Db 301 TGTGTAGTGTGTATCAAAATTCGTCATTCAGATCAGATCAGACGTTAGAGAG 360
 Qy 361 GCTGCTTCACAAAACCTTGAGAGACATTTTTCAAAACCAAGCTGTTTTCTGCTATT 420
 Db 361 GCTGCTTCACAAAACCTTGAGAGACATTTTTCAAAACCAAGCTGTTTTCTGCTATT 420
 Qy 421 AATACCAAGTATATACAGAAAGCTGCTACTGATGATGAGAACATTCCTTATATPA 480
 Db 421 AATACCAAGTATATACAGAAAGCTGCTACTGATGATGAGAACATTCCTTATATPA 480
 Qy 481 ACCTCAAAAAGGACCTTTTTCACAGGGTACCTTTAGTGGTCCAAATCTGGCATGCTGA 540
 Db 481 ACCTCAAAAAGGACCTTTTTCACAGGGTACCTTTAGTGGTCCAAATCTGGCATGCTGA 540
 Qy 541 ACAACCTGGTTATAAAACGTATACAGGTCCTGATGTCACATGCTGTTTAGCCGAGCAT 600
 Db 541 ACAACCTGGTTATAAAACGTATACAGGTCCTGATGTCACATGCTGTTTAGCCGAGCAT 600
 Qy 601 ACAACCAACAGCTCTAAATTTTGTGAGAGAGATGATCCTTAAAGAGATCATAGAT 660
 Db 601 ACAACCAACAGCTCTAAATTTTGTGAGAGAGATGATCCTTAAAGAGATCATAGAT 660
 Qy 661 AATGAAATATATGCTTCACTTACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA 720
 Db 661 AATGAAATATATGCTTCACTTACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA 720
 Qy 721 CAGTGAACAAGAGATATAACTAGTAAAGATGATTAACAGATTAACAGAAATTTGA 780
 Db 721 CAGTGAACAAGAGATATAACTAGTAAAGATGATTAACAGATTAACAGAAATTTGA 780
 Qy 781 GAAAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAAAGATCCAAAAAGCCTTA 840
 Db 781 GAAAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAAAGATCCAAAAAGCCTTA 840
 Qy 841 GAGAAACATTTTCTTGTGAGGCAATTCAGGACCTTTTTCCAATCTGAATTTCTCA 900
 Db 841 GAGAAACATTTTCTTGTGAGGCAATTCAGGACCTTTTTCCAATCTGAATTTCTCA 900
 Qy 901 TTCATGTATATGCTTTTAAAAAATGACATGTTTCTAAAAGTACTGATCAACCA 960
 Db 901 TTCATGTATATGCTTTTAAAAAATGACATGTTTCTAAAAGTACTGATCAACCA 960
 Qy 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 Db 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 Qy 1021 TAGTCCAGCTAGTACACACACAAATCATTAAGCATTAAGCCTTAGCTTAGATGACGATG 1080
 Db 1021 TAGTCCAGCTAGTACACACAAATCATTAAGCATTAAGCCTTAGCTTAGATGACGATG 1080
 Qy 1081 GCAATTCAGAGATCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATG 1140
 Db 1081 GCAATTCAGAGATCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATG 1140
 Qy 1141 TAGTATACCAAGATTAAGATCAAAATGAGAGCCCAAGAAACAGATGAGAAATTTGA 1200
 Db 1141 TAGTATACCAAGATTAAGATCAAAATGAGAGCCCAAGAAACAGATGAGAAATTTGA 1200
 Qy 1201 AAAAGTAAAGGGTTTTGCTGAATTTCAACGCTCTCCCACTTTTGAATCCTTTAACTTA 1260
 Db 1201 AAAAGTAAAGGGTTTTGCTGAATTTCAACGCTCTCCCACTTTTGAATCCTTTAACTTA 1260
 Qy 1261 CAAGAGATTTTATTTTGTGCTGATGAGTAAAGCCCAACATTTCTATTTGTTTACTAT 1320
 Db 1261 CAAGAGATTTTATTTTGTGCTGATGAGTAAAGCCCAACATTTCTATTTGTTTACTAT 1320
 Qy 1321 GTTAGACTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 Db 1321 GTTAGACTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 Qy 1381 ACAGATTAATCTTAGTGCATTTACTTACCAAGATCTTTTCAACATCAGATGCTTTTA 1440
 Db 1381 ACAGATTAATCTTAGTGCATTTACTTACCAAGATCTTTTCAACATCAGATGCTTTTA 1440

Qy 1441 TTTCGAACCTTTTTCACCTTTCACTAGTGTGAGAGGAGAGGCTTACAGACACA 1500
 Db 1441 TTTCGAACCTTTTTCACCTTTCACTAGTGTGAGAGGAGAGGCTTACAGACACA 1500
 Qy 1501 TTCTTGAATTTGGAAGAGTGAAGCAGACAGAGTGGCTCACACTGTAAATCCAGCACT 1560
 Db 1501 TTCTTGAATTTGGAAGAGTGAAGCAGACAGAGTGGCTCACACTGTAAATCCAGCACT 1560
 Qy 1561 TAGGGAAGACAGTCAAGAGATTTGATGAGTCAAGATTTAAGACCAAGCTGGGGCAAC 1620
 Db 1561 TAGGGAAGACAGTCAAGAGATTTGATGAGTCAAGATTTAAGACCAAGCTGGGGCAAC 1620
 Qy 1621 GTATTGAGACCATGCTATTAATAAATGAAATGAAAGAGAGATAGCTTATTTTCAA 1680
 Db 1621 GTATTGAGACCATGCTATTAATAAATGAAATGAAAGAGAGATAGCTTATTTTCAA 1680
 Qy 1681 AATATGAAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1740
 Db 1681 AATATGAAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTTCTCTTAAGTAT 1740
 Qy 1741 ACTTTTGAAGTATCACTTATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAAT 1800
 Db 1741 ACTTTTGAAGTATCACTTATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAAT 1800
 Qy 1801 AATTTGCAAAACATCATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1849
 Db 1801 AATTTGCAAAACATCATCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1849
 RESULT 4
 AAF4145
 ID AAF4145 standard; cDNA; 1849 BP.
 XX AAF4145;
 AC 02-APR-2001 (first entry)
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1013 (UNQ496) nucleotide sequence SEQ ID NO:157.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytoskeletal; cell death;
 KM cancer; chromosomal mapping; gene mapping; tissue typing;
 XX diagnostic assay; ss.
 XX
 OS Homo sapiens.
 XX
 FN W0200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000MO-US008439.
 XX
 PR 02-JUN-1999; 99MO-US012252.
 PR 23-JUN-1999; 98US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99MO-US021090.
 PR 15-SEP-1999; 99MO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.

PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US005884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GENTH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferreira N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Guirey AL, Kijavlin IJ, Napier NA, Pan J, Paon NP,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WR,
PI Zhang Z;
XX MPI; 2001-032160/04.
DR P-PSDB; AAB65189.
XX PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 2; Fig 94; 935bp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;
Query Match 100.0%; Score 1849; DB 5; Length 1849;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGGCGGCGGTAGATGAGGAGGAGAGTACGTGCGGCTTCTGCGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGGTAGATGAGGAGGAGAGTACGTGCGGCTTCTGCGGCTTTGTGCT 60
QY 61 CGGCGCATCTGCTTTCCAGACCTCAACGCGACGTGGAAGGTTTCTTCTTGG 120
DB 61 CGGCGCATCTGCTTTCCAGACCTCAACGCGACGTGGAAGGTTTCTTCTTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTTACTGATTCCTCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTTACTGATTCCTCAATGATGATGTAAGT 180
QY 181 TGTATTACATTGACATTCAGAAATATATTCATGCTATCACTTTTAACTTTTAA 240
DB 181 TGTATTACATTGACATTCAGAAATATATTCATGCTATCACTTTTAACTTTTAA 240
QY 241 TTCTTCAGGCGAAGTAAATGAGCAAGCATGAGAAATATTTATCAAAATGTCAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAAATGAGCAAGCATGAGAAATATTTATCAAAATGTCAAAAGAA 300
QY 301 TGTGTAGTGTGTGTACAAATTCGTGTCTTCAATGATGATGATGATGATGATGATG 360
DB 301 TGTGTAGTGTGTGTACAAATTCGTGTCTTCAATGATGATGATGATGATGATGATG 360
QY 361 GTGTCTTCAACAAAATCTGAGAGGATTTTCAAAAGCAAGCTTGTGTGTGTGTGTGT 420
DB 361 GTGTCTTCAACAAAATCTGAGAGGATTTTCAAAAGCAAGCTTGTGTGTGTGTGTGT 420
QY 421 AACACCAAGTATATATACAGAAAGCTGTCTACTCATGAGTGAACATTTCTTATATTA 480
DB 421 AACACCAAGTATATATACAGAAAGCTGTCTACTCATGAGTGAACATTTCTTATATTA 480

QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTAGTGGTCCCATCTGGGACATGTCTGA 540
DB 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTAGTGGTCCCATCTGGGACATGTCTGA 540
QY 541 ACAATGGGTATTAATCTGATACAGGTTCCTGATATCCAGTGGTTTGGCCGAGAGT 600
DB 541 ACAATGGGTATTAATCTGATACAGGTTCCTGATATCCAGTGGTTTGGCCGAGAGT 600
QY 601 ACAACACACAGCTCTAATTTTGTGAAGAGTGAATCCTTAAAGAGGATCAATAAT 660
DB 601 ACAACACACAGCTCTAATTTTGTGAAGAGTGAATCCTTAAAGAGGATCAATAAT 660
QY 661 AATGGAATGTATGCTTCTTCAAGAGGATTTAAAGATATATGCAAAAAAGTGGAGA 720
DB 661 AATGGAATGTATGCTTCTTCAAGAGGATTTAAAGATATATGCAAAAAAGTGGAGA 720
QY 721 CAGTGAACAAGCAGTATTAATCTGATTAAGATGATTAAGATTAAGCAAAATTTGA 780
DB 721 CAGTGAACAAGCAGTATTAATCTGATTAAGATGATTAAGATTAAGCAAAATTTGA 780
QY 781 GAAAAGAGAGGAGCAGACAGATTGAGCAGAGAGAGAGAGAAATCCAAAAGACCTCA 840
DB 781 GAAAAGAGAGGAGCAGACAGATTGAGCAGAGAGAGAGAGAAATCCAAAAGACCTCA 840
QY 841 GGAAGACATTTTCTTGTGAGGATTAAGGACCTTTTCCAAATCTGATTTCTTCA 900
DB 841 GGAAGACATTTTCTTGTGAGGATTAAGGACCTTTTCCAAATCTGATTTCTTCA 900
QY 901 TTCAATGATTAATCTTAAATTAAGATGATTTCTTAAAGATGATTAATCAACA 960
DB 901 TTCAATGATTAATCTTAAATTAAGATGATTTCTTAAAGATGATTAATCAACA 960
QY 961 CCATCTGATGATTAATCAATCTGATTAAGATGATTAAGATGATTAAGATGATTAAG 1020
DB 961 CCATCTGATGATTAATCAATCTGATTAAGATGATTAAGATGATTAAGATGATTAAG 1020
QY 1021 TAGTCAGCTAGTACACACCAATCATTAAGCATTAAGCCTTGAATGATGACAGATG 1080
DB 1021 TAGTCAGCTAGTACACACCAATCATTAAGCATTAAGCCTTGAATGATGACAGATG 1080
QY 1081 GCAATTCAGAGATCTGCTGTTGATGATCAACAGAAAGATCTTAAAGCAATTTCTGG 1140
DB 1081 GCAATTCAGAGATCTGCTGTTGATGATCAACAGAAAGATCTTAAAGCAATTTCTGG 1140
QY 1141 TAGTATGATTAATTAAGATCAAAATGAGCAGCCAGAAACAGATGAGAAATTTGA 1200
DB 1141 TAGTATGATTAATTAAGATCAAAATGAGCAGCCAGAAACAGATGAGAAATTTGA 1200
QY 1201 AAGATGAAGGTTTGGTGAATTTACAGGCTCTCTACATTTTGAATCTTTTAACTTGA 1260
DB 1201 AAGATGAAGGTTTGGTGAATTTACAGGCTCTCTACATTTTGAATCTTTTAACTTGA 1260
QY 1261 CAAGAGATTTTATTTTGGCTGATGAGTAAAGCCAAACATTTCTTATTTTAACTAT 1320
DB 1261 CAAGAGATTTTATTTTGGCTGATGAGTAAAGCCAAACATTTCTTATTTTAACTAT 1320
QY 1321 GTTGAATCTGATGATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1380
DB 1321 GTTGAATCTGATGATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1380
QY 1381 AAGATTAATCTGATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1440
DB 1381 AAGATTAATCTGATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1440
QY 1441 TTTCCTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1500
DB 1441 TTTCCTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1500
QY 1501 TTCTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1560
DB 1501 TTCTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1560

```

QY 1561 TAGGGAAGACAGTGCAGAGATTGATGAGAGTATGAGACCAAGCTGGGCAAC 1620
DB 1561 TAGGGAAGACAGTGCAGAGATTGATGAGAGTATGAGACCAAGCTGGGCAAC 1620
QY 1621 GTATTGAGACCATGTCTATTAAAAATGAAAAAGCAAGATAGCTTATTTTCAA 1680
DB 1621 GTATTGAGACCATGTCTATTAAAAATGAAAAAGCAAGATAGCTTATTTTCAA 1680
QY 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGATCTTAAATTCCTTAAGTAT 1740
DB 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGATCTTAAATTCCTTAAGTAT 1740
QY 1741 ACTTTTITGAGATGATGCTAGAGTGGCAGATGATGCTGATATCATGCAAT 1800
DB 1741 ACTTTTITGAGATGATGCTAGAGTGGCAGATGATGCTGATATCATGCAAT 1800
QY 1801 AATTTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAA 1849
DB 1801 AATTTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAA 1849

RESULT 5
ABS74388
ID ABS74388 standard; cDNA; 1849 BP.
XX
XX ABS74388;
XX
XX 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1013.
XX
XX Human; se; gene; secreted protein; transmembrane protein; antirheumatic;
XX antiarthritic; osteopathic; sports-related joint problem;
XX articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX US2002119130-A1.
XX
XX 29-AUG-2002.
XX
XX 06-DEC-2001; 2001US-0006867.
XX
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0064215P.
XX 22-APR-1998; 98US-0082797P.
XX 22-APR-1998; 98US-0083495P.
XX 15-MAY-1998; 98US-0085579P.
XX 02-JUN-1998; 98US-0087759P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088740P.
XX 10-JUN-1998; 98US-0088811P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088825P.
XX 11-JUN-1998; 98US-0088863P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089514P.
XX 16-JUN-1998; 98US-0089651P.
XX 19-JUN-1998; 98US-0089952P.
XX 22-JUN-1998; 98US-0090246P.
XX 24-JUN-1998; 98US-0090444P.
XX 25-JUN-1998; 98US-0090686P.
XX 26-JUN-1998; 98US-0090863P.
XX 02-JUL-1998; 98US-0091628P.
XX 10-AUG-1998; 98US-0096012P.
XX 17-AUG-1998; 98US-0096757P.
XX 18-AUG-1998; 98US-0096949P.
XX 18-AUG-1998; 98US-0096959P.
XX 26-AUG-1998; 98US-0097954P.

```

```

PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100663P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99US-00505028.
PR 14-MAY-1999; 99US-00510733.
PR 02-JUN-1999; 99US-00512252.
PR 01-SEP-1999; 99US-00520211.
PR 15-SEP-1999; 99US-00521090.
PR 15-SEP-1999; 99US-00521194.
PR 22-DEC-1999; 99US-00530720.
PR 18-FEB-2000; 2000US-00504341.
PR 18-FEB-2000; 2000US-00504414.
PR 22-FEB-2000; 2000US-00504414.
PR 01-MAR-2000; 2000US-00505601.
PR 30-MAR-2000; 2000US-00508449.
PR 02-MAY-2000; 2000US-00514042.
PR 02-JUN-2000; 2000US-00515264.
PR 23-AUG-2000; 2000US-00523528.
PR 24-AUG-2000; 2000US-00523528.
PR 10-NOV-2000; 2000US-00530873.
PR 01-DEC-2000; 2000US-00532378.
PR 20-DEC-2000; 2000US-00544956.
PR 28-FEB-2001; 2001US-00506620.
PR 01-MAR-2001; 2001US-00506666.
PR 30-MAY-2001; 2001US-00517443.
PR 01-JUN-2001; 2001US-00517800.
PR 20-JUN-2001; 2001US-00519692.
PR 29-JUN-2001; 2001US-00521066.
PR 09-JUL-2001; 2001US-00521735.

(GENTH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2002-731348/79.
XX P-PSB; ABG95861.
XX
XX New isolated secreted and transmembrane PRO polypeptide useful for
XX modulating biological activity of a cell, or for treating sports-related
XX joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX Claim 2; Fig 21; 399pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
XX polypeptide having 80 % sequence identity to a sequence appearing as
XX ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
XX extracellular domain of the proteins with their associated signal peptide
XX or lacking its associated signal peptide. Also included are the nucleic
XX acids encoding the proteins, vectors, host cells, fusion proteins and
XX antibodies which specifically bind to the proteins. The proteins are
XX useful for detecting a polypeptide designated as A, B, C or D in a sample
XX suspected of containing an A, B, C or D polypeptide, by contacting the
XX sample with a polypeptide designated as E, F, G, H or I (or vice versa)
XX and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide

```

CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
CC XX

Seq Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGGCGGTGAGTGAAGGGGAGAGTACGTGCGGCGGTCTCTCGGCGCTTTGTGCT 60
DB 1 CTGAGCGGCGGTGAGTGAAGGGGAGAGTACGTGCGGCGGTCTCTCGGCGCTTTGTGCT 60
QY 61 CGGCGCACTGCTTTCCAGACCTCAACACGCACTCGGACACGGAGGTTTCTTCTTG 120
DB 61 CGGCGCACTGCTTTCCAGACCTCAACACGCACTCGGACACGGAGGTTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCAAGAACACGATTAATGATCCCAATGGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGAACACGATTAATGATCCCAATGGATGATGTAAGT 180
QY 181 TGTATTACATTAATGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
DB 181 TGTATTACATTAATGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
QY 241 TTCTTCAGCGAATTAATGAGCAAGCACTGAAGAAATATTAATCAATGCAAAAAAGAA 300
DB 241 TTCTTCAGCGAATTAATGAGCAAGCACTGAAGAAATATTAATCAATGCAAAAAAGAA 300
QY 301 TGTGTAGAGTGTGATCAAAATCCGTGCTCATTCAGATCAATCAATGAGGAGAG 360
DB 301 TGTGTAGAGTGTGATCAAAATCCGTGCTCATTCAGATCAATCAATGAGGAGAG 360
QY 361 GCTGCTTACAAAAAAGTTCGAGAGCACTTTTCAACCAAGACCTGTTTTCGCTAT 420
DB 361 GCTGCTTACAAAAAAGTTCGAGAGCACTTTTCAACCAAGACCTGTTTTCGCTAT 420
QY 421 AACACCAAGTATTAATCAAGAAAGTGTCTACTCATCACTGGAACATTCCTATATAA 480
DB 421 AACACCAAGTATTAATCAAGAAAGTGTCTACTCATCACTGGAACATTCCTATATAA 480
QY 481 AACTCAAAAAGCACTTTTCAAGGATACCTTTAGTGTGCTCAATCGGCAATGCTGA 540
DB 481 AACTCAAAAAGCACTTTTCAAGGATACCTTTAGTGTGCTCAATCGGCAATGCTGA 540

QY 541 ACAACTGGCTTATTAACCTGATACAGTTCCTGATGCTCCAGTCGCTTTAGCCGAGAGT 600
DB 541 ACAACTGGCTTATTAACCTGATACAGTTCCTGATGCTCCAGTCGCTTTAGCCGAGAGT 600
QY 601 ACAACACAGAGCTCTAAATTTTGAAGAAGATGATCTCTTAAGAAGATCAATAGAT 660
DB 601 ACAACACAGAGCTCTAAATTTTGAAGAAGATGATCTCTTAAGAAGATCAATAGAT 660
QY 661 AAATGAATATGATCTCTTAATTAAGAAGATTAAGATATATGCAAAAAAGTGAAGA 720
DB 661 AAATGAATATGATCTCTTAATTAAGAAGATTAAGATATATGCAAAAAAGTGAAGA 720
QY 721 CAGTGAACAAGCAGTATTAATCAATGATTAAGATGTAACAGATTAACAGAAATTTGA 780
DB 721 CAGTGAACAAGCAGTATTAATCAATGATTAAGATGTAACAGATTAACAGAAATTTGA 780
QY 781 GAAAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAGAACATCCAAAAAGCCTCA 840
DB 781 GAAAAAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAGAACATCCAAAAAGCCTCA 840
QY 841 GAGAGACATTTTCTTTGTGAGGACATTAAGGACCTTTTCAATTCGATTTCTTCA 900
DB 841 GAGAGACATTTTCTTTGTGAGGACATTAAGGACCTTTTCAATTCGATTTCTTCA 900
QY 901 TTCAATGCTATGCTTTTAAAAAATGACATGTTTCTAAAAAGTGTAACTAACACCA 960
DB 901 TTCAATGCTATGCTTTTAAAAAATGACATGTTTCTAAAAAGTGTAACTAACACCA 960
QY 961 CCATTCGATGATGATGACATTCGACCTTAATGATGAACACGATCAATTCCTGAAGC 1020
DB 961 CCATTCGATGATGATGACATTCGACCTTAATGATGAACACGATCAATTCCTGAAGC 1020
QY 1021 TAGTCAAGTATGATCAGGACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1080
DB 1021 TAGTCAAGTATGATCAGGACATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1080
QY 1081 GCAATTCAGAGATTCGCTGTTGATGATGACCAAGACCAAGATCTTAAGAAATATCTGG 1140
DB 1081 GCAATTCAGAGATTCGCTGTTGATGATGACCAAGACCAAGATCTTAAGAAATATCTGG 1140
QY 1141 TAGTGTAAACCAAGTAAAGACATCCAAATATGAGCACCAGAAACAGATGAAGAAATGA 1200
DB 1141 TAGTGTAAACCAAGTAAAGACATCCAAATATGAGCACCAGAAACAGATGAAGAAATGA 1200
QY 1201 AAAGATGAAGGTTTGTGTAATATCAAGCTCTCTCAATTTGATCTCTTTAACTTA 1260
DB 1201 AAAGATGAAGGTTTGTGTAATATCAAGCTCTCTCAATTTGATCTCTTTAACTTA 1260
QY 1261 CAAGAGATTTTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 CAAGAGATTTTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GTTGAAGTATTCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GTTGAAGTATTCAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ACAAGTAACTCTTAATGATTAATCAAGATCAATTTTCAACATCAAGATGCTTTTA 1440
DB 1381 ACAAGTAACTCTTAATGATTAATCAAGATCAATTTTCAACATCAAGATGCTTTTA 1440
QY 1441 TTTCGAAACCTTTTTCACCTTTCAGTAAATGTTGAGGAGGAGGCTTACACAGACCA 1500
DB 1441 TTTCGAAACCTTTTTCACCTTTCAGTAAATGTTGAGGAGGAGGCTTACACAGACCA 1500
QY 1501 TTCTTTAAGATTTGAGAAAGTGAACAGGACAGGAGGCTCAACCTGTAATCCAGACT 1560
DB 1501 TTCTTTAAGATTTGAGAAAGTGAACAGGACAGGAGGCTCAACCTGTAATCCAGACT 1560
QY 1561 TAGGAGAGCAAGTCAAGAGATTAATGAAGATTAAGATTAAGATTAAGATTAAGAT 1620
DB 1561 TAGGAGAGCAAGTCAAGAGATTAATGAAGATTAAGATTAAGATTAAGATTAAGAT 1620
QY 1621 GTATTGAGACATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680

```
DB      1621 GATATTGAGACCATGCTATTATAAAAAATGAAAAAGCAAGATAGCTTATTTCGA 1680
QY      1681 AATATGGAAGAAATTTATATGAAAAATATATCGAGTCATTAATTCCTTAGTGAT 1740
DB      1681 AATATGGAAGAAATTTATATGAAAAATTTATCTGAGTCATTAATTCCTTAGTGAT 1740
QY      1741 ACTTTTGTGAAGTACATTATGCTAGAGTGCAGATAAATGCTGATATCATGCAAT 1800
DB      1741 ACTTTTGTGAAGTACATTATGCTAGAGTGCAGATAAATGCTGATATCATGCAAT 1800
QY      1801 AATATTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
DB      1801 AATATTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAA 1849

RESULT 6
ABX78594
ID      ABX78594 standard; cDNA; 1849 BP.
AC      ABX78594;
XX      15-APR-2003 (first entry)
DT      Human PRO polynucleotide #67.
XX      Human PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;
KW      liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; AdBPPT;
KW      antibody-dependent enzyme mediated prodng therapy.
XX      Homo sapiens.
XX      US2003027272-A1.
PD      06-FEB-2003.
PF      21-JUN-2002; 2002US-00176492.
XX      18-SEP-1997; 97US-0059263P.
PR      18-SEP-1997; 97US-0059266P.
PR      17-OCT-1997; 97US-0062250P.
PR      21-OCT-1997; 97US-0063486P.
PR      24-OCT-1997; 97US-0063120P.
PR      28-OCT-1997; 97US-0063540P.
PR      28-OCT-1997; 97US-0063541P.
PR      28-OCT-1997; 97US-0063544P.
PR      28-OCT-1997; 97US-0063564P.
PR      28-OCT-1997; 97US-0063744P.
PR      29-OCT-1997; 97US-0063870P.
PR      31-OCT-1997; 97US-0064103P.
PR      13-NOV-1997; 97US-0065311P.
PR      21-NOV-1997; 97US-0066120P.
PR      24-NOV-1997; 97US-0066466P.
PR      24-NOV-1997; 97US-0066772P.
PR      11-DEC-1997; 97US-0069335P.
PR      12-DEC-1997; 97US-0069425P.
PR      17-DEC-1997; 97US-0069870P.
PR      18-DEC-1997; 97US-0068017P.
PR      10-MAR-1998; 98US-0077450P.
PR      11-MAR-1998; 98US-0077649P.
PR      11-MAR-1998; 98US-0078886P.
PR      20-MAR-1998; 98US-0078939P.
PR      27-MAR-1998; 98US-0079664P.
PR      31-MAR-1998; 98US-0080107P.
PR      31-MAR-1998; 98US-0080194P.
PR      01-APR-1998; 98US-0080333P.
PR      08-APR-1998; 98US-0081049P.
PR      08-APR-1998; 98US-0081070P.
PR      09-APR-1998; 98US-0081195P.
```

```
PR      15-APR-1998; 98US-0081838P.
PR      21-APR-1998; 98US-0082568P.
PR      22-APR-1998; 98US-0082704P.
PR      28-APR-1998; 98US-0082797P.
PR      29-APR-1998; 98US-0083495P.
PR      29-APR-1998; 98US-0083496P.
PR      29-APR-1998; 98US-0083499P.
PR      29-APR-1998; 98US-0083599P.
PR      05-MAY-1998; 98US-0084366P.
PR      06-MAY-1998; 98US-0084414P.
PR      07-MAY-1998; 98US-0084639P.
PR      07-MAY-1998; 98US-0084640P.
PR      07-MAY-1998; 98US-0084643P.
PR      15-MAY-1998; 98US-0085580P.
PR      15-MAY-1998; 98US-0085582P.
PR      15-MAY-1998; 98US-0085700P.
PR      18-MAY-1998; 98US-0086023P.
PR      22-MAY-1998; 98US-0086392P.
PR      22-MAY-1998; 98US-0086466P.
PR      28-MAY-1998; 98US-0087088P.
PR      28-MAY-1998; 98US-0087208P.
PR      02-JUN-1998; 98US-0087609P.
PR      02-JUN-1998; 98US-0087759P.
PR      03-JUN-1998; 98US-0087827P.
PR      04-JUN-1998; 98US-0088025P.
PR      04-JUN-1998; 98US-0088028P.
PR      04-JUN-1998; 98US-0088029P.
PR      04-JUN-1998; 98US-0088033P.
PR      04-JUN-1998; 98US-0088366P.
PR      05-JUN-1998; 98US-0088167P.
PR      05-JUN-1998; 98US-0088202P.
PR      05-JUN-1998; 98US-0088212P.
PR      05-JUN-1998; 98US-0088217P.
PR      09-JUN-1998; 98US-0088655P.
PR      10-JUN-1998; 98US-0088722P.
PR      10-JUN-1998; 98US-0088738P.
PR      10-JUN-1998; 98US-0088740P.
PR      10-JUN-1998; 98US-0088811P.
PR      10-JUN-1998; 98US-0088824P.
PR      10-JUN-1998; 98US-0088825P.
PR      10-JUN-1998; 98US-0088826P.
PR      11-JUN-1998; 98US-0088861P.
PR      11-JUN-1998; 98US-0088863P.
PR      11-JUN-1998; 98US-0089090P.
PR      12-JUN-1998; 98US-0089105P.
PR      16-JUN-1998; 98US-0089512P.
PR      16-JUN-1998; 98US-0089514P.
PR      17-JUN-1998; 98US-0089538P.
PR      17-JUN-1998; 98US-0089539P.
PR      17-JUN-1998; 98US-0089653P.
PR      18-JUN-1998; 98US-0089908P.
PR      18-JUN-1998; 98US-0089952P.
PR      22-JUN-1998; 98US-0090246P.
PR      22-JUN-1998; 98US-0090252P.
PR      22-JUN-1998; 98US-0090254P.
PR      24-JUN-1998; 98US-0090428P.
PR      24-JUN-1998; 98US-0090435P.
PR      24-JUN-1998; 98US-0090444P.
PR      24-JUN-1998; 98US-0090461P.
PR      24-JUN-1998; 98US-0090535P.
PR      25-JUN-1998; 98US-0090540P.
PR      25-JUN-1998; 98US-0090678P.
PR      25-JUN-1998; 98US-0090688P.
PR      25-JUN-1998; 98US-0090690P.
PR      25-JUN-1998; 98US-0090694P.
PR      25-JUN-1998; 98US-0090695P.
PR      26-JUN-1998; 98US-00105413.
```

PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095298P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-01019330.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102300P.
PR 29-SEP-1998; 98US-0102311P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTGATGAGAGGGGAGAGTACGTCCGGCGGTGTCTCCGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGGTGATGAGAGGGGAGAGTACGTCCGGCGGTGTCTCCGGCTTTGTGCT 60
QY 61 CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGAGACGAGAGGTTTCTTCTTGG 120
DB 61 CGGCGCACTCGCTTCCAGCACTCAACAGCACTCGAGACGAGAGGTTTCTTCTTGG 120
QY 121 GGAAGTAAAGGTAAAGCCAAAGAACACATTAATGATTTCCCAATGATATGTAGACT 180
DB 121 GGAAGTAAAGGTAAAGCCAAAGAACACATTAATGATTTCCCAATGATATGTAGACT 180
QY 181 TGTATATACATTAATGATGAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
DB 181 TGTATATACATTAATGATGAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
QY 241 TTCTTCAGGCGAGTAAATGAGCAAGCACTGAGAGAAATATATCAATGTCAAAAAGAA 300
DB 241 TTCTTCAGGCGAGTAAATGAGCAAGCACTGAGAGAAATATATCAATGTCAAAAAGAA 300
QY 301 TGTGTAGGTGATGACAAATCCGTCATTCATGATCAGATCACTGAGCTTTAGAGAG 360
DB 301 TGTGTAGGTGATGACAAATCCGTCATTCATGATCAGATCACTGAGCTTTAGAGAG 360
QY 361 GCTGCTTCACAAAACCTTGACAGAGCACTTTTCAACCAAGACCTTGTTCGTATTT 420
DB 361 GCTGCTTCACAAAACCTTGACAGAGCACTTTTCAACCAAGACCTTGTTCGTATTT 420
QY 421 AACACAAAGTATATACAGAAAGCTGCTACATCACTGAGCAATTCCTATATTA 480
DB 421 AACACAAAGTATATACAGAAAGCTGCTACATCACTGAGCAATTCCTATATTA 480
QY 481 ACCTCAAAAAGACTTTTTCACAGGTAACCTTTAGTGTTGCCAATCGGCACTGTCTGA 540
DB 481 ACCTCAAAAAGACTTTTTCACAGGTAACCTTTAGTGTTGCCAATCGGCACTGTCTGA 540
QY 541 ACAACTGGGTATTAACCTGATACAGGTAACCTTTAGTGTTGCCAATCGGCACTGTCTGA 600
DB 541 ACAACTGGGTATTAACCTGATACAGGTAACCTTTAGTGTTGCCAATCGGCACTGTCTGA 600
QY 601 ACAACACACAGCTCTAATTTTGAAGAGATGATCCTTAAGAGGATCATAGAT 660
DB 601 ACAACACACAGCTCTAATTTTGAAGAGATGATCCTTAAGAGGATCATAGAT 660
QY 661 AATGAAATGATGCTTCAATTAACAAGAGATTAAGATATGCAAAAAGTGAAGA 720
DB 661 AATGAAATGATGCTTCAATTAACAAGAGATTAAGATATGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAGCAGTATTAACCTAGTAAGATGTAAGAGATTAAGAGAAATTGA 780
DB 721 CAGTGAACAGCAGTATTAACCTAGTAAGATGTAAGAGATTAAGAGAAATTGA 780
QY 781 GAAAAGAGAGAGACACAGATTCAGGACAGAGAGAGAGACATCCAAAAGACCTCA 840
DB 781 GAAAAGAGAGAGACACAGATTCAGGACAGAGAGAGAGACATCCAAAAGACCTCA 840
QY 841 GGAAGACATTTTCTTTGTGAGGATTAAGGACCTTTTCCAAATCTGATTTCTTCA 900
DB 841 GGAAGACATTTTCTTTGTGAGGATTAAGGACCTTTTCCAAATCTGATTTCTTCA 900
QY 901 TTCAATGATTAATGCTTTAAATAAGATGTTCTTAAAGTGTGAATCTAACCA 960
DB 901 TTCAATGATTAATGCTTTAAATAAGATGTTCTTAAAGTGTGAATCTAACCA 960
QY 961 CCATCTGATGATTAAGACATCTGACCTTAAGTGTGAACACACTGACATTCCTGAAGC 1020
DB 961 CCATCTGATGATTAAGACATCTGACCTTAAGTGTGAACACACTGACATTCCTGAAGC 1020
QY 1021 TAGTCAAGCTAGTACACACAAATCATTAAGCATTAAGCCTTAGACTGACAGATG 1080

Db 1021 TAGTCAGCTAGTACGACCAATATCATTAAGCATAAAGCTTAGAGCTTAGAGATGAGATG 1080
 Qy 1081 GCATTTCAAGAATCTCGGTGTGTAGATACACAAAGCAAGATCTTAAAGCAAAATCTGG 1140
 Db 1081 GCATTTCAAGAATCTCGGTGTGTAGATACACAAAGCAAGATCTTAAAGCAAAATCTGG 1140
 Qy 1141 TAGTGTATCAAGATTAAGATCCAAATAGAGAGCCAGAAAGATGAAGAAATGA 1200
 Db 1141 TAGTGTATCAAGATTAAGATCCAAATAGAGAGCCAGAAAGATGAAGAAATGA 1200
 Qy 1201 AAAAGATGAAGGTTTGGTGAATATTCAGCGTCTCTTACATTTTGTATCTTTAACTTA 1260
 Db 1201 AAAAGATGAAGGTTTGGTGAATATTCAGCGTCTCTTACATTTTGTATCTTTAACTTA 1260
 Qy 1261 CAAGAGATTTTATTTTGGCTGATGGTAAAGCAAACTTTGATTTTGTATTTACTAT 1320
 Db 1261 CAAGAGATTTTATTTTGGCTGATGGTAAAGCAAACTTTGATTTTGTATTTACTAT 1320
 Qy 1321 GTTGAAGCTTCTGAGTAAGTTCATTTGTTTACTAGTTCACCTGTTTGCATGATATAC 1380
 Db 1321 GTTGAAGCTTCTGAGTAAGTTCATTTGTTTACTAGTTCACCTGTTTGCATGATATAC 1380
 Qy 1381 ACAGATTAAGCTTGTAGAGATTTTCAAGATGCTTTTCAAGATCAGATGCTTTTA 1440
 Db 1381 ACAGATTAAGCTTGTAGAGATTTTCAAGATGCTTTTCAAGATCAGATGCTTTTA 1440
 Qy 1441 TTTCAGAACTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCAC 1500
 Db 1441 TTTCAGAACTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCAC 1500
 Qy 1501 TTCTTTAGAAATTTGAAAGTGAAGCAAGGCAAGTGGCTTCAACCTGTTAACTCCAGCAGCT 1560
 Db 1501 TTCTTTAGAAATTTGAAAGTGAAGCAAGGCAAGTGGCTTCAACCTGTTAACTCCAGCAGCT 1560
 Qy 1561 TAGGGAAGCAAGTTCAGAGATTTGATTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1620
 Db 1561 TAGGGAAGCAAGTTCAGAGATTTGATTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1620
 Qy 1621 GTATTTAGAACATGCTATTTAAATAAATGAATAAGCAAGATAGCTTATTTTCAA 1680
 Db 1621 GTATTTAGAACATGCTATTTAAATAAATGAATAAGCAAGATAGCTTATTTTCAA 1680
 Qy 1681 AATATGGAAGAAATTTATATGAATTTATCTGAGTCAATTAATTCCTTTAAGTAT 1740
 Db 1681 AATATGGAAGAAATTTATATGAATTTATCTGAGTCAATTAATTCCTTTAAGTAT 1740
 Qy 1741 ACTTTTGTAGAGTATTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1800
 Db 1741 ACTTTTGTAGAGTATTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1800
 Qy 1801 AAATTTGCAAAATCATCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 1849
 Db 1801 AAATTTGCAAAATCATCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 1849

XX US2003032127-A1.
 PN 13-FEB-2003.
 XX 26-JUN-2002; 2002US-00183012.
 XX 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063545P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063970P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 11-DEC-1997; 97US-0066772P.
 PR 12-DEC-1997; 97US-0069335P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080337P.
 PR 01-APR-1998; 98US-0080339P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 09-APR-1998; 98US-0081195P.
 PR 15-APR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 28-APR-1998; 98US-0083332P.
 PR 29-APR-1998; 98US-0083485P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 05-MAY-1998; 98US-0083559P.
 PR 06-MAY-1998; 98US-0084366P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 18-MAY-1998; 98US-0086033P.
 PR 22-MAY-1998; 98US-0086382P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088033P.

RESULT 7
 ACAT75566
 ID ACAT75566 standard; cDNA; 1849 BP.
 ACAT75566;
 07-JUN-2003 (first entry)
 Novel human secreted and transmembrane protein PRO1013 cDNA.
 Human; secreted and transmembrane protein; PRO; gene therapy;
 tumour necrosis factor-alpha release; TNF-alpha release;
 chondrocyte proliferation; chondrocyte differentiation; tumour;
 adrenal tumour; lung tumour; colon tumour; breast tumour;
 prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
 Homo sapiens.


```

Db      421 AACACCAACTATATAACAGAAAGCTGCTCTACTCATGCATGGAACAATCTCTATATAA 480
Qy      481 AACTCAAAAGAGACTTTTTCACAGGGTACCTTAGTGGTTCGCAATCTGGGATGTCTGA 540
Db      481 AACTCAAAAGAGACTTTTTCACAGGGTACCTTAGTGGTTCGCAATCTGGGATGTCTGA 540
Qy      541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGCTCACTGGTTTACCCGACGCT 600
Db      541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGCTCACTGGTTTACCCGACGCT 600
Qy      601 ACAACACACAGCTCTAAATTTTGAAGAAGTGGATCTTAAAGAGGTACATAGAT 660
Db      601 ACAACACACAGCTCTAAATTTTGAAGAAGTGGATCTTAAAGAGGTACATAGAT 660
Qy      661 AATATGAATGTATGCTTCAATACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA 720
Db      661 AATATGAATGTATGCTTCAATACAGAGAAATTAAGATATATGCAAAAAAGTGAAGA 720
Qy      721 CAGTGAACAAGCAGTGAATTAAGTAAAGATGTAACAGATTAAACGAAATTGA 780
Db      721 CAGTGAACAAGCAGTGAATTAAGTAAAGATGTAACAGATTAAACGAAATTGA 780
Qy      781 GAAAGAGAGAGACACAGATTCAGGACAGCAAGAGAAACATCCAAAAAGACCTTCA 840
Db      781 GAAAGAGAGAGACACAGATTCAGGACAGCAAGAGAAACATCCAAAAAGACCTTCA 840
Qy      841 GAGAAACATTTTCTTTGTCAGGATTAAGGACCTTTTCCAAATCTGAAATTTCTCA 900
Db      841 GAGAAACATTTTCTTTGTCAGGATTAAGGACCTTTTCCAAATCTGAAATTTCTCA 900
Qy      901 TTCAATGTTATGCTTTTAAAAATAGACATGTTCTTAAAGTACGTGACTACACCA 960
Db      901 TTCAATGTTATGCTTTTAAAAATAGACATGTTCTTAAAGTACGTGACTACACCA 960
Qy      961 CCATCTCGATGTAGTACACATCTGACCTTAATGTAAGACACACAGCAATCTCGAAGC 1020
Db      961 CCATCTCGATGTAGTACACATCTGACCTTAATGTAAGACACACAGCAATCTCGAAGC 1020
Qy      1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCAATTAAGCTTGAATGATGACAGATG 1080
Db      1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCAATTAAGCTTGAATGATGACAGATG 1080
Qy      1081 GCAATTCAGAGATCTGGTGTGATATACACAGCAAAACGATCTTAAAGCAATCTGG 1140
Db      1081 GCAATTCAGAGATCTGGTGTGATATACACAGCAAAACGATCTTAAAGCAATCTGG 1140
Qy      1141 TAGTAGTACCAAGATTAAGATCCAAATGAGAGCCGAGAAACAGATGAGAAATTGA 1200
Db      1141 TAGTAGTACCAAGATTAAGATCCAAATGAGAGCCGAGAAACAGATGAGAAATTGA 1200
Qy      1201 AAAGATGAAGGTTTGGTGAATAATCAGCGTCTCTTACATTTGATCTTTTAACCTTA 1260
Db      1201 AAAGATGAAGGTTTGGTGAATAATCAGCGTCTCTTACATTTGATCTTTTAACCTTA 1260
Qy      1261 CAAAGAGATTTTATTTTGGCTGATAGGTAAACCCAAACATTTCTATTTTCTACTAT 1320
Db      1261 CAAAGAGATTTTATTTTGGCTGATAGGTAAACCCAAACATTTCTATTTTCTACTAT 1320
Qy      1321 GTTAGGCTACTGAGTAAAGTTCATTTGTTTAACTATGTCACCTGTTGACGTATAC 1380
Db      1321 GTTAGGCTACTGAGTAAAGTTCATTTGTTTAACTATGTCACCTGTTGACGTATAC 1380
Qy      1381 ACAGATTAAGCTTTAGTATTAATTAATGATTAAGTAAAGTAAAGTAAAGTAAAGT 1440
Db      1381 ACAGATTAAGCTTTAGTATTAATTAATGATTAAGTAAAGTAAAGTAAAGTAAAGT 1440
Qy      1441 TTTCGAAACCTTTTTCACCTTCACTAAGTGTGAGGGAGGCTTACACAGACACA 1500
Db      1441 TTTCGAAACCTTTTTCACCTTCACTAAGTGTGAGGGAGGCTTACACAGACACA 1500
Qy      1501 TTCTTTAATTTGAAAGTGAAGCAGGCAAGTGGCTCACACTGTAATCCAGCACT 1560

```

```

Db      1501 TTCTTTAATTTGAAAGTGAAGCAGGACAGTGGCTCACACTGTAATCCAGCACT 1560
Qy      1561 TAGGAAAGACAGTCAAGAGATTAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
Db      1561 TAGGAAAGACAGTCAAGAGATTAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
Qy      1621 GTATTTGAGCAGTCTATTAATTAATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1680
Db      1621 GTATTTGAGCAGTCTATTAATTAATTAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1680
Qy      1681 AATATGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Db      1681 AATATGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Qy      1741 ACTTTTAAAGTCACTTATGCTAGTGAAGTGCAGATTAATGATGATATCATGCAAT 1800
Db      1741 ACTTTTAAAGTCACTTATGCTAGTGAAGTGCAGATTAATGATGATATCATGCAAT 1800
Qy      1801 AATTTGCAAAACATCATCTTAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAA 1849
Db      1801 AATTTGCAAAACATCATCTTAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAA 1849

RESULT 8
ACA71046
ID ACA71046 standard; cDNA; 1849 BP.
XX
AC ACA71046;
XX
DT 02-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #67.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032112-A1.
XX
PD 13-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176756.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063545P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 31-OCT-1997; 97US-0064103P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0065312P.
PR 21-NOV-1997; 97US-0065466P.
PR 24-NOV-1997; 97US-0066772P.
PR 24-NOV-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069817P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077645P.
PR 20-MAR-1998; 98US-0077886P.
PR 20-MAR-1998; 98US-0077939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.

```

PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080134P.
PR 01-APR-1998; 98US-0080347P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 26-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088366P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089539P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.

PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-010105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 02-JUL-1998; 98US-0091633P.
PR 04-AUG-1998; 98US-0094066P.
PR 10-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 17-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 18-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0097023P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 01-SEP-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 02-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101766P.
PR 25-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.

PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGCGGTAGCATGAGGCGGAGAGTACGTGCGCGGTGCTCGGCGCTTTGTCT 60
Db 1 CTGAGGCGCGGTAGCATGAGGCGGAGAGTACGTGCGCGGTGCTCGGCGCTTTGTCT 60
QY 61 CCGGCGCTGCTTCCAGACCTCAACAGACTGGAGACGGAGGTTTCTTTGG 120
Db 61 CCGGCGCTGCTTCCAGACCTCAACAGACTGGAGACGGAGGTTTCTTTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAAAGACGATTACTGATCCCAATGATGATGATGAT 180
Db 121 GGAAGTAAAGGTGAAGCCAAAGACGATTACTGATCCCAATGATGATGATGAT 180
QY 181 TGTATATACATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATATA 240
Db 181 TGTATATACATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATATA 240
QY 241 TTCTTCAGGCGAGTAAATGAGCAAGCACTGAGAAATATATCAATGTCAAAAGAA 300
Db 241 TTCTTCAGGCGAGTAAATGAGCAAGCACTGAGAAATATATCAATGTCAAAAGAA 300
QY 301 TGTGTAGGTGTGATCAAAATCCGTGCTCATTCAGATCAGATCAGATCAGATCAG 360
Db 301 TGTGTAGGTGTGATCAAAATCCGTGCTCATTCAGATCAGATCAGATCAGATCAG 360
QY 361 GCTGCTTCAAAAACCTTGAGAGGCACTTTTCAACCAAGACCTGTTTCTGCTAT 420
Db 361 GCTGCTTCAAAAACCTTGAGAGGCACTTTTCAACCAAGACCTGTTTCTGCTAT 420
QY 421 AACACCAAGTATATAACAGAAAGCTGCTACTCATGACTGAAACATTCCTTATATA 480
Db 421 AACACCAAGTATATAACAGAAAGCTGCTACTCATGACTGAAACATTCCTTATATA 480
QY 481 ACCCTCAAAAAGGACTTTTCAAGGGTACCTTTAGTGTGCTCAATCTGGCATGTCTGA 540
Db 481 ACCCTCAAAAAGGACTTTTCAAGGGTACCTTTAGTGTGCTCAATCTGGCATGTCTGA 540
QY 541 ACAACTGCGTTATATAAAGCTGATCAGGTTCTGATGTCACCTGTTTACCGAGCAGT 600
Db 541 ACAACTGCGTTATATAAAGCTGATCAGGTTCTGATGTCACCTGTTTACCGAGCAGT 600
QY 601 ACAAAACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTATATAGAT 660
Db 601 ACAAAACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTATATAGAT 660
QY 661 AAATGAATGATGCTCATTAACAAGAGATTTAAAGATTTGCAAAAAGTGAAGA 720
Db 661 AAATGAATGATGCTCATTAACAAGAGATTTAAAGATTTGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAGAGTAACTAGTAAAGATGTAACAGATTAACAGAAATTTGA 780
Db 721 CAGTGAACAGAGTAACTAGTAAAGATGTAACAGATTAACAGAAATTTGA 780
QY 781 GAAAGAGAGAGAGACAGATTCAGGAGCAAGAGAGAAACATCCAAAAGCCCTCA 840
Db 781 GAAAGAGAGAGAGACAGATTCAGGAGCAAGAGAGAAACATCCAAAAGCCCTCA 840
QY 841 GGAGAACATTTTCTTGTGAGGATTAAGGACCTTTTTCAAAATTTCTGAATTTCTCA 900
Db 841 GGAGAACATTTTCTTGTGAGGATTAAGGACCTTTTTCAAAATTTCTGAATTTCTCA 900
QY 901 TTCTATGTTATGCTTTTAAATATAGCATGTTTCTAAAGATGCTGTAATCAACCA 960
Db 901 TTCTATGTTATGCTTTTAAATATAGCATGTTTCTAAAGATGCTGTAATCAACCA 960

Db 901 TTCTATGTTATGCTTTTAAATATAGCATGTTTCTAAAGATGCTGTAATCAACCA 960
QY 961 CCATCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 CCATCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACATG 1080
Db 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACATG 1080
QY 1081 GCAATTCAGAGATCTGCTGTTTGTATGATCAACAAAGACAAAGATCTTAAGCAATCTGG 1140
Db 1081 GCAATTCAGAGATCTGCTGTTTGTATGATCAACAAAGACAAAGATCTTAAGCAATCTGG 1140
QY 1141 TAGTATGATCAACATTAAGATCAAAATGAGAGCCAGAAACAGATGAAGAATTTGA 1200
Db 1141 TAGTATGATCAACATTAAGATCAAAATGAGAGCCAGAAACAGATGAAGAATTTGA 1200
QY 1201 AAAGATGAAGGTTTGTGATATATCAAGCTCTCTACATTTTGTATCTTTTAACTTTA 1260
Db 1201 AAAGATGAAGGTTTGTGATATATCAAGCTCTCTACATTTTGTATCTTTTAACTTTA 1260
QY 1261 CAAGAGATTTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 CAAGAGATTTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GTTGAGCTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 GTTGAGCTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 AAGATTAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 AAGATTAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 TTTCCAAACCTTTTTCACCTTCACTAAGTTGTAAGGAGGAGCTTACACAGACA 1500
Db 1441 TTTCCAAACCTTTTTCACCTTCACTAAGTTGTAAGGAGGAGCTTACACAGACA 1500
QY 1501 TTTCTTGAATTTGAAAAGTGAACCAAGCAAGTGTGCTCAACCTGTAATCCAGCACT 1560
Db 1501 TTTCTTGAATTTGAAAAGTGAACCAAGCAAGTGTGCTCAACCTGTAATCCAGCACT 1560
QY 1561 TAGGGAAGCAAGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 TAGGGAAGCAAGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GTATGAGACATGCTATTAATAAATTAAGTGAAGCAAGAAATGCTTATTTTCA 1680
Db 1621 GTATGAGACATGCTATTAATAAATTAAGTGAAGCAAGAAATGCTTATTTTCA 1680
QY 1681 AATATGAAGAATTTTATGAATAATTTATCTGATGATTAATTTCTCTTAAGTAT 1740
Db 1681 AATATGAAGAATTTTATGAATAATTTATCTGATGATTAATTTCTCTTAAGTAT 1740
QY 1741 ACTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 ACTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTTAAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 AAATTTGCAAAACATCATCTAAATTTTAAATTAATTAATTAATTAATTAATTAAT 1860
RESULT 9
ACC87574
ID ACC87574 strand: cDNA, 1849 BP.
XX ACC87574;
XX AC
XX AC
XX 05-AUG-2003 (first entry)
XX DT
XX DE
XX Human secreted polypeptide PRO1013-encoding cDNA, SEQ ID NO:133.
XX

KM Human; PRO; secreted protein; transmembrane protein;
KM extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KM Chondrocyte; proliferation; differentiation; cartilage disorder;
KM bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KM adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KM liver; drug screening; transgenic animal; genetic analysis;
KM antithrptic; vulnery; gene therapy; gene; ss.
XX Homo sapiens.
XX US2003027278-A1.
XX 06-FEB-2003.
PD 21-JUN-2002; 2002US-00176987.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 13-NOV-1997; 97US-0065111P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 27-MAR-1998; 98US-0079644P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 01-APR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 08-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 09-APR-1998; 98US-0081070P.
PR 15-APR-1998; 98US-0081195P.
PR 21-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 22-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 28-APR-1998; 98US-0082977P.
PR 29-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 05-MAY-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 07-MAY-1998; 98US-0084114P.
PR 07-MAY-1998; 98US-0084399P.
PR 07-MAY-1998; 98US-0084409P.
PR 15-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085779P.
PR 15-MAY-1998; 98US-0085880P.
PR 15-MAY-1998; 98US-0085882P.
PR 18-MAY-1998; 98US-0085700P.
PR 22-MAY-1998; 98US-0086233P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086392P.

PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088325P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089513P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089539P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089508P.
PR 19-JUN-1998; 98US-0089525P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090697P.
PR 26-JUN-1998; 98US-0090698P.
PR 26-JUN-1998; 98US-0090699P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 04-AUG-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 17-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096767P.
PR 17-AUG-1998; 98US-0096881P.
PR 17-AUG-1998; 98US-0096877P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.

PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098502P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Fred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTGAGTGAAGGAGGAGAGTACGTCGGCGGTCTCTCGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGGTGAGTGAAGGAGGAGAGTACGTCGGCGGTCTCTCGGCTTTGTGCT 60
QY 61 CGGCGCACTCGCTTTCCAGCACTTCAACAGGACTCGGACACGGAAGTTTCTTCTTG 120
DB 61 CGGCGCACTCGCTTTCCAGCACTTCAACAGGACTCGGACACGGAAGTTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCAAGCAAGCACTACTGATTTCCCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGCAAGCACTACTGATTTCCCAATGATGATGTAAGT 180
QY 181 TGTATTACATTGACATTCAGAAATATTCATGCTATGACGTTTGTAGCTTTTATA 240
DB 181 TGTATTACATTGACATTCAGAAATATTCATGCTATGACGTTTGTAGCTTTTATA 240
QY 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAATATTTATCAATGTCAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAATATTTATCAATGTCAAAAGAA 300
QY 301 TGTGTAGTGTGTAACAATTCGTCGTCATTCAGATCAATGATGACGTTTGAAGAG 360
DB 301 TGTGTAGTGTGTAACAATTCGTCGTCATTCAGATCAATGATGACGTTTGAAGAG 360

DB 301 TGTGTAGTGTGTAACAATTCGTCGTCATTCAGATCAATGATGACGTTTGAAGAG 360
QY 361 GCTGCTTCACAAAAACCTTGAGAGAGCATTTTTCAAAACAGACCTGTTTCTGCTATT 420
DB 361 GCTGCTTCACAAAAACCTTGAGAGAGCATTTTTCAAAACAGACCTGTTTCTGCTATT 420
QY 421 AACACGAATTAATTAACAAAGCTGCTACTGATCGACTGAAACATTCCTTAATAA 480
DB 421 AACACGAATTAATTAACAAAGCTGCTACTGATCGACTGAAACATTCCTTAATAA 480
QY 481 ACCTCAAAAAGACTTTTTCAGAGGTAACCTTAGTGTTGCCAATCTGAGCATGTCTGA 540
DB 481 ACCTCAAAAAGACTTTTTCAGAGGTAACCTTAGTGTTGCCAATCTGAGCATGTCTGA 540
QY 541 ACAACTGGTTATTAACCTGATACAGTCTCTGTAAGTCCAGCGTTTATGCCGAGAT 600
DB 541 ACAACTGGTTATTAACCTGATACAGTCTCTGTAAGTCCAGCGTTTATGCCGAGAT 600
QY 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAGAGAGGTACATAAGAT 660
DB 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAGAGAGGTACATAAGAT 660
QY 661 AATGAAATGTATCTCTTCAATTAACAGGAATTTAAAGATTAATGCAAAAAGTGAGAGA 720
DB 661 AATGAAATGTATCTCTTCAATTAACAGGAATTTAAAGATTAATGCAAAAAGTGAGAGA 720
QY 721 CAGTGAACAAGCAGTATTAACCTAGTAAGATGTAACAGATTAACAGAAATTTGA 780
DB 721 CAGTGAACAAGCAGTATTAACCTAGTAAGATGTAACAGATTAACAGAAATTTGA 780
QY 781 GAAAGAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAAACATCCAAAAGACCTCA 840
DB 781 GAAAGAGAGAGAGACACAGATTCAGGACGACAGAGAGAGAAACATCCAAAAGACCTCA 840
QY 841 GGAGACATTTTCTTTGTGAGCATTCAGGACCTTTTTCAAATTCGATTTCTTCA 900
DB 841 GGAGACATTTTCTTTGTGAGCATTCAGGACCTTTTTCAAATTCGATTTCTTCA 900
QY 901 TTCATGTGTTATGTCCTTAAAAAATAGACATGTTTCTAAAGTGTGATCTACACCA 960
DB 901 TTCATGTGTTATGTCCTTAAAAAATAGACATGTTTCTAAAGTGTGATCTACACCA 960
QY 961 CCATCTGATGATGAGACATTCGACCTTAATGTAAGCACTGACATTCCTGAGC 1020
DB 961 CCATCTGATGATGAGACATTCGACCTTAATGTAAGCACTGACATTCCTGAGC 1020
QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAGCATTAAGCCTTAAGCTTAGATGACAGATG 1080
DB 1021 TAGTCCAGCTAGTACACCAAAATCATTAGCATTAAGCCTTAAGCTTAGATGACAGATG 1080
QY 1081 GCAATTCAGAGATCTCGTGTGTAATGATACAGAGCAAAAGATCTAAAGCAATCTG 1140
DB 1081 GCAATTCAGAGATCTCGTGTGTAATGATACAGAGCAAAAGATCTAAAGCAATCTG 1140
QY 1141 TAGTGAACCAAGTAAGACATCCAAATGAGAGCCCAAGAACAGATGAAGAAATGA 1200
DB 1141 TAGTGAACCAAGTAAGACATCCAAATGAGAGCCCAAGAACAGATGAAGAAATGA 1200
QY 1201 AAAGATGAAGGTTTGTGTAATTAATCAAGCTCTCTCAATTTGATCTTTTAACCTTA 1260
DB 1201 AAAGATGAAGGTTTGTGTAATTAATCAAGCTCTCTCAATTTGATCTTTTAACCTTA 1260
QY 1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAGCCAAACATTTCTATGTTTACTAT 1320
DB 1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAGCCAAACATTTCTATGTTTACTAT 1320
QY 1321 GTTGAAGCTTCTGAGTAAGTTCATTTTATTAATAGTTCACCTGTTTGAAGTAATAC 1380
DB 1321 GTTGAAGCTTCTGAGTAAGTTCATTTTATTAATAGTTCACCTGTTTGAAGTAATAC 1380
QY 1381 ACAGATTACTTGAAGCTTACTTCAAAAGTACCTTTTCAACATCAATGATGCTTTTA 1440
DB 1381 ACAGATTACTTGAAGCTTACTTCAAAAGTACCTTTTCAACATCAATGATGCTTTTA 1440

QY 1441 TTTCAAACCTTTTTCACCTTCACTAAGTGTGAGGGAGGCTTACACAGACACA 1500
Db 1441 TTTCAAACCTTTTTCACCTTCACTAAGTGTGAGGGAGGCTTACACAGACACA 1500
QY 1501 TTCTTTAGATTGGAAAAGTGAACAGGACAGTGGCTCACACCTGTATCCCGCACT 1560
Db 1501 TTCTTTAGATTGGAAAAGTGAACAGGACAGTGGCTCACACCTGTATCCCGCACT 1560
QY 1561 TAGGGAAGACAGTCAAGAGAGATTGATGAGAGTTAGAGACACGCTGGGCAAC 1620
Db 1561 TAGGGAAGACAGTCAAGAGAGATTGATGAGAGTTAGAGACACGCTGGGCAAC 1620
QY 1621 GATTTAGACCACTGCTATTAATAAATGAAAAGAGAAATGAGCTTATTTTCA 1680
Db 1621 GATTTAGACCACTGCTATTAATAAATGAAAAGAGAAATGAGCTTATTTTCA 1680
QY 1681 AATATGGAAGAAATTTATATGAAAATTTATCTGAGTCAATTAATTCCTTAAGTGAT 1740
Db 1681 AATATGGAAGAAATTTATATGAAAATTTATCTGAGTCAATTAATTCCTTAAGTGAT 1740
QY 1741 ACTTTTAAAGTACATTATGGCTAGAGTGGCAGATAAATGCTGATATCTATGCAAT 1800
Db 1741 ACTTTTAAAGTACATTATGGCTAGAGTGGCAGATAAATGCTGATATCTATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTTTTTTTTTTTTTTTTTT 1849
Db 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTTTTTTTTTTTTTTTTTT 1849

RESULT 10

ACC86960 standard; cDNA; 1849 BP.

ID ACC86960 standard; cDNA; 1849 BP.

XX ACC86960;

DT 05-AUG-2003 (first entry)

XX Human secreted polypeptide PRO1013-encoding cDNA, SEQ ID NO:133.

XX Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor- α ; TNF- α ;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy; gene; ss.

XX Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00186773.

PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059263P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0068707P.
PR 31-OCT-1997; 97US-0068103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082566P.
PR 21-APR-1998; 98US-0082566P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 22-MAY-1998; 98US-0086709P.
PR 28-MAY-1998; 98US-0087088P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087759P.
PR 02-JUN-1998; 98US-0087827P.
PR 03-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088126P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088217P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088875P.
PR 12-JUN-1998; 98US-0088909P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.

PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-00902552P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-01005413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 04-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-01019310.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.

PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 25-SEP-1998; 98US-0102240P.
PR 25-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1849; Conservative 0;

QY 1 CTGAGGCGGCGTAGCATGAGGCGGAGTAGTACGTGCGCGTCTCTCGGCTTTGTGCT 60
DB 1 CTGAGGCGGCGTAGCATGAGGCGGAGTAGTACGTGCGCGTCTCTCGGCTTTGTGCT 60
QY 61 CGGCGCACTGCTTTCCAGCACTTCAACAGCACTGGAACCGAAGCTTTTCTCTTG 120
DB 61 CGGCGCACTGCTTTCCAGCACTTCAACAGCACTGGAACCGAAGCTTTTCTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCAAGAACAGCATTACTGATCCCAATGGATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGAACAGCATTACTGATCCCAATGGATGTTGAAGT 180
QY 181 TGTATTACATTTGACATTCAGAAATATTCATGCTATCAGCTTTTGTGCTTTTAA 240
DB 181 TGTATTACATTTGACATTTGACAAATATTCATGCTATCAGCTTTTGTGCTTTTAA 240
QY 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATTTATCAATGCAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATTTATCAATGCAAAAGAA 300
QY 301 TGTGTAGTGTGTACAAATTCGTCGTATTCAGATCATGACGTTTGAAGAG 360
DB 301 TGTGTAGTGTGTACAAATTCGTCGTATTCAGATCATGACGTTTGAAGAG 360
QY 361 GCTGCTTCAAAAACCTTGCGAGCACTTTTCAACCAAGACCTTTTTCGCTATT 420
DB 361 GCTGCTTCAAAAACCTTGCGAGCACTTTTCAACCAAGACCTTTTTCGCTATT 420
QY 421 AACACCAAGTAAATTAACAGAAAGCTGCTACTCATGACTGGAACATTCCTATATA 480
DB 421 AACACCAAGTAAATTAACAGAAAGCTGCTACTCATGACTGGAACATTCCTATATA 480
QY 481 ACCTTAAAGACCTTTTTCAGAGTACCTTTGAGGCAATCGGGCATGCTGA 540
DB 481 ACCTTAAAGACCTTTTTCAGAGTACCTTTGAGGCAATCGGGCATGCTGA 540
QY 541 ACAACTGGTTATAAAGCTGATCAGTTCCGTATGTCACCTGTTTACCCGACAGT 600
DB 541 ACAACTGGTTATAAAGCTGATCAGTTCCGTATGTCACCTGTTTACCCGACAGT 600
QY 601 ACAAAACACAGCTTTAATTTTGAAGAAATGATCCCTTAAAGGATGATCAAT 660
DB 601 ACAAAACACAGCTTTAATTTTGAAGAAATGATCCCTTAAAGGATGATCAAT 660
QY 661 AAATGAATGTATGCTTCAATACAGAGAAATTAAGATATGCAAAAAAGTGAAGA 720
DB 661 AAATGAATGTATGCTTCAATACAGAGAAATTAAGATATGCAAAAAAGTGAAGA 720
QY 721 CAGTGAACAGAGTATGATTAATCTATGAAGATGTAACAGATTTAAACGGAATTTGA 780
DB 721 CAGTGAACAGAGTATGATTAATCTATGAAGATGTAACAGATTTAAACGGAATTTGA 780
QY 781 GAAAGGAGAGAGACAGATTCAAGAGCAAGAGAGAAACATCCAAAAGACCTTCA 840
DB 781 GAAAGGAGAGAGACAGATTCAAGAGCAAGAGAGAAACATCCAAAAGACCTTCA 840

QY 841 GGAGACATTTTCTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTCCTCA 900
DB 841 GGAGACATTTTCTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTCCTCA 900
QY 901 TTGATGTGTATGTCTTTAAAAATGACATGTTTCTAAAAGTGTGTAACAACA 960
DB 901 TTGATGTGTATGTCTTTAAAAATGACATGTTTCTAAAAGTGTGTAACAACA 960
QY 961 CCATCTGATGTGTGACATCTGACCTTAATGTGAGAACACATGACATTCCTGAAC 1020
DB 961 CCATCTGATGTGTGACATCTGACCTTAATGTGAGAACACATGACATTCCTGAAC 1020
QY 1021 TAGTCCAGCTAGTACACCAACCAATCAATTAAGCATTAAGCCTTGAATGACAGATG 1080
DB 1021 TAGTCCAGCTAGTACACCAACCAATCAATTAAGCATTAAGCCTTGAATGACAGATG 1080
QY 1081 GCAATTCAGAGATCTCGGTTGTAGTACACAAGCAAAAGATCTAAAGCAATACCTG 1140
DB 1081 GCAATTCAGAGATCTCGGTTGTAGTACACAAGCAAAAGATCTAAAGCAATACCTG 1140
QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGACAGCCCAAGAACATGAAGAAATGA 1200
DB 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGACAGCCCAAGAACATGAAGAAATGA 1200
QY 1201 AAAGATGAAGGTTTGTGTAATATTCACGCTCTTACATTTGATCCCTTTAACTTA 1260
DB 1201 AAAGATGAAGGTTTGTGTAATATTCACGCTCTTACATTTGATCCCTTTAACTTA 1260
QY 1261 CAAGAGATTTTATTTGGCTGATGGTAAAGCAAAATTTCTATTGTTTACTAT 1320
DB 1261 CAAGAGATTTTATTTGGCTGATGGTAAAGCAAAATTTCTATTGTTTACTAT 1320
QY 1321 GTTGAGTACTTGCAGTAATCATTTGTTTACTACTATGTTCCCTGTTGAGTAATAC 1380
DB 1321 GTTGAGTACTTGCAGTAATCATTTGTTTACTACTATGTTCCCTGTTGAGTAATAC 1380
QY 1381 ACAGATTAATCTAGTATCATTTTCTTCAACAAGTATTTTCAATCATGATGCTTTA 1440
DB 1381 ACAGATTAATCTAGTATCATTTTCTTCAACAAGTATTTTCAATCATGATGCTTTA 1440
QY 1441 TTTCCAAACCTTTTTCACCTTTCACTAAAGTTGAGGGGAAAGCTTACACAGACAC 1500
DB 1441 TTTCCAAACCTTTTTCACCTTTCACTAAAGTTGAGGGGAAAGCTTACACAGACAC 1500
QY 1501 TTCTTTGAATTTGGAAAGTGAGACAGGACAGTGGCTACACCTGTAAATCCAGACACT 1560
DB 1501 TTCTTTGAATTTGGAAAGTGAGACAGGACAGTGGCTACACCTGTAAATCCAGACACT 1560
QY 1561 TAGGGAAGACAGTCAAGAGATTAAGAGTGAAGCTAGAGTGAAGACCAAGCTGGCAAC 1620
DB 1561 TAGGGAAGACAGTCAAGAGATTAAGAGTGAAGCTAGAGTGAAGACCAAGCTGGCAAC 1620
QY 1621 GTATTTGACATGTCTATTAATAAATAAGAAAGCAAAATAGCCTTTTTCAA 1680
DB 1621 GTATTTGACATGTCTATTAATAAATAAGAAAGCAAAATAGCCTTTTTCAA 1680
QY 1681 AATATGAAGAAATTAATTAAGAAATTTATCTGAGTCATTAATTTCTCCTTAAGTAT 1740
DB 1681 AATATGAAGAAATTAATTAAGAAATTTATCTGAGTCATTAATTTCTCCTTAAGTAT 1740
QY 1741 ACTTTTAAAGTACATTAATGCTAGAGTTGCCAGATAAAAGCTGAGATATATGCAAT 1800
DB 1741 ACTTTTAAAGTACATTAATGCTAGAGTTGCCAGATAAAAGCTGAGATATATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849
DB 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849

RESULT 11
ACD04133
ID ACD04133 standard, cDNA, 1849 BP.

XX ACD04133;
AC 09-AUG-2003 (first entry)
XX
DT
XX
DE Human secreted/transmembrane protein (PRO) cDNA #67.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
FN US2003040070-A1.
XX
PD 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059263P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080335P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083455P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0083566P.
PR 05-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.

PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086492B.
PR 22-MAY-1998; 98US-0086486P.
PR 26-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088555P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 18-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089652P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105613.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.

PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100622P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102310P.
PR 29-SEP-1998; 98US-0102310P.
PR 29-SEP-1998; 98US-0102310P.
PR 29-SEP-1998; 98US-0102310P.
PR 30-SEP-1998; 98US-0102311P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102664P.
PR 01-OCT-1998; 98US-0102664P.
PR 02-OCT-1998; 98US-0102665P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGTGCATGAGGCGGAGAGTACCTCGCGGCTGCTTCGCGCTTTGCT 60
DB 1 CTGAGCGCGCGTGCATGAGGCGGAGAGTACCTCGCGGCTGCTTCGCGCTTTGCT 60
QY 61 CGGCGCATTCGCTTCCGACCTCAACACGCGCTCGGACCGAGAGTTTCTCTTG 120
DB 61 CGGCGCATTCGCTTCCGACCTCAACACGCGCTCGGACCGAGAGTTTCTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCAAGAAAGAGTACTGATTTCCAAATGATGATTTGAGT 180
DB 121 GGAAGTAAAGGTGAAGCAAGAAAGAGTACTGATTTCCAAATGATGATTTGAGT 180
QY 181 TGTATTACATTGACATTGAGAAATATATTCAGATGATCAGCTTTTACCTTTATA 240
DB 181 TGTATTACATTGACATTGAGAAATATATTCAGATGATCAGCTTTTACCTTTATA 240

QY 241 TTCTTCAGGCGAATAATGAGCAGACCTGAAGAAAAATATATCAATGTCAAAAAA 300
 Db 241 TTCTTCAGGCGAATAATGAGCAGACCTGAAGAAAAATATATCAATGTCAAAAAA 300
 QY 301 TGTGTAGGTGTGACAAATTCGGTGTGATTCAGATCAGATGACGTGTAAGAG 360
 Db 301 TGTGTAGGTGTGACAAATTCGGTGTGATTCAGATCAGATGACGTGTAAGAG 360
 QY 361 GGTGCTTCACAAAACTTGACAGAGCATTTTTCACCAAGACCTGTGTTCTGCTAT 420
 Db 361 GGTGCTTCACAAAACTTGACAGAGCATTTTTCACCAAGACCTGTGTTCTGCTAT 420
 QY 421 AACGCAAGATATATACAGAAAGCTGCTACTCATCGACTGGAACATCTCTATATA 480
 Db 421 AACGCAAGATATATACAGAAAGCTGCTACTCATCGACTGGAACATCTCTATATA 480
 QY 481 ACCTCAAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCAACTGGGCACTGTCTGA 540
 Db 481 ACCTCAAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCAACTGGGCACTGTCTGA 540
 QY 541 ACAACTGGGTATATAAAGTGTATAGGTTCTGTATGTCACTGGTATTACCGAGAGT 600
 Db 541 ACAACTGGGTATATAAAGTGTATAGGTTCTGTATGTCACTGGTATTACCGAGAGT 600
 QY 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCTCTTAAAGAGGTACATAAGAT 660
 Db 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCTCTTAAAGAGGTACATAAGAT 660
 QY 661 AATGAAATGTATGCTTCATTACAGAGAAATTAAGATTAATGCAAAAAAGTGAAGA 720
 Db 661 AATGAAATGTATGCTTCATTACAGAGAAATTAAGATTAATGCAAAAAAGTGAAGA 720
 QY 721 CAGTGAACAAGCAGTATATACTAGTAAGAGATGTAACAGATTAAAGAGAAATTTGA 780
 Db 721 CAGTGAACAAGCAGTATATACTAGTAAGAGATGTAACAGATTAAAGAGAAATTTGA 780
 QY 781 GAAAAGAGAGAGACAGATTCAGGAGCAGAGAGAGAGAGACATCCAAAAGACCTCA 840
 Db 781 GAAAAGAGAGAGACAGATTCAGGAGCAGAGAGAGAGAGACATCCAAAAGACCTCA 840
 QY 841 GAGAGAACTTTTCTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTTCTTCA 900
 Db 841 GAGAGAACTTTTCTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTTCTTCA 900
 QY 901 TTCAATGTATGCTTTTAAATAATAGACATGTTCTTAAAGTGTGTAACAACA 960
 Db 901 TTCAATGTATGCTTTTAAATAATAGACATGTTCTTAAAGTGTGTAACAACA 960
 QY 961 CCATCTGATGTATGACAAATCTGACCTTAATGTGTAACAACAATCTGTAAGC 1020
 Db 961 CCATCTGATGTATGACAAATCTGACCTTAATGTGTAACAACAATCTGTAAGC 1020
 QY 1021 TAGTCAGCTAGTACCAACAATCATTAAGCATTAAGCTTAAGCTTGAAGATG 1080
 Db 1021 TAGTCAGCTAGTACCAACAATCATTAAGCATTAAGCTTGAAGATG 1080
 QY 1081 GCAATTCAGAGATCTGCTGTTGTAATACACAAGCAACGATCTTAAAGCAAAATCTG 1140
 Db 1081 GCAATTCAGAGATCTGCTGTTGTAATACACAAGCAACGATCTTAAAGCAAAATCTG 1140
 QY 1141 TAGTAGTACCAAGATTAAGCATCCAAATGAGAGCCGAGAAACGATGAAAGATTA 1200
 Db 1141 TAGTAGTACCAAGATTAAGCATCCAAATGAGAGCCGAGAAACGATGAAAGATTA 1200
 QY 1201 AAAGATGAAGGCTTTGTGTAATATTCACGCTCTCTACATTTGATCTTTTAACTTA 1260
 Db 1201 AAAGATGAAGGCTTTGTGTAATATTCACGCTCTCTACATTTGATCTTTTAACTTA 1260
 QY 1261 CAAGGAAATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTATGTTTACTAT 1320
 Db 1261 CAAGGAAATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTATGTTTACTAT 1320

QY 1321 GTTAGCTACTTGACAGTAAGTTCATTTGTTTACTATGTTCACTGTTGCAATATAC 1380
 Db 1321 GTTAGCTACTTGACAGTAAGTTCATTTGTTTACTATGTTCACTGTTGCAATATAC 1380
 QY 1381 ACAGTAATCTGTATGATTTACTTCAAGATACCTTTTCAACATCAGATGCTTTTA 1440
 Db 1381 ACAGTAATCTGTATGATTTACTTCAAGATACCTTTTCAACATCAGATGCTTTTA 1440
 QY 1441 TTTCAAAACCTTTTTCACCTTTCATTAAGTGTGAGGGAAGGCTTACACAGACA 1500
 Db 1441 TTTCAAAACCTTTTTCACCTTTCATTAAGTGTGAGGGAAGGCTTACACAGACA 1500
 QY 1501 TTCTTAAGATTTGAAAGTGAACCAAGCAAGTGGCTCACTCTGTAATCCAGCACT 1560
 Db 1501 TTCTTAAGATTTGAAAGTGAACCAAGCAAGTGGCTCACTCTGTAATCCAGCACT 1560
 QY 1561 TAGGAGAGCAAGTCAAGAGATTTGATTAAGTGAAGTGAAGACCAAGCCTGGCAAC 1620
 Db 1561 TAGGAGAGCAAGTCAAGAGATTTGATTAAGTGAAGTGAAGACCAAGCCTGGCAAC 1620
 QY 1621 GTATTGAACCATGCTCTTTTAAATAATTAATGGAAGCAAGATACCTTATTTTCA 1680
 Db 1621 GTATTGAACCATGCTCTTTTAAATAATTAATGGAAGCAAGATACCTTATTTTCA 1680
 QY 1681 AATATGAAGAAATTTATGAAATTTATCTGAGTCAATTAATCTCCTTAAAGTAT 1740
 Db 1681 AATATGAAGAAATTTATGAAATTTATCTGAGTCAATTAATCTCCTTAAAGTAT 1740
 QY 1741 ACTTTTGAAGATTAATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAAT 1800
 Db 1741 ACTTTTGAAGATTAATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAAT 1800
 QY 1801 AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849
 Db 1801 AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849

RESULT 12

ABX77815
ID ABX77815 standard; cDNA, 1849 BP.

XX ABX77815;

DT 14-APR-2003 (first entry)

XX Human PRO polynucleotide #36.

KW Human; PRO; gene; se; cytosolic; tumour; cancer; breast; lung; stomach;

KW liver; horse; cow; cat; sheep; pig; goat; rabbit; ADPRT;

XX antibody-dependent enzyme mediated prodng therapy.

OS Homo sapiens.

PN US2003027163-A1.

XX 06-FEB-2003.

PF 15-NOV-2001; 2001US-00997666.

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0068707P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088367P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088867P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089589P.
 PR 17-JUN-1998; 98US-0089593P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089949P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 22-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.
 PR 23-JUN-1998; 98US-0090355P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090431P.
 PR 24-JUN-1998; 98US-0090435P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090445P.
 PR 24-JUN-1998; 98US-0090472P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 24-JUN-1998; 98US-0090542P.
 PR 24-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090698P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 01-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.

PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095323P.
 PR 04-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095916P.
 PR 10-AUG-1998; 98US-0095929P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 11-AUG-1998; 98US-0096143P.
 PR 11-AUG-1998; 98US-0096146P.
 PR 12-AUG-1998; 98US-0096329P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
 PR 17-AUG-1998; 98US-0096791P.
 PR 17-AUG-1998; 98US-0096867P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 17-AUG-1998; 98US-0096894P.
 PR 17-AUG-1998; 98US-0096895P.
 PR 17-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096950P.
 PR 18-AUG-1998; 98US-0096952P.
 PR 18-AUG-1998; 98US-0096954P.
 PR 18-AUG-1998; 98US-0096960P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097214P.
 PR 20-AUG-1998; 98US-0097261P.
 PR 24-AUG-1998; 98US-0097661P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019347.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98US-0113296P.
 PR 22-DEC-1998; 99WO-US000106.
 PR 05-JAN-1999; 99WO-US005028.
 PR 08-MAR-1999; 99US-0123957P.
 PR 12-MAR-1999; 99WO-US012252.
 PR 02-JUN-1999; 99US-0141037P.
 PR 23-JUN-1999; 99US-0143048P.
 PR 07-JUL-1999; 99US-0144758P.
 PR 20-JUL-1999; 99US-0145688P.
 PR 26-JUL-1999; 99US-0145688P.
 PR 28-JUL-1999; 99US-0146223P.
 PR 17-AUG-1999; 99US-0149366P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US028634.
 PR 20-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.

Db 1801 AATTGCAAAACATCATTAATAAAAAAAAAAAAAAAAAAAAAA 1849

RESULT 13

ABX80227 standard; DNA; 1849 BP.

ABX80227;

28-APR-2003 (first entry)

Novel human secreted or transmembrane protein PRO937 DNA.

Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
cardiac insufficiency disorder; cancer; tumour; immune response;
adrenal cortical capillary endothelial growth; c-fos induction;
vascular endothelial growth factor inhibition; VEGF inhibition;
endothelial cell growth inhibitor; T-lymphocytes stimulation;
retinal neurons cell survival; rod photoreceptor cell survival;
retinal disorder; retinitis pigmentosa; kidney disorder;
mammalian kidney mesangial cell proliferation; Berger disease;
dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

Homo sapiens.

US2002132252-A1.

19-SEP-2002.

14-NOV-2001; 2001US-00990442.

16-JUN-1997; 97US-0049787P.
17-OCT-1997; 97US-0062250P.
05-NOV-1997; 97WO-US020069.
12-NOV-1997; 97US-0065186P.
13-NOV-1997; 97US-0065311P.
24-NOV-1997; 97US-0066770P.
25-FEB-1998; 98US-0075945P.
20-MAR-1998; 98US-0078810P.
28-APR-1998; 98US-0083322P.
07-MAY-1998; 98US-0084600P.
28-MAY-1998; 98US-0087106P.
02-JUN-1998; 98US-0087607P.
02-JUN-1998; 98US-0087759P.
02-JUN-1998; 98US-0087827P.
03-JUN-1998; 98US-0088021P.
04-JUN-1998; 98US-0088025P.
04-JUN-1998; 98US-0088026P.
04-JUN-1998; 98US-0088028P.
04-JUN-1998; 98US-0088029P.
04-JUN-1998; 98US-0088030P.
04-JUN-1998; 98US-0088033P.
04-JUN-1998; 98US-0088326P.
05-JUN-1998; 98US-0088167P.
05-JUN-1998; 98US-0088202P.
05-JUN-1998; 98US-0088212P.
05-JUN-1998; 98US-0088217P.
09-JUN-1998; 98US-0088655P.
10-JUN-1998; 98US-0088734P.
10-JUN-1998; 98US-0088738P.
10-JUN-1998; 98US-0088742P.
10-JUN-1998; 98US-0088810P.
10-JUN-1998; 98US-0088824P.
10-JUN-1998; 98US-0088826P.
11-JUN-1998; 98US-0088858P.
11-JUN-1998; 98US-0088861P.
11-JUN-1998; 98US-0088876P.
12-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.

16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089589P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
17-JUN-1998; 98US-0089633P.
18-JUN-1998; 98US-0089601P.
18-JUN-1998; 98US-0089607P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUN-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023528.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kijavlin IO, Napier MA, Pan U, Paoletti NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FW, Wood WI;
Zhang Z;
WPI; 2003-247083/24.
P-PsDB; ABUS9083.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
are therapeutically useful for enhancing immune response and in cancer
treatments.

Claim 2; Fig 96; 648bp; English.

The invention describes an isolated human PRO polypeptide. The PRO

CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO1326,
CC PRO1943, PRO1826, PRO1068 or PRO1068, PRO1068, PRO1068, PRO1068,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and angiogenesis of this polypeptide are
CC useful for treating cancerous tumours. PRO1312 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth. PRO1068,
CC PRO1068, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO1068, PRO1068, PRO1068 or PRO1312 enhance survival of
CC retinal neurons cells (PRO1312 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO1068, PRO1068,
CC and PRO1068 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO1068, PRO1312, PRO1312 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide

XX Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGGAGTACGAGGAGAGTACGTCGCGGCTCTCGGCTTTGCT 60
DB 1 CTGAGCGCGGAGTACGAGGAGAGTACGTCGCGGCTCTCGGCTTTGCT 60
QY 61 CGGCGACTCGCTTTCCAGACCTCAACGAGCTGGACAGGAGTTCTTTGG 120
DB 61 CGGCGACTCGCTTTCCAGACCTCAACGAGCTGGACAGGAGTTCTTTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACGACTTCTGATCCCAATGATGATGAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAGAACGACTTCTGATCCCAATGATGATGAGT 180
QY 181 TGTATTACATTTGACATTCAGAAATATATTCATGCTTATGCTTTTATTA 240
DB 181 TGTATTACATTTGACATTCAGAAATATATTCATGCTTATGCTTTTATTA 240
QY 241 TTTCTTACGAGGAGTAAATGAGAGCACTGAAGAAATATATTAATGCAAAA 300
DB 241 TTTCTTACGAGGAGTAAATGAGAGCACTGAAGAAATATATTAATGCAAAA 300
QY 301 TGTGTAGTGTGTATCAAAATTCGTGTCATTCAGATCATGATGATGAGAG 360
DB 301 TGTGTAGTGTGTATCAAAATTCGTGTCATTCAGATCATGATGATGAGAG 360
QY 361 GGTGTCTCAAAAATTTGAGAGATTTTCAACCAAGACTTTTCTGCTAT 420
DB 361 GGTGTCTCAAAAATTTGAGAGATTTTCAACCAAGACTTTTCTGCTAT 420
QY 421 AACACCAAGTATATTAACAGAAAGTGTCTATCTATGATGATGATGATGAT 480
DB 421 AACACCAAGTATATTAACAGAAAGTGTCTATCTATGATGATGATGATGAT 480
QY 481 AACTCAAAAAGACTTTTCAAGAGTACTTTAGTGTGTCATTCGGAGATTTG 540
DB 481 AACTCAAAAAGACTTTTCAAGAGTACTTTAGTGTGTCATTCGGAGATTTG 540
QY 541 ACAACTGGGTATTAATACTGTATCAGTTCCTGTATGTCACCTGTTTACG 600
DB 541 ACAACTGGGTATTAATACTGTATCAGTTCCTGTATGTCACCTGTTTACG 600

DB 541 ACAACTGGGTATTAATACTGTATCAGTTCCTGTATGTCACCTGTTTACG 600
QY 601 ACAACACACAGCTCTTAATTTTGAAGAGTATGATCCTTTAAGAGTATCA 660
DB 601 ACAACACACAGCTCTTAATTTTGAAGAGTATGATCCTTTAAGAGTATCA 660
QY 661 AATGAATGTATGCTTATTAACAGAGATTAAGATATGCAAAAAGTGAAGA 720
DB 661 AATGAATGTATGCTTATTAACAGAGATTAAGATATGCAAAAAGTGAAGA 720
QY 721 CAGTGAACAGCAATATTAATCTAGTAAAGATGTAACAGATTTAAAGAG 780
DB 721 CAGTGAACAGCAATATTAATCTAGTAAAGATGTAACAGATTTAAAGAG 780
QY 781 GAAAGAGAGAGAGACAGATTTACGAGAGCAAGAGAGAGAGAGAGAGAG 840
DB 781 GAAAGAGAGAGAGACAGATTTACGAGAGCAAGAGAGAGAGAGAGAGAG 840
QY 841 GGAAGACATTTTCTTTGTCAGGATTAAGGACCTTTTCCAAATTTGAT 900
DB 841 GGAAGACATTTTCTTTGTCAGGATTAAGGACCTTTTCCAAATTTGAT 900
QY 901 TTGATGTATGCTTATTAATAATAGACATGTTCTTAAAGTATGATCAACA 960
DB 901 TTGATGTATGCTTATTAATAATAGACATGTTCTTAAAGTATGATCAACA 960
QY 961 CCATCTGATGTATGATGACATCTGACCTTAATGATGAGACACATGATCT 1020
DB 961 CCATCTGATGTATGATGACATCTGACCTTAATGATGAGACACATGATCT 1020
QY 1021 TAGTCCAGCTATGACACACAAATCAATTAAGCTTGAATGATGATGAT 1080
DB 1021 TAGTCCAGCTATGACACACAAATCAATTAAGCTTGAATGATGATGAT 1080
QY 1081 GCAATTCAGAGATCTCGTGTGTATGATCAACAAGCAAGATCTTAAGCA 1140
DB 1081 GCAATTCAGAGATCTCGTGTGTATGATCAACAAGCAAGATCTTAAGCA 1140
QY 1141 TAGTATGACCAAGATTAAGCAATCCAAATAGACAGCCAGAGAGAGAG 1200
DB 1141 TAGTATGACCAAGATTAAGCAATCCAAATAGACAGCCAGAGAGAGAG 1200
QY 1201 AAGATGAAGGATTTGATGATATTCACGCTCTCAATTTGATCTTTTAA 1260
DB 1201 AAGATGAAGGATTTGATGATATTCACGCTCTCAATTTGATCTTTTAA 1260
QY 1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAAGCCAAATCTTATTT 1320
DB 1261 CAAGAGATTTTATTTATTTGCTGATGAGTAAAGCCAAATCTTATTT 1320
QY 1321 GTTGTACTCTGACGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GTTGTACTCTGACGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ACGATATCTTATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 ACGATATCTTATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 TTTCAAACTTTTTCACCTTCACTTAAGTGTGAGGAGAGGCTTCAACA 1500
DB 1441 TTTCAAACTTTTTCACCTTCACTTAAGTGTGAGGAGAGGCTTCAACA 1500
QY 1501 TTTCTTGAATTTGAAGAGTGAACAGGACAGTGTCTCACTGATATCC 1560
DB 1501 TTTCTTGAATTTGAAGAGTGAACAGGACAGTGTCTCACTGATATCC 1560
QY 1561 TAGGAG 1620
DB 1561 TAGGAG 1620
QY 1621 GTATTGAGACATGTCTATTTAAATAATGAAGAGAGAGAGAGAGAG 1680
DB 1621 GTATTGAGACATGTCTATTTAAATAATGAAGAGAGAGAGAGAGAG 1680

PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096899P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097619P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0101943P.
PR 07-OCT-1998; 98US-0102114P.
PR 01-DEC-1998; 98US-0102510P.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0100010P.
PR 08-MAR-1999; 98US-0123957P.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98US-0123957P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
PR 15-SEP-1999; 98US-0150210P.
PR 15-SEP-1999; 98US-0150215P.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98US-0158663P.
PR 01-DEC-1999; 98US-0158663P.
PR 01-DEC-1999; 98US-0158663P.
PR 16-DEC-1999; 98US-0158663P.
PR 20-DEC-1999; 98US-0158663P.
PR 05-JAN-2000; 98US-0158663P.
PR 06-JAN-2000; 98US-0158663P.
PR 11-FEB-2000; 98US-0158663P.
PR 18-FEB-2000; 98US-0158663P.
PR 22-FEB-2000; 98US-0158663P.
PR 24-FEB-2000; 98US-0158663P.
PR 02-MAR-2000; 98US-0158663P.
PR 10-MAR-2000; 98US-0158663P.
PR 15-MAR-2000; 98US-0158663P.
PR 20-MAR-2000; 98US-0158663P.
PR 30-MAR-2000; 98US-0158663P.
PR 15-MAY-2000; 98US-0158663P.
PR 17-MAY-2000; 98US-0158663P.
PR 22-MAY-2000; 98US-0158663P.
PR 30-MAY-2000; 98US-0158663P.
PR 02-JUN-2000; 98US-0158663P.
PR 23-JUN-2000; 98US-0158663P.
PR 28-JUL-2000; 98US-0158663P.
PR 11-AUG-2000; 98US-0158663P.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGGTAGCATGAGGAGGAGTACGTGCGCGTCTCTCGGCGTTTGCT 60
Db 1 CTGAGCGCGCGGTAGCATGAGGAGGAGTACGTGCGCGTCTCTCGGCGTTTGCT 60
QY 61 CGGCGCATCTGCTTTTCAAGCATCTCAACAGCTGCGACAGGAGGTTTCTCTG 120
Db 61 CGGCGCATCTGCTTTTCAAGCATCTCAACAGCTGCGACAGGAGGTTTCTCTG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCTTACTGATTCGCAATGATGTTGAAGT 180
Db 121 GGAAGTAAAGGTGAAGCCAGAACAGCTTACTGATTCGCAATGATGTTGAAGT 180
QY 181 TGTATTATACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TGTATTATACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 TTCTTCAGCGGAGTAAATGAGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 241 TTCTTCAGCGGAGTAAATGAGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 301 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GCTGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 GCTGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 AACACCAAGTATATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 AACACCAAGTATATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 ACCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 481 ACCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 ACAACGCGGTTTAAACCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 541 ACAACGCGGTTTAAACCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 601 ACAACGCGGTTTAAACCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 601 ACAACGCGGTTTAAACCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 AAATGAATGTATGCTTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 661 AAATGAATGTATGCTTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 CAGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 CAGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 CCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TAGTCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 TAGTCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080

PR 09-JUN-1998; 98US-008655P.
PR 10-JUN-1998; 98US-0086722P.
PR 10-JUN-1998; 98US-0086738P.
PR 10-JUN-1998; 98US-0086740P.
PR 10-JUN-1998; 98US-0086811P.
PR 10-JUN-1998; 98US-0086824P.
PR 10-JUN-1998; 98US-0086825P.
PR 10-JUN-1998; 98US-0086826P.
PR 11-JUN-1998; 98US-0086861P.
PR 11-JUN-1998; 98US-0086863P.
PR 11-JUN-1998; 98US-0086867P.
PR 12-JUN-1998; 98US-0086900P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089808P.
PR 19-JUN-1998; 98US-0089852P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100663P.
PR 17-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101044P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0016897P.
PR 07-OCT-1998; 98US-0103395P.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTGACATGAGGCGGAGAGTACGTCGCGGTCTTGGGCTTGTGCT 60
DB 1 CTGAGGCGGCGGTGACATGAGGCGGAGAGTACGTCGCGGTCTTGGGCTTGTGCT 60
QY CGGCGCACTGCTTCCAGACCTCAACACGCACTGGACACGGAAGTTTCTTCTTG 120
DB CGGCGCACTGCTTCCAGACCTCAACACGCACTGGACACGGAAGTTTCTTCTTG 120
QY 61 CGGCGCACTGCTTCCAGACCTCAACACGCACTGGACACGGAAGTTTCTTCTTG 120
DB 61 CGGCGCACTGCTTCCAGACCTCAACACGCACTGGACACGGAAGTTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAGCCAGAAACAGCACTTACTGATTCGCAATGATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAGCCAGAAACAGCACTTACTGATTCGCAATGATGTTGAAGT 180
QY 121 GGAAGTAAAGGTGAGCCAGAAACAGCACTTACTGATTCGCAATGATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAGCCAGAAACAGCACTTACTGATTCGCAATGATGTTGAAGT 180
QY 181 TGTATTACATTCATTCAGAAATATATTCATGCTATCAGTTTAACTTTTAA 240
DB 181 TGTATTACATTCATTCAGAAATATATTCATGCTATCAGTTTAACTTTTAA 240
QY 241 TTCTTCAGGCGCAATGATGAGCAAGCACTGAGAAAATATTCAAATGTCAAAAGAA 300
DB 241 TTCTTCAGGCGCAATGATGAGCAAGCACTGAGAAAATATTCAAATGTCAAAAGAA 300
QY 301 TGTGTAGTGTGATCAATTCGCTGCTATTCAGATCAGATCAGATCAGATCAGATCAG 360
DB 301 TGTGTAGTGTGATCAATTCGCTGCTATTCAGATCAGATCAGATCAGATCAGATCAG 360
QY 361 GCTGCTTCAAAAAGTTCAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATT 420
DB 361 GCTGCTTCAAAAAGTTCAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATT 420
QY 421 AACACCAAGTATATTAACAGAAAGCTGCTACATCAGATCAGATCAGATCAGATCAG 480
DB 421 AACACCAAGTATATTAACAGAAAGCTGCTACATCAGATCAGATCAGATCAGATCAG 480

QY 481 ACCGAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCAACTGGCATGTCTGA 540
 Db 481 ACCGAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCAACTGGCATGTCTGA 540
 QY 541 ACACTGGGTATTAACACTGTATCAGGTCCCTGTATGTCACACTGGTTTAAAGGAGCT 600
 Db 541 ACACTGGGTATTAACACTGTATCAGGTCCCTGTATGTCACACTGGTTTAAAGGAGCT 600
 QY 601 ACAACACACAGCTCTAAATTTTGTGAAGAGATGATCTTAAAGAGATACATAGAT 660
 Db 601 ACAACACACAGCTCTAAATTTTGTGAAGAGATGATCTTAAAGAGATACATAGAT 660
 QY 661 AAATGAATGTATGCTTCAATTACAGAGAAATTAAGAGATATATGCAAAAAGTGAAGA 720
 Db 661 AAATGAATGTATGCTTCAATTACAGAGAAATTAAGAGATATATGCAAAAAGTGAAGA 720
 QY 721 CAGTGAACAGAGATGATTAAGTAAAGATGTAACAGATTAAACAGAAATTGA 780
 Db 721 CAGTGAACAGAGATGATTAAGTAAAGATGTAACAGATTAAACAGAAATTGA 780
 QY 781 GAAAGAGAGAGAGACAGATTCAGGACCAAGAGAAACATCCAAAAGACCTCA 840
 Db 781 GAAAGAGAGAGAGACAGATTCAGGACCAAGAGAAACATCCAAAAGACCTCA 840
 QY 841 GAGAACATTTTCTTCTTCAGGCAATTAAGACCTTTTCCAAATTCGAATTTCTCA 900
 Db 841 GAGAACATTTTCTTCTTCAGGCAATTAAGACCTTTTCCAAATTCGAATTTCTCA 900
 QY 901 TTCATGTATATGTCCTTAAATAATAGACATGTTCTAAAGTAGCTGTAACACCA 960
 Db 901 TTCATGTATATGTCCTTAAATAATAGACATGTTCTAAAGTAGCTGTAACACCA 960
 QY 961 CCATCTCGATGTATGACAACTGACCTTAATGAGAGAACACATGACCTGGAAGC 1020
 Db 961 CCATCTCGATGTATGACAACTGACCTTAATGAGAGAACACATGACCTGGAAGC 1020
 QY 1021 TAGTCCAGCTAGTACACCAAAATCCTTAAGCATTAAGCCTTGAAGCTTATGACAGATG 1080
 Db 1021 TAGTCCAGCTAGTACACCAAAATCCTTAAGCATTAAGCCTTGAAGCTTATGACAGATG 1080
 QY 1081 GCAATTCAGAGATCTCGGTGTTAGTATACAAAGCAACGATCTAAAGCAAAATCTGG 1140
 Db 1081 GCAATTCAGAGATCTCGGTGTTAGTATACAAAGCAACGATCTAAAGCAAAATCTGG 1140
 QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCCAAGAAACGATGAAGAAATTGA 1200
 Db 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCCAAGAAACGATGAAGAAATTGA 1200
 QY 1201 AAAGATGAAGGGTTTGTGTAATATTCAGGGTCTCTTAATTTGATCTTTAACTTA 1260
 Db 1201 AAAGATGAAGGGTTTGTGTAATATTCAGGGTCTCTTAATTTGATCTTTAACTTA 1260
 QY 1261 CAAGGAGATTTTATTTGGCTGATGGGTAAGCCAAACATTTCTATGTTTACTAT 1320
 Db 1261 CAAGGAGATTTTATTTGGCTGATGGGTAAGCCAAACATTTCTATGTTTACTAT 1320
 QY 1321 GTTAGCTACTTGCAGTAAGTCAATTTGTTTACTATGTTTCACTGTTGCAATATAC 1380
 Db 1321 GTTAGCTACTTGCAGTAAGTCAATTTGTTTACTATGTTTCACTGTTGCAATATAC 1380
 QY 1381 ACAGATTAACCTTAGTACATTTCTTCAAAAGTACTTTTCAAAATCAGATGCTTTA 1440
 Db 1381 ACAGATTAACCTTAGTACATTTCTTCAAAAGTACTTTTCAAAATCAGATGCTTTA 1440
 QY 1441 TTTCCTTGAATTTGAAGAGAGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 Db 1441 TTTCCTTGAATTTGAAG 1500
 QY 1501 TTCTTTGAATTTGAAG 1560
 Db 1501 TTCTTTGAATTTGAAG 1560

QY 1561 TAGGAAAGACAGTCAAGAGATTTGATTTGAAGCTAGAGATTAGACACAGCTGGGCAAC 1620
 Db 1561 TAGGAAAGACAGTCAAGAGATTTGATTTGAAGCTAGAGATTAGACACAGCTGGGCAAC 1620
 QY 1621 GTATTAAGACCATGTCTATTAATAATTAATAATGAAGAAACAGAAATAGCTTATTTTCA 1680
 Db 1621 GTATTAAGACCATGTCTATTAATAATTAATAATGAAGAAACAGAAATAGCTTATTTTCA 1680
 QY 1681 AATATGAAGAAATTTATATGAATAATTAATCTGAGTCAATTAATTTCTTAAAGTAT 1740
 Db 1681 AATATGAAGAAATTTATATGAATAATTAATCTGAGTCAATTAATTTCTTAAAGTAT 1740
 QY 1741 ACTTTTGAAGTACATTAATGAGCTAGAGTCCAGATTAATGATGATATCATGCAAT 1800
 Db 1741 ACTTTTGAAGTACATTAATGAGCTAGAGTCCAGATTAATGATGATATCATGCAAT 1800
 QY 1801 AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1849
 Db 1801 AAATTTGCAAAACATCATCTTAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1849

Search completed: April 17, 2004, 18:46:51
 Job time : 773 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 10:11:17 ; Search time 147 Seconds

(without alignments)
6980.301 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctagagcgcgcgtagcatg.....aaaaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

5: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

6: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

7: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

8: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

9: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

10: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

11: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

12: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

13: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

14: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

15: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

16: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

17: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

18: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

19: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

20: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

21: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

22: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

23: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

24: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

25: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

26: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

27: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	454.6	24.6	480	4	US-09-621-976-57
2	96	5.2	3590	1	US-08-587-889-1
3	96	5.2	3590	4	US-09-016-434-1093
4	96	5.2	3590	5	PCT-US96-09193-1
5	94.6	5.1	813	4	US-09-288-143-30
6	94.2	5.1	15231	3	US-09-128-155-16
7	94	5.1	64467	4	US-09-803-6718-3
8	93.8	5.1	81001	4	US-09-750-580-1
9	93.2	5.0	7680	4	US-09-210-748A-3
10	92.6	5.0	1014	4	US-09-257-179-32
11	92.6	5.0	43950	4	US-09-735-934A-3
12	92.6	5.0	43950	4	US-10-060-332-3
13	92	5.0	391	4	US-09-621-976-14255
14	91.8	5.0	66804	4	US-09-740-041-3
15	91.4	4.9	533	1	US-08-049-283A-1
16	90.6	4.9	1061	4	US-09-489-847-88
17	90	4.9	330	3	US-09-078-294-24
18	90	4.9	1001	4	US-09-671-317-238
19	90	4.9	1001	4	US-09-671-317-239
20	89.8	4.9	4066	4	US-09-367-750-1
21	89.8	4.9	99500	4	US-09-798-096-10
22	89.4	4.8	444	4	US-09-621-976-12675
23	89.2	4.8	1354	4	US-09-620-312D-308
24	89.2	4.8	3117	4	US-09-146-580-6
25	89.2	4.8	59065	4	US-09-813-817-3
26	89.2	4.8	59065	4	US-09-978-197-3
27	89	4.8	2923	1	US-08-480-449-1

C	28	89	4.8	2923	2	US-08-660-542-1	Sequence 1, Appl
C	29	89	4.8	2923	4	US-08-479-603-1	Sequence 1, Appl
C	30	89	4.8	2923	4	US-08-939-107-1	Sequence 1, Appl
C	31	89	4.8	2923	4	US-08-931-764-1	Sequence 1, Appl
C	32	89	4.8	2923	4	US-09-591-992-1	Sequence 1, Appl
C	33	89	4.8	2927	3	US-09-232-878-5	Sequence 5, Appl
C	34	89	4.8	62804	4	US-10-096-960-3	Sequence 3, Appl
C	35	89	4.8	62804	4	US-10-096-960-3	Sequence 3, Appl
C	36	88.4	4.8	45716	4	US-08-965-048-5	Sequence 5, Appl
C	37	88.4	4.8	45889	4	US-08-965-048-5	Sequence 5, Appl
C	38	88.4	4.8	66804	4	US-09-740-041-3	Sequence 6, Appl
C	39	88	4.8	16063	4	US-09-801-052-3	Sequence 3, Appl
C	40	88	4.8	16063	4	US-10-020-121-3	Sequence 3, Appl
C	41	87.6	4.7	2042	3	US-09-063-237-2	Sequence 2, Appl
C	42	87.6	4.7	2043	1	US-07-914-281-1	Sequence 1, Appl
C	43	87.6	4.7	2043	1	US-08-393-246-1	Sequence 1, Appl
C	44	87.6	4.7	2043	1	US-08-273-411-4	Sequence 1, Appl
C	45	87.6	4.7	2043	1	US-08-525-058A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1	US-09-621-976-57
Sequence 57, Application US/09621976	
Patent No. 6639063	
GENERAL INFORMATION:	
APPLICANT: Dumas Milne Edwards, J.B.	
APPLICANT: Giordano, J.Y.	
TITLE OF INVENTION: ESTS and Encoded Human Proteins.	
FILE REFERENCE: GENSET.054PR2	
CURRENT APPLICATION NUMBER: US/09/621,976	
CURRENT FILING DATE: 2000-07-21	
NUMBER OF SEQ ID NOS: 19335	
SOFTWARE: Patent.pm	
SEQ ID NO 57	
LENGTH: 480	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: CDS	
LOCATION: 27..479	
NAME/KEY: sig_peptide	
LOCATION: 27..83	
OTHER INFORMATION: Von Heljne matrix	
OTHER INFORMATION: score 8.80000019073486	
OTHER INFORMATION: seq SAVLSGFLVGLHA/FQ	
US-09-621-976-57	
Query Match	24.6%; Score 454.6; DB 4; Length 480;
Best Local Similarity	99.8%; Pred. No. 2.7e-106;
Matches 454; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
16 CATGAGGGGAGAGTACTGCTGCGGGTCTCGGGCTTTGTGCTCGGCACCTGCTT	75
26 SATGAGGGGAGAGTACTGCTGCGGGTCTCGGGCTTTGTGCTCGGCACCTGCTT	85
76 CCAGACCTTCAACGAGCTCGACACGAGAGTTTCTTCTGGGGAATGAAGTGA	135
86 CCAGACCTTCAACGAGCTCGACACGAGAGTTTCTTCTGGGGAATGAAGTGA	145
136 AGCAAGAACGACTTACTGATTCCTCAATGATGATGAAGTTGTTATCAATTGA	195
146 AGCAAGAACGACTTACTGATTCCTCAATGATGATGAAGTTGTTATCAATTGA	205
196 CATTCAGAAATATTTCCATGCTATTCAGCTTTTATGTTTATTAATCTTCAAGGAGT	255
206 CATTCAGAAATATTTCCATGCTATTCAGCTTTTATGTTTATTAATCTTCAAGGAGT	265
256 AATGACCAAGCACTGAAGAAATATTTATCAAAATGTCAAAAGATGTGATGTTGTA	315

Db 266 AATGAGCAAGCAGTGAAGAAAATATTATCAAAATGTGTAGTTGGTA 325
QY 316 CAAATCCGTCGTCATTCAGATCAGATCAGTGAAGAGGCGCTCCACAAAA 375
Db 326 CAAATTCGTCGTCATTCAGATCAGATCAGTGAAGAGGCGCTCCACAAAA 385
QY 376 CTTCAGAGACATTTTCAAAACCAAGACCTTTTCTATTATTAACCAAGTAAAT 435
Db 386 CTTCAGAGACATTTTCAAAACCAAGACCTTTTCTATTATTAACCAAGTAAAT 445
QY 436 AACGAAAGCTGCTACTACATCAGATGGAACCT 470
Db 446 AACGAAAGCTGCTACTACATCAGATGGAACCT 480

RESULT 2

US-08-587-889-1
Sequence 1, Application US/08587889
Patent No. 5634397
GENERAL INFORMATION:
APPLICANT: CAO, Zhaodan
APPLICANT: CROSTON, Glenn E.
APPLICANT: GOEDDEL, David V.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,889
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-60916
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3590 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-587-889-1

Query Match 5.2%; Score 96; DB 1; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 135; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1458 CACCTTCACTAAGTTGTTAGAGGGAAGGCTTACACAGACATCTTTAGAAATGAAA 1517
Db 2623 CACCTTCACAAATGGGGCCACGAGGCGCTAGGGCCCTCTACCTTACAAATTTGAAA 2682
QY 1518 AGTAGAGCCAGGCACTAGGCTCACACCTGAATCCAGACCTTAGGAGAACAGTCAG 1577
Db 2683 AGTAGAGCCAGGCTAGGCTCACACCTGAATCCAGACCTTTGGAGGCCAAGCAG 2742
QY 1578 GAGGATGATGAAGCTAGAGATTAGAGACCAAGCTGGGCAACGTATGAGACCATGCT 1637

Db 2743 GAGGATGCTGAGGCCAGCTAGGTCAAGACCAAGGCAAGATGAGACCTGTCT 2802
QY 1638 ATTAAAAATAAATGAAA 1657
Db 2803 CTGCCAAAAATTTTAAA 2822

RESULT 3

US-09-016-434-1093
Sequence 1093, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Selthamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1093:
SEQUENCE CHARACTERISTICS:
LENGTH: 3590 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91220312
US-09-016-434-1093

Query Match 5.2%; Score 96; DB 4; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 135; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1458 CACCTTCACTAAGTTGTTAGAGGGAAGGCTTACACAGACATCTTTAGAAATGAAA 1517
Db 2623 CACCTTCACAAATGGGGCCACGAGGCGCTAGGGCCCTCTACCTTACAAATTTGAAA 2682
QY 1518 AGTAGAGCCAGGCACTAGGCTCACACCTGAATCCAGACCTTAGGAGAACAGTCAG 1577
Db 2683 AGTAGAGCCAGGCTAGGCTCACACCTGAATCCAGACCTTTGGAGGCCAAGCAG 2742
QY 1578 GAGGATGATGAAGCTAGAGATTAGAGACCAAGCTGGGCAACGTATGAGACCATGCT 1637
Db 2743 GAGGATGCTGAGAGCCAGTGTCAAGACCAAGGCAAGCATGATGAGACCATGCT 2802
QY 1638 ATTAAAAATAAATGAAA 1657

Db 2803 CTGCCAAAAATTTTAA 2822

```
RESULT 4
PCT-US96-09193-1
; Sequence 1, Application PC/TUS9609193
; GENERAL INFORMATION:
; APPLICANT: Tularik, Inc.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
; TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBERTSON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09193
; FILING DATE: JUNE 5 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 08/587,889
; FILING DATE: JAN 16 1996
; CLASSIFICATION:
; APPLICATION NUMBER: U.S. Serial No. 08/494,006
; FILING DATE: JUNE 23 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Brezner
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: FP-62191-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US96-09193-1
```

```
Query Match 5.2%; Score 96; DB 5; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 15; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
```

```
QY 1458 CACCTTTCACTAGTGTGAGGGGAAGCTTACACAGACATTTAGATTGAAA 1517
Db 2623 CACCTTGCACAAATGGGGCCGACAGGCTAGGCTCTCTACTGTTCAATTTGAAA 2682
QY 1518 AGTGAACCAAGGACAGTGGCTACACCTGTAAATCCAGACTTGGGAAAGCAAGTCAG 1577
Db 2683 AGTGTGGCCGGGCGCGGTGCTCACCGCTGTATCCACACCTTGGGAGGCCAAGGCAAG 2742
QY 1578 GAGGATTTAGATTGAGTAGAGTTAGACCAAGCCTGGGCAAGTATTAGACCAATGCT 1637
Db 2743 GAGGATCGCTGGAGCCCAAGTAGTCAAGACCAAGCCAGGCAATGATGAGACCTGTCT 2802
QY 1638 ATTAAAAAATTAATGAAA 1657
Db 2803 CTGCCAAAAATTTTAA 2822
```

RESULT 5

```
US-09-288-143-30
; Sequence 30, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (691)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-288-143-30
```

```
Query Match 5.1%; Score 94.6; DB 4; Length 813;
Best Local Similarity 75.2%; Pred. No. 1.4e-14;
Matches 118; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 1501 TTCTTAGAATTGAAAAGTGAAGCCAGCAAGTGGCTACACCTGTAATCCAGACT 1560
Db 479 TTCAATATATAGAGAAAGTTAGGCGAGATCCAGTGGCTCACCTGTAAATCCAACTT 538
QY 1561 TAGGAAAGACAAAGTCAGAGAGATTGATTGAAGCTTAGAGATTAGACCAAGCTGGCAAC 1620
Db 539 TTGGGAATCCAGGCAAGAGATGCTTTAGCCTTAGAGATTGAGACCAAGATGGCAAC 598
QY 1621 GTATTGAGCATCTCTATTAAAAAATTAATGAAA 1657
Db 599 ATAAACAAGACCTGTCTCTACTAAAAAATAATAA 635
```

```
RESULT 6
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
;; SEQ ID NO 16
;; LENGTH: 152331
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(152331)
;; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
```

```
Query Match
Best Local Similarity 70.4%; Score 94.2; DB 3; Length 152331;
Pred. No. 2e-13;
Matches 126; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
QY 1487 CTTCACACACACATCTTTAGAAATGGAAGTGGACAGCAGTGGCTCAGACCT 1546
DB 49282 CTCACACATACAGAGCTACATTTAAACAACTAATGAGCCAGGCGAGTGGCTCAGACCT 49341
QY 1547 GTAATCCAGCAGCTTAGGAGAGCAAGTCAGAGAGATTGAAAGTAACTAGAGTTAGAGA 1606
DB 49342 GTAATCCAGCAGCTTAGGAGAGCAAGTCAGAGAGATTGAAAGTAACTAGAGTTAGAGA 49401
QY 1607 CCAAGCTGGGCAACGATTTAGAGCCATGCTCTTAAATAATGAAAGCAAGAA 1665
DB 49402 CCAAGCTGGGCAACGATTTAGAGCCATGCTCTTAAATAATGAAAGCAAGAA 49460
```

RESULT 7

```
US-09-803-671B-3
; Sequence 3, Application US/09803671B
; Patent No. 6582946
```

```
;; GENERAL INFORMATION:
;; APPLICANT: WEBSTER, Marion et al
;; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: CL001161
;; CURRENT APPLICATION NUMBER: US/09/803,671B
;; CURRENT FILING DATE: 2001-03-12
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 64467
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(64467)
;; OTHER INFORMATION: n = A,T,C or G
US-09-803-671B-3
```

```
Query Match
Best Local Similarity 71.3%; Score 94; DB 4; Length 64467;
Pred. No. 1.5e-13;
Matches 124; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
```

```
QY 1507 AGAATTGAAAGTGAAGCAGGACAGTGGCTCAGACCTGTATCCAGCACTTAGGGA 1566
DB 34449 AAAACAAGGAGAGGAGGAGCCAGGCTGCTCAGACCTGGAATCCAGAACTTTGGGA 34508
QY 1567 AGACAAGTCAGAGAGATTGATTTAGAGTGAAGATTAGAGACCCGCTGGGCAACGATNTG 1626
DB 34509 AGCCAGAGAGGAGAGATTGTTGAGCTTAGAGATTGAGCCAGCTGGGCAATACAGTA 34568
QY 1627 AGACCATGTCTATTTAAATAATGAAAGCAAGATAGCCTTATTTTCA 1680
DB 34569 AGACCCGTCTATTAACAAAATTTAAATAATTTTAAATAATAGCA 34622
```

```
RESULT 8
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
```

```
;; APPLICANT: Yen, Frances
;; APPLICANT: Denison, Blake
;; APPLICANT: Bour, Barbara
;; APPLICANT: Bluhm, Bernard
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;; APPLICANT: Duclert, Aymeric
;; APPLICANT: Bougueleret, Lydie
;; APPLICANT: Ebbets-Reed, Dana
;; APPLICANT: Salter-Cid, Luisa
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
;; FILE REFERENCE: 89. US2. CIP
;; CURRENT APPLICATION NUMBER: US/09/750,580
;; CURRENT FILING DATE: 2000-12-28
;; PRIOR APPLICATION NUMBER: US 09/599,362
;; PRIOR FILING DATE: 2000-06-21
;; PRIOR APPLICATION NUMBER: PCT/IB00/0101
;; PRIOR FILING DATE: 2000-06-21
;; PRIOR APPLICATION NUMBER: PCT/IB99/02058
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: US 49/469/099
;; PRIOR FILING DATE: 1999-12-21
;; PRIOR APPLICATION NUMBER: US 60/113,686
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: US 60/141,032
;; PRIOR FILING DATE: 1999-06-25
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: Patent.pm
;; SEQ ID NO 1
;; LENGTH: 81001
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 10946..12946
;; OTHER INFORMATION: 5'regulatory region
;; NAME/KEY: exon
;; LOCATION: 12947..12958
;; OTHER INFORMATION: exon 1
;; NAME/KEY: exon
;; LOCATION: 13470..13526
;; OTHER INFORMATION: exon 2
;; NAME/KEY: exon
;; LOCATION: 13641..13752
;; OTHER INFORMATION: exon 3
;; NAME/KEY: exon
;; LOCATION: 14271..15968
;; OTHER INFORMATION: exon 4
;; NAME/KEY: misc_feature
;; LOCATION: 15969..17969
;; OTHER INFORMATION: 3'regulatory region
;; NAME/KEY: allele
;; LOCATION: 1239
;; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
;; NAME/KEY: allele
;; LOCATION: 12347
;; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
;; NAME/KEY: allele
;; LOCATION: 15241
;; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
;; NAME/KEY: allele
;; LOCATION: 42218
;; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
;; NAME/KEY: allele
;; LOCATION: 45442
;; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
;; NAME/KEY: allele
;; LOCATION: 77058
;; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
;; NAME/KEY: primer_bind
;; LOCATION: 929..949
;; OTHER INFORMATION: 20-828-pu
;; NAME/KEY: primer_bind
;; LOCATION: 1357..1377
```

```
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
```

```
NAME/KEY: misc binding
LOCATION: 15225..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match
Best Local Similarity 73.9%; Pred. No. 1.9e-13;
Matches 119; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
```

```
Qy 1503 CTTTGAATTTGAAAGTGAACGAGGACAGTGGCTCAACCTGTATCCGCACTTA 1562
Db 893 CTTTATCATTTAAATTTTGAAGCTGGGACAGTGGCTCAACCTGTATCCGCACTTT 834
Qy 1563 GGAAGACAAAGTCAGAGGATTTGATTGAGCTAGAGTGAAGCCAGCTGGGCAAGT 1622
Db 833 GAGAAGCAAGGAGGAGGAGTGGCTTGAAGCCAGGAGTTGATTCAGAGCTGGGCAATGT 774
Qy 1623 ATTGAGACATGTCTATTAAATTAATGAAGCAAG 1663
Db 773 AGCAGACCCCTGTCTGCAAAAGATTCAAAATTAAGCCAG 733
```

```
RESULT 9
US-09-210-748A-3
Sequence 3, Application US/09210748A
Patent No. 6335156
GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107.77810
CURRENT APPLICATION NUMBER: US/09/210.748A
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/069,416
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 7680
TYPE: DNA
ORGANISM: Homo sapiens
US-09-210-748A-3
```

```
Query Match
Best Local Similarity 79.7%; Pred. No. 8.9e-14;
Matches 110; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
```

```
Qy 1523 GACCAGGACAGTGGCTCAACCTGTATCCGCACTTGAAGGACAAAGTCAGAGGA 1582
Db 6293 GGCAGGTGTAGTACTCACACCTGTATCCGCACTTGGGAAAGCCAGAGGA 6352
Qy 1583 TTGATTGAAGTGAAGTGAAGCCAGCTGGGCAAGTATGAGCAATGTCTATTAA 1642
Db 6353 TTGCTTGAACCAAGTTGAGACAGCTTGGGCAACATGATGAGCCTGTCTACA 6412
Qy 1643 AAAATTAATGAAAAGC 1660
Db 6413 AAAATACAAAATTAAGC 6430
```

```
RESULT 10
US-09-257-179-32
Sequence 32, Application US/09257179
```


Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29. Human Secreted Proteins
FILE REFERENCE: P2015PL
CURRENT APPLICATION NUMBER: US/09/257,179
EARLIER FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
US-09-257-179-32

Query Match
Best Local Similarity 5.0%; Score 92.6; DB 4; Length 1014;
Best Local Similarity 68.4%; Pred. No. 4,9e-14;
Matches 128; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1507 AGAATGGAAGTGAAGACGAGGACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
DB 19 AACTTAAATAATGCGCCAGCATAGTCTCATGCTGTAATCTTAAGCAATTGGGA 78
QY 1567 AGACAAAGTCAGAGATTGATTGAAGCTTAGAGAGACCAAGCTGGGCAAGCTATG 1626
DB 79 GGGCGAGCGCGAGATCCCTGAATCCAGAGATTCAGACCAAGCTGGGCAAGCACTG 138
QY 1627 AGACCTGTCTATTAATAATAATGAAGAAAGCAAGATACCTTATTTCAAAATNG 1686
DB 139 AGACCTGTCTATTAATAATAATGAAGAAATTAATTAATTTTGTATTAACCA 198
QY 1687 GAAAGAA 1693
DB 199 CAAAAA 205

RESULT 11
US-09-735-934A-3
Sequence 3, Application US/09735934A
Patent No. 6372468
GENERAL INFORMATION:
APPLICANT: Li, Jiajin et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C1000851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 43950
TYPE: DNA
ORGANISM: Homo sapiens
US-09-735-934A-3

Query Match
Best Local Similarity 5.0%; Score 92.6; DB 4; Length 43950;
Best Local Similarity 73.0%; Pred. No. 2,9e-13;
Matches 119; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1501 TTCTTAGAATTGGAAGTGAAGACGAGGACAGTGGCTCACACCTGTATCCAGCACT 1560
DB 4215 TTAAATATAAGTAAATAATGCGCCAGCTGAGTGGCTCACACCTGTATCCAGCACT 4274

QY 1561 TAGGAAGACAAGTCAGAGATTGATTGAAGTGAAGTGAAGACCAAGCAAGCTGGGCAAC 1620
DB 4275 TTGGAGGCTGAGAGTGGAGATCGCTGAGAGCCCGAGATTTGAAGCCAGGCTGGGCAAC 4334
QY 1621 GTATTGAGACCATGTCTATTAAATAATAATGAAGAAAGCAAG 1663
DB 4335 ATAGAGAGACCCCATCTTTAAAAAAGG 4377
RESULT 12
US-10-060-332-3
Sequence 3, Application US/10060332
Patent No. 6528294
GENERAL INFORMATION:
APPLICANT: Li, Jiajin et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C1000851DIV
CURRENT APPLICATION NUMBER: US/10/060,332
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 43950
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-332-3

Query Match
Best Local Similarity 5.0%; Score 92.6; DB 4; Length 43950;
Best Local Similarity 73.0%; Pred. No. 2,9e-13;
Matches 119; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1501 TTCTTAGAATTGGAAGTGAAGACGAGGACAGTGGCTCACACCTGTATCCAGCACT 1560
DB 4215 TTAAATATAAGTAAATAATGCGCCAGCTGAGTGGCTCACACCTGTATCCAGCACT 4274
QY 1561 TAGGAAGACAAGTCAGAGATTGATTGAAGTGAAGTGAAGACCAAGCTGGGCAAC 1620
DB 4275 TTGGAGGCTGAGAGTGGAGATCGCTGAGAGCCCGAGAGTTGAAGCCAGGCTGGGCAAC 4334
QY 1621 GTATTGAGACCATGTCTATTAAATAATAATGAAGAAAGCAAG 1663
DB 4335 ATAGAGAGACCCCATCTTTAAAAAAG 4377

RESULT 13
US-09-621-976-14255
Sequence 3, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14255
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-14255

Query Match
Best Local Similarity 5.0%; Score 92; DB 4; Length 391;
Best Local Similarity 72.6%; Pred. No. 4,4e-14;
Matches 119; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1503 CTTTAGAATTGGAAGTGAAGACGAGGACAGTGGCTCACACCTGTATCCAGCACTTA 1562

Mon Apr 19 12:46:08 2004

us-10-063-523-21.rn1

Page 7

Db 78 CTATTGAATCTCAAGAGCTGGCCAGTGCAGTGCCTCAAGCTTAAATCCAGCACTTT 137
Qy 1563 GGGAGACAAAGTCAGAGAGTATGATTGAAGCTAGAGATTAGACCACTGGGCAAGCT 1622
Db 138 GGGAGAGCCAGAGCGGGGTGATGTTCTGAGCTCAGAGATTCCAGACCACTGGGCAAGCT 197
Qy 1623 ATTGAGACCATGTCTATTAAAAATTAATGAAGAAAGCAAGAT 1666
Db 198 AGTGAACCCGCTCTCTACTGAAATACAAAACAAAACAAAAT 241

RESULT 14
US-09-740-041-3/c
Sequence 3, Application US/09740041
Patent No. 6562593
GENERAL INFORMATION:
APPLICANT: MERKULOV, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001001
CURRENT APPLICATION NUMBER: US/09/740,041
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 66804
TYPE: DNA
ORGANISM: Human
US-09-740-041-3

Query Match 5.0%; Score 91.8; DB 4; Length 66804;
Best Local Similarity 73.6%; Pred. No. 5.7e-13;
Matches 117; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 1505 TTAGATTGAAAAGTGAAGACCAAGCAAGTGGCTCAGCACTGTATCCAGCACTTAG 1564
Db 51491 TTAATAATTAATTAAGCAAGCCAGGCGAGGTGGCTCATGCTGTATCCAGCACTTAG 51432
Qy 1565 GAAGCAAGTCAAGAGATTTGATTGAAGTGAAGTGAAGCCAGCTGGGCAAGCTAT 1624
Db 51431 AAGGCGAGCGCGGCGATTAATTGAGTCAAGAGTTGAAGCCAGCTGGGCAATATAG 51372
Qy 1625 TGAGACCATGTCTATTAAAAATTAATGAAGAAAGCAAG 1663
Db 51371 TGAAACCTGTCTCTACAAAATTAAGAAATTAAGCAG 51333

RESULT 15
US-08-049-283A-1/c
Sequence 1, Application US/08049283A
Patent No. 5502176
GENERAL INFORMATION:
APPLICANT: Teren, Daniel G.
APPLICANT: Paul, Helke U.
APPLICANT: Burt, Timothy C.
TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,283A
FILING DATE: 14-APR-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,465
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/837,776
FILING DATE: 13-FEB-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: B1H91-03/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-049-283A-1

Query Match 4.9%; Score 91.4; DB 1; Length 533;
Best Local Similarity 67.7%; Pred. No. 7.3e-14;
Matches 128; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Qy 1460 CCTTCACTAAGTTGTTAGGGGAGGCTTACACAGACATCTTAGATTGAAAAG 1519
Db 190 CATATGACAGAGTGAATATAGCTTAGGCTCCCTCGGAATGTGTCTAAACATTAAT 131
Qy 1520 TGAGACCAAGCAAGTGGCTCAGCACTGTATATCCAGCACTTAGGGAAGCAAGTCAAG 1579
Db 130 ACGGCGCAGCGAGAGTGGCTCAGCCTGTATATCCAGCACTTTGGAGGCGCAAGGAGGA 71
Qy 1580 GAATTGATTGAAGCTAGAGTGAAGCCAGCTGGGCAAGCTATTGAGACATGTCTAT 1639
Db 70 GGAATGCTTAGGCTGGAGATTGAAACAGCCTGGGCAACATAGAGAGACCTGTCTCT 11
Qy 1640 TAAAAATA 1648
Db 10 ACAAATAA 2

Search completed: April 16, 2004, 11:20:20
Job time : 155 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 21:04:36 ; Search time 4891 Seconds

(without alignments)
11312.266 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctagagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estrom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pln:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rnd:*
26: em_gse_png:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	852	46.1	883	BQ21560	BQ21560 AGENCOURT
2	791.8	42.8	1018	BM479419	BM479419 AGENCOURT
3	771.8	41.7	2500	AK051816	AK051816 Mus muscu
4	757.4	41.0	1078	BQ216065	BQ216065 AGENCOURT

5	701.4	37.9	703	13	EX089041	EX089041
6	696.8	37.7	1599	11	AK042001	AK042001 Mus muscu
7	696.8	37.7	1599	11	AK042339	AK042339 Mus muscu
8	681.8	36.9	736	9	AU125653	AU125653
9	681.4	36.9	1606	11	AK014420	AK014420
10	671.4	36.3	789	13	BQ221128	BQ221128
11	658.6	35.6	665	14	CA429280	CA429280
12	654.2	35.4	778	12	BG570593	BG570593
13	649.2	35.1	665	12	BQ019837	BQ019837
14	648	35.0	744	12	BG311177	BG311177
15	646	34.9	701	12	B1909258	B1909258
16	635.2	34.4	688	10	BE888265	BE888265
17	616.8	33.4	620	14	CB135704	CB135704
18	616	33.3	706	12	B1771321	B1771321
19	613.6	33.2	1597	11	BC043923	BC043923
20	608	32.9	623	9	AL602519	AL602519
21	577.8	31.2	581	14	CB135111	CB135111
22	568.4	30.7	668	9	AU139555	AU139555
23	559.2	30.2	643	10	BF812538	BF812538
24	556.4	30.1	778	12	B1912725	B1912725
25	547.4	29.6	549	9	AA781435	AA781435
26	543.6	29.4	716	12	B1626210	B1626210
27	536.2	29.0	645	9	AU144581	AU144581
28	519.4	28.1	886	13	BQ422301	BQ422301
29	504.6	27.3	886	12	B1464110	B1464110
30	503.8	27.2	509	9	A1830957	A1830957
31	498.8	27.0	702	14	CD372794	CD372794
32	498	26.9	967	13	B1713601	B1713601
33	464	25.1	641	10	BB600368	BB600368
34	463.8	25.1	487	10	AM978650	AM978650
35	463	25.0	812	13	B0258945	B0258945
36	462.4	25.0	523	9	AM977201	AM977201
37	446	24.1	523	9	A1820814	A1820814
38	442	23.9	602	12	BC087655	BC087655
39	436.8	23.6	508	9	A1820815	A1820815
40	435	23.5	465	10	AM467456	AM467456
41	433.4	23.4	634	12	BG922020	BG922020
42	432.2	23.4	437	9	AA831922	AA831922
43	430.6	23.3	618	10	BB638750	BB638750
44	429	23.2	622	13	BY737205	BY737205
45	427.4	23.1	798	10	BF139015	BF139015
46	418.6	22.6	577	14	CF750268	CF750268
47	418.6	22.6	577	14	CF750268	CF750268
48	418.2	22.6	570	14	CA551388	CA551388
49	415.6	22.5	600	10	BB639240	BB639240
50	408	22.1	422	14	W51769	W51769
51	407.4	22.0	869	10	BF240591	BF240591
52	404.2	21.9	466	12	BM089787	BM089787
53	402.4	21.8	563	9	AU144027	AU144027
54	396.6	21.4	848	14	CB959860	CB959860
55	390.2	21.1	533	14	CAS54083	CAS54083
56	388.4	21.0	665	14	CF734052	CF734052
57	388.2	21.0	472	12	BM254410	BM254410
58	368.4	19.9	370	9	AA456838	AA456838
59	367.6	19.9	694	13	B0251196	B0251196
60	366.2	19.8	499	9	AA475460	AA475460
61	364	19.7	400	12	BG933348	BG933348
62	360	19.5	360	9	A1472709	A1472709
63	353.2	19.1	592	13	B0376799	B0376799
64	347.4	18.8	546	13	BX520913	BX520913
65	343	18.6	584	10	AW915167	AW915167
66	337.4	18.2	346	14	F08936	F08936
67	337.4	18.2	463	14	CAS52283	CAS52283
68	335.6	18.2	857	10	BF218805	BF218805
69	330.6	17.9	451	14	CF158609	CF158609
70	328	17.7	328	9	AA774511	AA774511
71	325.4	17.6	379	10	BF742611	BF742611
72	321.8	17.4	526	9	A1821443	A1821443
73	316.4	17.1	596	12	BM538053	BM538053
74	310.8	16.8	750	9	AJ453281	AJ453281
75	310.6	16.8	678	12	BJ617828	BJ617828
76	310	16.8	579	10	BE309999	BE309999
77	303.2	16.4	652	9	AA905493	AA905493

78 299.8 16.2 505 9 A1821445 ypl6d11.x
 79 299.4 16.2 377 14 R83736 ypl5h11.r1
 80 298.8 16.2 466 10 BB858985 BB858985
 81 297.8 16.1 427 9 AA880079 AA880079
 82 294 15.9 316 9 A1014808 A1014808
 83 288.8 15.6 619 12 B0613510 B0613510
 84 287.8 15.6 617 12 B094725 B094725
 85 286.6 15.5 350 10 AM315813 AM315813
 86 285.4 15.4 347 14 R83667 ypl6d11.r1
 87 279 15.1 592 12 B3625593 B3625593
 88 278.2 15.0 455 12 B331995 B331995
 89 276.2 14.9 371 13 B267461 B267461
 90 276 14.9 948 10 B894160 B894160
 91 270 14.6 950 13 B0901917 B0901917
 92 263 14.2 264 13 C01486 C01486
 93 262.2 14.2 686 9 AL635982 AL635982
 94 257.8 13.9 356 13 BY058043 BY058043
 95 253.8 13.7 469 14 R83653 ypl6d12.s1
 96 247.8 13.4 701 13 B847858 B847858
 97 246.4 13.3 940 13 B916415 B916415
 98 245.4 13.3 372 13 B3299482 B3299482
 99 232.6 12.6 841 13 B0311834 B0311834
 100 229 12.4 977 13 B0431082 B0431082

ALIGNMENTS

RESULT 1 883 bp mRNA linear EST 20-AUG-2002
 BQ921560
 LOCUS AGENCOURT 8959812 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6471798
 DEFINITION 5' mRNA Sequence.

ACCESSION BQ921560
 VERSION BQ921560.1 GI:22336591
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 883)
 NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL4004 row: 1 column: 07
 High quality sequence stop: 710.

FEATURES

Source

1. 883
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6471798"
 /tissue_type="leiomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN

Query Match 46.1%; Score 852; DB 13; Length 883;
 Best Local Similarity 98.4%; Pred. NO. 1.3e-119;
 Matches 869; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 295 AAAGAATGTGTAGTGTGTGTAACAATTCCTGTCATTTAGATCAGATCAGTTCGTTG 354
 Db 1 AAAGAATGTGTAGTGTGTGTAACAATTCCTGTCATTTAGATCAGATCAGTTCGTTG 60
 QY 355 AGAGAGGCTGCTTCACAAAAAGCTGAGAGAGATTTTCAAAACAAGACCTGTTTTC 414
 Db 61 AGAGAGGCTGCTTCACAAAAAGCTGAGAGAGATTTTCAAAACAAGACCTGTTTTC 120
 QY 415 GCTATTAAACCAAGATATATAACAGAAAGCTGCTTACTATCGATCGTGAACATTCCT 474
 Db 121 GCTATTAAACCAAGATATATAACAGAAAGCTGCTTACTATCGATCGTGAACATTCCT 180
 QY 475 ATATTAACCTCAAAAAGACCTTTTCAAGAGGATCTTAGTGTGTCATCTGGACATCTGGACAT 534
 Db 181 ATATTAACCTCAAAAAGACCTTTTCAAGAGGATCTTAGTGTGTCATCTGGACATCTGGACAT 240
 QY 535 GTCTGAACAACCTGGTTATTAACCTGTATCAGGTTCTGTATGTCATCTGTTTACCG 594
 Db 241 GTCTGAACAACCTGGTTATTAACCTGTATCAGGTTCTGTATGTCATCTGTTTACCG 300
 QY 595 AGAGATTAACAACACAGAGCTTAATTTTGAAGAAGATGATCCTTAAAGAGGTACA 654
 Db 301 AGAGATTAACAACACAGAGCTTAATTTTGAAGAAGATGATCCTTAAAGAGGTACA 360
 QY 655 TAAGATTAATGAATGTATGCTTCAATTAACAAGAAATTAAGATTAATGAATGAAT 714
 Db 361 TAAGATTAATGAATGTATGCTTCAATTAACAAGAAATTAAGATTAATGAATGAAT 420
 QY 715 GGAAGACAGTGAACAAGCAGTATATACTAGTAAGATTAAGATTAAGATTAAGATTAAG 774
 Db 421 GGAAGACAGTGAACAAGCAGTATATACTAGTAAGATTAAGATTAAGATTAAGATTAAG 480
 QY 775 AATTGAAGAAAGAGAGAGACAGATTCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAG 834
 Db 481 AATTGAAGAAAGAGAGAGACAGATTCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 835 CCTCAGAGAGACATTTTCTTTGTCAAGGATTAAGGACCTTTTCCAAATCTGAAT 894
 Db 541 CCTCAGAGAGACATTTTCTTTGTCAAGGATTAAGGACCTTTTCCAAATCTGAAT 600
 QY 895 TCTTCATTCAATGTGTATGCTTTTAAATAAGACATGTTCTTAAAGTATGCTGTAATA 954
 Db 601 TCTTCATTCAATGTGTATGCTTTTAAATAAGACATGTTCTTAAAGTATGCTGTAATA 660
 QY 955 CAACCAACATCTGATGTATGATCAATCTGACCTTAATGTATGAACACACCTGACCTTC 1014
 Db 661 CAACCAACATCTGATGTATGATCAATCTGACCTTAATGTATGAACACACCTGACCTTC 720
 QY 1015 TGAAGCTAGTCCAGCTAGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGA 1074
 Db 721 TGAAGCTAGTCCAGCTAGTACACCAAAATCATTAAGCATTAAGCCTTAGACTTAGATGA 780
 QY 1075 CAGATGCAATTCAGAGATCTCGGTTGTTAGATACAGAGCAAAAGCATTTAAAGCAA 1133
 Db 781 CAGATGCAATTCAGAGATCTCGGTTGTTAGATACAGAGCAAAAGCATTTAAAGCAA 840
 QY 1134 ATACTGTAAGTATTAACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 1176
 Db 841 ATACTGTAAGTATTAACCAAGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCAT 883

RESULT 2
 BQ479419 1018 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT 6418807 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502357
 DEFINITION 5' mRNA Sequence.
 ACCESSION BQ479419
 VERSION BQ479419.1 GI:18528461
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1018)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
 Plate: LLNL2140 row: f column: 22
 High quality sequence stop: 634.
 Location/Qualifiers
 1..1018
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5502357"
 /issue_type="retinoblastoma"
 /lab_host="PH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN
 Query Match 42.8%; Score 791.8; DB 12; Length 1018;
 Best Local Similarity 97.0%; Pred. No. 1.5e-110;
 Matches 839; Conservative 0; Mismatches 22; Indels 4; Gaps 3;

QY 20 GAGGGGAGAGTACGCGCGGCTCTCGGCTTTGGCTGGGCGACCTGCTTCAG 79
 DB 1 GAGGGGAGAGTACGCGCGGCTCTCGGCTTTGGCTGGGCGACCTGCTTCAG 60
 QY 80 CACCTCAACACGCGACTCGACACGGAAGGTTTCTTCTGGGGAAGTAAGAGTAAAGCC 139
 DB 61 CACCTCAACACGCGACTCGACACGGAAGGTTTCTTCTGGGGAAGTAAGAGTAAAGCC 120
 QY 140 AAGAAAGAGTATCTATTCCTCCAAATGATGATGTAAGTGTATTAATCAATTGACAT 199
 DB 121 AAGAAAGAGTATCTATTCCTCCAAATGATGATGTAAGTGTATTAATCAATTGACAT 180
 QY 200 CAGAAATATATTCATGCTATCAAGCTTTTATGCTTTATATTTCTTCAAGCGAAGTAAT 259
 DB 181 CAGAAATATATTCATGCTATCAAGCTTTTATGCTTTATATTTCTTCAAGCGAAGTAAT 240
 QY 260 GAGCAAGCACTGAAGAAATATTTATCAATGTCAAAAGATGTGTAGTGTGTAACAA 319
 DB 241 GAGCAAGCACTGAAGAAATATTTATCAATGTCAAAAGATGTGTAGTGTGTAACAA 300
 QY 320 TTCCTGCGCAATTCAGATCAGATCATGAGCTTTAGAGAGAGGCTGCTTCAAAAACCTTG 379
 DB 301 TTCCTGCGCAATTCAGATCAGATCATGAGCTTTAGAGAGAGGCTGCTTCAAAAACCTTG 360
 QY 380 CAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATTAACCAACCAATTAATTAACA 439
 DB 361 CAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATTAACCAACCAATTAATTAACA 420
 QY 440 GAAAGTGTCTACTATGAGTGAACATTCCTTAATAAAGCTCAAAAAGAGCTTTT 499
 DB 421 GAAAGTGTCTACTATGAGTGAACATTCCTTAATAAAGCTCAAAAAGAGCTTTT 480
 QY 500 CACAGGGTACTTTAGTGTGCGCAATCTGGGCAATCTGAAACAATGGTATTAATAACT 559
 DB 481 CACAGGGTACTTTAGTGTGCGCAATCTGGGCAATCTGAAACAATGGTATTAATAACT 540
 QY 560 GTATCGGTTCCGTATGTCACATGTTTAAAGCGAGTCAAAACACAGCTCTAA 619
 DB 541 GTATCGGTTCCGTATGTCACATGTTTAAAGCGAGTCAAAACACAGCTCTAA 600

QY 620 TTTTGAAGAGATGATCCTTAAGAGAGTACATTAAGTAATGATGATGCTTCA 679
 DB 601 TTTTGAAGAGATGATCCTTAAGAGAGTACATTAAGTAATGATGATGCTTCA 660
 QY 680 TTACAGAGAGAAATTAAGATATATGCAAAAAGTGAAGACAGTGAACAGAGTAGAT 739
 DB 661 TTACAGAGAGAAATTAAGATATATGCAAAAAGTGAAGACAGTGAACAGAGTAGAT 720
 QY 740 AAACCTAAGAGATGTAACAGATTAACAGAAATTTAG-AAAAGAGAGAGACACA 798
 DB 721 AAACCTAAGAGATGTAACAGATTAACAGAAATTTAG-AAAAGAGAGAGACACC 780
 QY 799 GATTCAGGCA-GCAGAGAGAGAGACATCCAAAAGACCTCGAGG-AGAACATTTTCT 855
 DB 781 GATTCAGGCA-GCAGAGAGAGAGACATCCAAAAGACCTCGAGGAGAACATTTTCT 840
 QY 856 TTGTGAGGCAATTACGGAACCTTTT 880
 DB 841 TTGTGAGGCAATTACGGAACCTTT 865

RESULT 3
 AK051816
 LOCUS
 DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23004N03 product:hypothetical protein, full insert sequence.
 ACCESSION AK051816
 VERSION AK051816.1 GI:26342235
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, J., Nishii, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer
 Nature 409, 685-690 (2001)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	1260	-----TTTCTTACTGACTGAGGTTTCGGGCACTGTTTATTTTACTCTTTCGCTTCTG	1315									
Qy	1326	GCTACTTGACAGTACTTATTTGTTTACTATGTCACCTGTTTGACGTA	1376									
Db	1316	GATTAAATACA-CAGAAAGTTGGTTTACTATCTATTCACCTGTTGTATA	1365									
RESULT 4	LOCUS	BO216065	1078 bp	mRNA	linear	EST 02-MAY-2002						
	DEFINITION	AGENCOURT_7595259 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042359										
	ACCESSION	BO216065										
	VERSION	BO216065.1	GI:20397465									
	KEYWORDS	EST.										
	SOURCE	Homo sapiens (human)										
	ORGANISM	Homo sapiens										
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
	AUTHORS	1 (bases 1 to 1078)										
	TITLE	NIH-MGC http://mgc.nci.nih.gov/.										
	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)										
	COMMENT	Unpublished (1999)										
		Contact: Robert Strausberg, Ph.D.										
		Email: cgaabs-remail.nih.gov										
		Tissue Procurement: ATCC										
		cDNA Library Preparation: Life Technologies, Inc.										
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)										
		DNA Sequencing by: Agencourt Bioscience Corporation										
		Clone distribution: MGC clone distribution information can be										
		found through the I.M.A.G.E. Consortium/LNL at:										
		http://image.lnl.gov										
		Plate: L1AM13281 row: 24										
		High quality sequence stop: 494.										
FEATURES	location	sequence	stop: 494.									
SOURCE	location	sequence	stop: 494.									
	1..1078											
	/organism="Homo sapiens"											
	/mol_type="mRNA"											
	/db_xref="taxon:9606"											
	/clone="IMAGE:6042359"											
	/tissue_type="Embryonal carcinoma, cell line"											
	/lab_host="RDH10B (phage-resistant)"											
	/clone_lib="NIH_MGC_92"											
	/note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."											
ORIGIN												
	Query Match	41.0%	Score 757.4;	DB 13;	Length 1078;							
	Best Local Similarity	94.9%;	Pred. No. 2.3e-105;									
	Matches 838;	Conservative 0;	Mismatches 36;	Indels 9;	Gaps 5;							
Qy	7	CGGCGGTAGCATGAGGGGAGAGTACGTCGCGCGTGTCTCGGGCTTGTGCTCGGGC	66									
Db	1	CGGCGGTAGCATGAGGGGAGAGTACGTCGCGCGTGTCTCGGGCTTGTGCTCGGGC	60									
Qy	67	ACTGCGTTTCAGACCTCAACAGGACTCGGACCGGAAAGTTTCTTCTTG										

D	b		241	AGGGGAAGTAATGACGAAGCACTGAAAGAAAATTATCAAATGCACAAAAAAGATGTGCT	300
Oy			307	AGTTTGTTACAATAATTCGTGCTCATTTCAATCAGATCATGACGTTTTAGAGAGAAGCGTCT	366
D	b		301	AGGTTGGTACAAATTTCCGTGCTCATTTAGATCAACATCATGACGTTTAGAGAGAAGCGTCT	360
Oy			367	TCAAAAACCTCTGACGAGGACATTTTCAAAACCAGAACCTTTCTTTTTCGCATTATPACAC	426
D	b		361	TCAABAAACTCTGACGAGGACATTTTCAAAACCAGAACCTTTTTCGCATTATPACAC	420
Oy			427	AAGTATATATAACAGAAAAGCTGCTCTACTCATGACCTGGACATTTCTTATATPAACCTCA	486
D	b		421	AAGTATATATAACAGAAAAGCTGCTCTACTCATGACCTGGACATTTCTTATATPAACCTCA	480
Oy			487	AAAGGACTTTTTCACAGGGGTACCTTTAGTGGTGGCCAATCGGGCAATGCTGSAACACT	546
D	b		481	AAAGGACTTTTTCACAGGGGTACCTTTAGTGGTGGCCAATCGGGCAATGCTGSAACACT	540
Oy			547	GGGTTATPAAAAGCTGTATCAGGTTCCGTATGCTCCACTGGTTTAAAGCCAGACGATPACAAAC	606
D	b		541	GGGTTATPAAAAGCTGTATCAGGTTCCGTATGCTCCACTGGTTTAAAGCCAGACGATPACAAAC	600
Oy			607	ACACAGCTCTAAATTTTGTGAAGAAGATGAT - CCTTAAAGAGGTACATTAAGATPAATG	665
D	b		601	ACACAGCTCTAAATTTTGTGAAGAAGATGATCCTTTAAAGAGGTACATTAAGATPAATG	660
Oy			666	AAATGTATGCTTCATTAACAAGAGATTTAAAGATATATGCAAAAAAGTGGAAACAGCTG	725
D	b		661	AAATGTATGCTTCATTAACAAGAGATTTAAAGATATATGCAAAAAAGTGGAAACAGCTG	720
Oy			726	AACAAGCATGTATGATTAACCTA-GTAAAGATGTAAACGATTA-AAACAGAAATTGAGAA	783
D	b		721	AACAAGCATGTATGATTAACCTA-GTAAAGATGTAAACGATTAACAACAGAAATTGAGAA	780
Oy			784	AAGGAGAGAGACACAGATTCAGGACGAGACAAGAGAGAG- ---AACATCAAAAAGACCCCTC	839
D	b		781	AAGGAGAGAGACCCCGAGATTCGCCGCGCCCGAGAGAGAAAGAACTCCCMAAAAGACCCCTC	840
Oy			840	AGGAGAAACATTTTT - CTTTGTACAGGCAATTACGGACCTTTTT	880
D	b		841	AGGAGAAACCTTTTTCTTTTGTGTCCGCTTTAACCGAACCCCTTTT	883

RESULT_5 EST 23-JAN-2003
EXOS9041 LOCUS IMAGE:J391437.rna
DEFINITION BK089041 Soares, testis NIH Homo sapiens cDNA clone IMAGE998N14513
VERSION EXOS9041
KEYWORDS BK089041.1 GI:27823633
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)

REFERENCE Deert.L., Heil.O., Hennig.S., Neubert.P., Parsch.E., Peters.M.,
AUTHORS Radelet.F., Schneider.D. and Korn.B.
TITLE Human UniGeneSet - RPFD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMG998N14513.
RZPDLB: I.M.A.G.E.B.cDNA Clone Collection;
Human UniGeneSet - RPFD3 (RZPDLB.Nr.972)
[http://www.rzpd.de/ClsnCards/cgsl-](http://www.rzpd.de/ClsnCards/cgsl-bin/showlib.pl.cgi?response#libno=972)
bin/showlib.pl.cgi?response#libno=972 Contact: Ina Rolfs
RPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel.: +49 30 32639 101
Fax: +49 30 32639 111

www.rzpd.de
This clone is available royalty-free from RZPD.
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTGACACAGGAAACAGCTATGAC.
Location/Qualifiers

FEATURES

Source

1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE988N143513 ; IMAGE1391437"
/sex="male"
/lab_host="DH10B"
/clone_1ib="Soares testis NHT"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTTCACATCTGAAGTGGAGGCGGCCCAATTTTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT73 vector. Library
went through one round of normalization to Cots5 and was
constructed by Bento Soares and M. Patricia Bonaldo."

ORIGIN

Query Match 37.9%; Score 701.4; DB 13; Length 703;
Best Local Similarity 99.9%; Pred. No. 8.7e-97;
Matches 702; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 915 CTTTAAAAATAGACATGTTTCTTAAAGAGCTGTACTACACACCATTCGATGAG 974
1 CTTTAAAAATAGACATGTTTCTTAAAGAGCTGTACTACACACCATTCGATGAG 60
DB 975 TAGACATCTGACCTTAATGCTGAGACACATGACATCTCTGAGCTAGTCCAGTAGTA 1034
61 TAGACATCTGACCTTAATGCTGAGACACATGACATCTCTGAGCTAGTCCAGTAGTA 120
QY 1035 CACCAACAAATCATTAAAGCATTAAGCCTTGAATGACATGACATGATGCAATCAAGAT 1094
121 CACCAACAAATCATTAAAGCATTAAGCCTTGAATGACATGACATGATGCAATCAAGAT 180
DB 1095 CTGGGTGTAGATACACAGACAAACGATCTTAAGCAATCTGGTAGTAGTAACCAAG 1154
181 CTGGGTGTAGATACACAGACAAACGATCTTAAGCAATCTGGTAGTAGTAACCAAG 240
QY 1155 ATAAAGCATCCAAATGAGCAGCCAGAAACAGATGAAGAAATGAAAGATGAAGGTT 1214
241 ATAAAGCATCCAAATGAGCAGCCAGAAACAGATGAAGAAATGAAAGATGAAGGTT 300
DB 1215 TTGGTGAATTCACCGCTCCCAACATTTGATCCTTTTAACTTCAAGAGATTTT 1274
301 TTGGTGAATTCACCGCTCCCAACATTTGATCCTTTTAACTTCAAGAGATTTT 360
QY 1275 TATTGGCTAGTGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTTC 1334
361 TATTGGCTAGTGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTTC 420
DB 1335 AGTAACTTCAATTTGTTTACTATGTTGACCTGTTGGAGTATTAACAGATTAACCTCTTA 1394
421 AGTAACTTCAATTTGTTTACTATGTTGACCTGTTGGAGTATTAACAGATTAACCTCTTA 480
QY 1395 GTGCAATTACTTCAACAGTACTTTTCAACATTCAGATCTTTTATTTCACAACTTTT 1454
481 GTGCAATTACTTCAACAGTACTTTTCAACATTCAGATCTTTTATTTCACAACTTTT 540
DB 1455 TTTTACCTTTCACTAAATGTTTGAAGGGAGAGCTTACACAGACATCTTTTGAATTTGG 1514
541 TTTTACCTTTCACTAAATGTTTGAAGGGAGAGCTTACACAGACATCTTTTGAATTTGG 600
QY 1515 AAAAGTAGACACAGCAGATGGCTCACACCTGTATATCCAGACTTGAAGGAAGACAGT 1574
601 AAAAGTAGACACAGCAGATGGCTCACACCTGTATATCCAGACTTGAAGGAAGACAGT 660

QY 1575 CAGAGGATTGATTGATTAAGCTAGAGCTTAGAGACACAGCTGGGC 1617
DB 661 CAGAGGATTGATTGATTAAGCTAGAGCTTAGAGACACAGCTGGGC 703

RESULT 6
AK042001
LOCUS
DEFINITION
MUS musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A63005112 product: hypothetical protein, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK042001
AK042001.1 GI:26334856
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PMID
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PMID
REFERENCE
AUTHORS

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042155
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsumi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Kikuchi, A. and Hayashizaki, Y.
Okazaki, Y., Muramatsu, M., Inoue, Y., Kikuchi, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1599)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imoto, K., Ishii, Y., Itoh, M., Kaga, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komuro, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

LOCUS AK042339 1599 bp mRNA linear HTC 19-SEP-2003
DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630083X16 product:hypothetical protein, full insert sequence.
ACCESSION AK042339
VERSION AK042339.1 GI:26335056
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE 11042159
PubMed 11076861
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujimake, S., Inoue, K., Togawa, I., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE 11076861
PubMed 11076861
REFERENCE 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
JOURNAL 20530913
MEDLINE 11076861
PubMed 11076861
REFERENCE 5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL 20530913
MEDLINE 11076861
PubMed 11076861
REFERENCE 6
Adachi, T., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, S., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Muraoka, M., Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>
Location/Qualifiers
1..1599
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM,DB:A630083X16"
/db_xref="MGI:2407373"
/db_xref="taxon:10090"
/clone="A630083X16"
/issue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="3 days neonate"
28..813
/note="unnamed protein product; hypothetical protein (evidence: Procest)
putative"
/codon_start=1
/protein_id="BAC31229.1"
/db_xref="GI:26335057"
/translation="MEGSTGLVLSGFVYALTFHRLNTSDTEGLLEKMGKXANS
ITDSQDNVAVVYIDICKYIPCYRLFVNSLGEVHNLKRVSNVKTAVGWKF
RRSDQIMFRELRLNLTSLSELTLSLTSITSSCSGDLKLYKPOKGL
FHRVPIVMTMGSDQLGYKTBASCTSVFBRVAVTHSSOFFNEGSLKEVAKINEM
YAAVGEIKRLRPREALPMDLEALRALVYAAKLVNKK"

CDS

ORIGIN
Query Match 37.7%; Score 696.8; DB 11; Length 1599;
Best Local Similarity 71.4%; Pred. No. 2,6e-96;
Matches 1025; Conservative 0; Mismatches 332; Indels 79; Gaps 5;
6 GCGCGGCTACATGACGAGGGGAGAGTACGTCGGCGGCTTCGCGCTTTGTCCTGGG 65
17 GAGCGCGCACTATGAGGGGAGAGGACGTTGGGGGCTGCTTGGCTTCGCTGGG 76
66 CACTCGCTTCCAGCACTTCACACGAGCTCGACACGAGAGGTTTCTTGGGGAAG 125
77 CGCTCACTTCCATCATCTCAACACAGACTCAACACGAGAGGTTTCTTGGGGAAG 136
126 TAAAGGTGAAGCCAGAGACGATTAATGATTTCCCAATGATGATGATGAGTGT 185
137 TGAAGGTGAAGCCAGAGACGATTAATGATTTCCCAATGATGATGATGAGTGT 196
186 ATACATTTGACATTCAGAAATATATTCATGATGATGATGATGATGATGATGAT 245
197 ATACATTTGACATTCAGAAATATATTCATGATGATGATGATGATGATGATGAT 256
246 CAGCGGAGTGAATGAGACGACGACGACGACGACGACGACGACGACGACGACGAC 305
257 TAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 316
306 TAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 365
317 TGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 376
366 TTCAAAAACCTTCAGAGAGATTTTCAAAACCAAGCTTTGTTTCTGCTATTAC 425
377 TCCACAGAACTTCAGACACATCTTCAAGCCCTGAGCGTGTTCCTGTTTAAAC 436
426 CAGGATTAATTAAGAAAGTGTCTACTCATGACGAGAAACATCTTATTAATTA 485
437 CGAGTATTAACACGAAAGTGTCTACTCATGACGAGAAACATCTTATTAATTA 496
486 AAAAGGACCTTTTCAAGGATCTTATGTTGTCGAATCTGGCATGTGAAAC 545

Db 497 AAGAGGAGCTTTTCTATAGGATCCATTTGGTGTACCAATCTGGGAATGTGTATCAAC 556
 QY 546 TGGGTTATATAAAGCTGTATCAGGTTCTGTATGTCCATGCTTTTATAGCCAGAGATACAA 605
 Db 557 TGGGTTATATAAAGAGAACTGCTCTCTGTACGTCACCTCTTTTATAGATGCTGTAGAGA 616
 QY 606 CACACAGCTCTAATTTTGTGAAGATGATGATCCCTTAAGAGGATGATGATGATGATG 665
 Db 617 CACACAGCTCTCTCTTTTATGAAGATGATGATTAAGAGAGTCCATTAAGATTAAG 676
 QY 666 AATGTATGCTCTCTTATCAAGAGATTAAG----- 697
 Db 677 AATGTATGCTCTGTATCAAGAGATTAAGTCCCTGTGAGCCAGAGAGGACCTTG 736
 QY 698 -----AGTATGTGAAAAAGTGGAGA 720
 Db 737 TTCCATGATCTGATGAGCAGATTCGAGCTGCCCTGTATATATGCAAAAAGTTGAACA 796
 QY 721 CAGTGAACAAGCAGTATGATTAAGATTAAGAGATTAAGAGATTAAGAGAGAAATTTGA 780
 Db 797 AAGTGAACAAGAGATGAGAACTATGATGATGATGATGATGATGATGATGATGATGATG 853
 QY 781 GAAAAGAGAGAGCAGATTCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 854 AAGAGCCAG 913
 QY 841 GAGAGACATTTTCTTTTCTGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 914 GAGAGACATTTTCTTTTCTGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 973
 QY 901 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 974 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
 QY 961 CCACTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 Db 1034 CCACTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1093
 QY 1021 TAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 Db 1094 TAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1153
 QY 1081 GCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 Db 1154 GTCTGAG 1213
 QY 1141 TAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 Db 1214 CAGCAG 1270
 QY 1201 AAG 1260
 Db 1271 GAGCCAG 1330
 QY 1261 CAGAGAGATTTTATTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 Db 1331 CA-----TTCTTACTAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
 QY 1321 GTTGAAGTACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1376
 Db 1384 TTCTGATTAATACA-CAGAAAAGTTGTTTACTCTATTCACCTGTTGTAATA 1438

RESULT 8
 AUI25653 736 bp mRNA linear EST 01-ANG-2002
 LOCUS AUI25653 NT2RM4 Homo sapiens cDNA clone NT2RM4001965 5', mRNA
 DEFINITION
 ACCESSION AUI25653
 VERSION AUI25653.1 GI:10950369
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

TITLE
 HRI human cDNA project (Ota, T., Makamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Sugano, S., Isozaki, T., Nagai, T., Suzuki, Y., Sugano, S., and Isozaki, T.)
 JOURNAL
 COMMENT
 CONTACT: Takao Isozaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES
 source
 Location/Qualifiers
 1..736
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RM4001965"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_id="NT2RM4"
 /note="Vector: pME18SFLJ; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN
 Query Match 36.9%; Score 681.8; DB 9; Length 736;
 Best Local Similarity 99.0%; Pred. No. 7,8e-94;
 Matches 694; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Db 1 CTGAGGCGCGGTGATGATGAGAGGAGAGAGTACGTCCGCGGTGCTCCGCGCTTTGTGCT 60
 QY 36 CTGAGGCGCGGTGATGATGAGAGGAGAGAGTACGTCCGCGGTGCTCCGCGCTTTGTGCT 95
 Db 61 CGGCGCACTGCTTTCCAGAGACCTCAACAGGAGTGGAGACGGAAGTTCCTCTTG 120
 QY 96 CGGCGCACTGCTTTCCAGAGACCTCAACAGGAGTGGAGACGGAAGTTCCTCTTG 155
 Db 121 GGAAGTAAAGGTGAG 180
 QY 156 GGAAGTAAAGGTGAG 215
 Db 181 TGTTTATCAATTTACATTCAGAAATATTTCCATGCTATACAGCTTTTATGATTA 240
 QY 216 TGTTTATCAATTTACATTCAGAAATATTTCCATGCTATACAGCTTTTATGATTA 275
 Db 241 TTCTTCAGGCGAGATTAATGAGCAGAGCAGTGAAGAAATATTAATGATGCAAAAGAA 300
 QY 276 TTCTTCAGGCGAGATTAATGAGCAGAGCAGTGAAGAAATATTAATGATGCAAAAGAA 335
 Db 301 TGTGTAGCTTGTGATCAATTCGCTGCTCATTCAGATCAATCATGACGTTTAAAGAG 360
 QY 336 TGTGTAGCTTGTGATCAATTCGCTGCTCATTCAGATCAATCATGACGTTTAAAGAG 395
 Db 361 GGTGCTTCAAAAAGCTTGACAGAGAGATTTTCAACAGAGAGCTGTTTCTGCTATT 420
 QY 396 GGTGCTTCAAAAAGCTTGACAGAGAGATTTTCAACAGAGAGCTGTTTCTGCTATT 455
 Db 421 AACACCAAGTATTAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 456 AACACCAAGTATTAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 515
 Db 481 AACTCAAAAAGAGATTTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 516 AACTCAAAAAGAGATTTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 575

Db 181 TACAAATGACATTCAGAAATATATATTCATGCTATCAGCTTTTACGTTTAAATCTTC 240

QY 247 AGCGGAGTAATAGGACAGCACTGAGAAATATATTCATCAATGCAAAAAGATGCT 306

Db 241 AGCGGAGTAATAGGACAGCACTGAGAAATATATTCATCAATGCAAAAAGATGCT 300

QY 307 AGGTTGGTCAAAATTCGCTGCTCATTCAGATCAGATCAGATGAGCTTTAGAGAGGCTGCT 366

Db 301 AGGTTGGTCAAAATTCGCTGCTCATTCAGATCAGATCAGATGAGCTTTAGAGAGGCTGCT 360

QY 367 TCACAAAACTGCGAGAGCACTTTTTCACAAACCAACCTGTTTTCGCTATTACACC 426

Db 361 TCACAAAACTGCGAGAGCACTTTTTCACAAACCAACCTGTTTTCGCTATTACACC 420

QY 427 AAGTATATACAGAAAGCTGCTCTACTCATCAGATGAGCAATCTCTTATATTAACCTCA 486

Db 421 AAGTATATACAGAAAGCTGCTCTACTCATCAGATGAGCAATCTCTTATATTAACCTCA 480

QY 487 AAAAGACCTTTTTCACAGAGGATCTTATAGTGGTTCGCAATCTGGGCAATGCTGAACACT 546

Db 481 AAAAGACCTTTTTCACAGAGGATCTTATAGTGGTTCGCAATCTGGGCAATGCTGAACACT 540

QY 547 GGGTTATAAAACGTATACAGGTTCTGATGTCCTCACTGGTTTACCCGAGCAGTACCAAC 606

Db 541 GGGTTATAAAACGTATACAGGTTCTGATGTCCTCACTGGTTTACCCGAGCAGTACCAAC 600

QY 607 ACACAGCTCTAAATTTTTCAGAAAGATGATGATCTTTTAAAGAGGTACATTAAGATAATG 665

Db 601 ACACAGCTCTAAATTTTTCAGAAAGATGATGATCTTTTAAAGAGGTACATTAAGATAATG 660

QY 666 AATATGATGC-TTCATTACAGAGGAA-TTAAAGATATATGCAAAAAA 712

Db 661 AATATGATGC-TTCATTACAGAGGAA-TTAAAGATATATGCAAAAAA 709

RESULT 11
CA429280/c 665 bp mRNA linear EST 07-NOV-2002
LOCUS UI-H-FH1-bf1-n-12-0-UI.s1 NCI CGAP_FH1 Homo sapiens cDNA clone
DEFINITION UI-H-FH1-bf1-n-12-0-UI 3', mRNA sequence.
ACCESSION CA429280
VERSION CA429280.1 GI:24792006
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 188-316, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1. .665
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FH1-bf1-n-12-0-UI"
/tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"

/clone lib="NCI CGAP FH1"
/note="Organ: Chondrosarcoma; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library
obtained from a cell line derived from grade I
chondrosarcoma tissue. The library was constructed and
normalized according to Bonaldi, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGATCCGCGC. The cell line was provided by Dr. James Martin
from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
TAG LIB=UI-H-FH1
TAG_SEQ=AGATCCGCGC"

ORIGIN
Query Match 35.6%; Score 658.6; DB 14; Length 665;
Best Local Similarity 99.4%; Pred. No. 2,7e-90;
Matches 661; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1174 CAGCCGAGAAACAGATGAGAAATTTGAAAGAGGTTTGGTGAATTTACAGGTC 1233

Db 665 CAGCCGAGAAACAGATGAGAAATTTGAAAGAGGTTTGGTGAATTTACAGGTC 606

QY 1234 TCCGACATTTGATCCCTTTTACCTTACAGAGATTTTATTTGGCTGATGGTAA 1293

Db 605 TCCGACATTTGATCCCTTTTACCTTACAGAGATTTTATTTGGCTGATGGTAA 546

QY 1294 GCCAAACATTTGATTTTATCTATGTTGAGCTTCTGAGAAAGTTGATTTT 1353

Db 545 GCCAAACATTTGATTTTATCTATGTTGAGCTTCTGAGAAAGTTGATTTT 486

QY 1354 ACTATGTTACCTGTTTGGAGTAATACAGATACCTTATGATTTACTTACAAAG 1413

Db 485 ACTATGTTACCTGTTTGGAGTAATACAGATACCTTATGATTTACTTACAAAG 426

QY 1414 TACTTTTCAACATCAGATGCTTTTATTTTCAAACTTTTTCACCTTTCACTAA 1473

Db 425 TACTTTTCAACATCAGATGCTTTTATTTTCAAACTTTTTCACCTTTCACTAA 366

QY 1474 GTTGAAGGGAGAGCTTACAGAGACACTTCTTATGAAATGGAAAGTGAACAGGACA 1533

Db 365 GTTGAAGGGAGAGCTTACAGAGACACTTCTTATGAAATGGAAAGTGAACAGGACA 306

QY 1534 GTGGCTCACACTGTATATCCAGACTTTAGGAAGACAACTGAGAGATTTGAAAGC 1593

Db 305 GTGGCTCACACTGTATATCCAGACTTTAGGAAGACAACTGAGAGATTTGAAAGC 246

QY 1594 TAGAGCTTAGAGACACCTGCGGCAACGTTATGAGACCACTGCTATTAATAATG 1653

Db 245 TAGAGCTTAGAGACACCTGCGGCAACGTTATGAGACCACTGCTATTAATAATG 186

QY 1654 GAAAGCAGAAATAGCTTTATTTTCAAAATATGAAAGAAATTTATGAAATTTATCT 1713

Db 185 GAAAGCAGAAATAGCTTTATTTTCAAAATATGAAAGAAATTTATGAAATTTATCT 126

QY 1714 GAGTCATTTAAATTTCTCTTATAGATATCTTTTATGAAATTTATGCTGAGAGTGC 1773

Db 125 GAGTCATTTAAATTTCTCTTATAGATATCTTTTATGAAATTTATGCTGAGAGTGC 66

QY 1774 CAGATTAATAATGCTGATATCATGCAATTAATTTGCAAAACATCATCTTAATTTAAAAA 1833

Db 65 CAGATTAATAATGCTGATATCATGCAATTAATTTGCAAAACATCTTTAAAAA 6

QY 1834 AAAAA 1838

Db 5 AAAA 1

RESULT 12
BG570593

LOCUS 778 bp mRNA linear EST 10-APR-2001
602591278F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717987 5',
MNA sequence.

ACCESSION BG570593
VERSION BG570593.1 GI:13578246
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 778)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IL0M1568 row: 1 column: 20
High quality sequence stop: 673.
Location/Qualifiers
1..778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4717987"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_77"
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccgcggcc); Site 2: SfiI (ggcgccgcggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.4%; Score 654.2; DB 12; Length 778;
Best Local Similarity 96.9%; Pred. No. 1.1e-89;
Matches 753; Conservative 0; Mismatches 13; Indels 11; Gaps 8;

QY 194 GACATTGAGAAATATATTCCTATCAGCTTTTACGTTTATATCTTCAGCGCA 253
DB 1 GACATTGAGAAATATATTCCTATCAGCTTTTACGTTTATATCTTCAGCGCA 60

QY 254 GTAATGAGAGACACTGAGAAATATATTCCTATCAGCTTTTACGTTTATATCTTCAGCGCA 313
DB 61 GTAATGAGAGACACTGAGAAATATATTCCTATCAGCTTTTACGTTTATATCTTCAGCGCA 119

QY 314 TACAAATTCGCTGTCATTCAGATCATCATGCTTTAGAGAGGCTGCTTCACAA 373
DB 120 TACAAATTCGCTGTCATTCAGATCATCATGCTTTAGAGAGGCTGCTTCACAA 179

QY 374 AACTTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGTATA 433
DB 180 AACTTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGTATA 239

QY 434 ATTAAGAAAGGCTCTTACTCATGAGTGAACATTCCTTATATAAAGCTCAAAAAGA 493
DB 240 ATTAAGAAAGGCTCTTACTCATGAGTGAACATTCCTTATATAAAGCTCAAAAAGA 299

QY 494 CTTTTCACAGGATCCTTTAGTGTGTCATGCGCATGTCGAAACAACCTGGTTAT 553
DB 300 CTTTTCACAGGATCCTTTAGTGTGTCATGCGCATGTCGAAACAACCTGGTTAT 359

QY 554 AAACTGATCAGGTTCTCTGATGTCATCTGTTTACCGAGAGATCAACACACAGC 613
DB 360 AAACTGATCAGGTTCTCTGATGTCATCTGTTTACCGAGAGATCAACACACAGC 419

QY 614 TCTAAATTTTGAAGAAGATGATCCTTAAGAGAGTACATTAAGTAAATGATGAT 673
DB 420 TCTAAATTTTGAAGAAGATGATCCTTAAGAGAGTACATTAAGTAAATGATGAT 479

QY 674 GCTTCATTACAAGAGATTAAGAGTATATGCAAAAAAGTGAAGACAGTAAACAGCA 733
DB 480 GCTTCATTACAAGAGATTAAGAGTATATGCAAAAAAGTGAAGACAGTAAACAGCA 539

QY 734 GTAGTAACTAGTAAAGATGATTAACAGATTAAGAGAAATGGAAGAGAGAGA 793
DB 540 GTAGTAACTAGTAAAGATGATTAACAGATTAAGAGAAATGGAAGAGAGAGA 599

QY 794 GCACAGATTCAAGAGAGAGAGAGAGAGATCC-AAAAAGCCCTCAGAGAAACATTT 852
DB 600 GCACAGATTCAAGAGAGAGAGAGAGAGATCC-AAAAAGCCCTCAGAGAAACATTT 659

QY 853 TCT-TTTGCAGGATTA--CGACCTTTTTCGCAATTC- GAATTTCTTATCATGT- 907
DB 660 TCTCTTGCAGGATTA--CGACCTTTTTCGCAATTC- GAATTTCTTATCATGT- 719

QY 908 GTATAGTCTTAAAAATAGA--CATGTTCTAAAA-GTAGTGTACTACACCA 960
DB 720 GTATAGTCTTAAAAATAGA--CATGTTCTAAAA-GTAGTGTACTACACCA 776

RESULT 13
B0019837/C

LOCUS B0019837.1

DEFINITION UI-H-ED0-exe-c-16-0-UI-s1 NCI CGAP_ED0 Homo sapiens cDNA clone
IMAGE:5827527 3', mRNA sequence.

ACCESSION B0019837
VERSION B0019837.1 GI:19755114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 665)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 8-136, >Alu (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source 1..665
Location/Qualifiers
1..665
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5827527"
/tissue_type="chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI_CGAP_ED0"

/note="Organ: Left Pubic Bone; Vector: p1773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP ED0 is a cDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p1773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=CCTCAAGGCT"

ORIGIN

Query Match 35.1%; Score 649.2; DB 12; Length 665;
Best Local Similarity 99.4%; Pred. No. 7.1e-89;
Matches 662; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

QY 993 TGGTAGACACACTGACATTCCTGAAGCTAGTCAGCTAGTACACCAAAATCATTAGC 1052
Db 665 TGGTAGACACACTGACATTCCTGAAGCTAGTCAGCTAGTACACCAAAATCATTAGC 606
QY 1053 ATTAAGCCTTAGCTTAGATGACAGATGGCAATTCAGAGATTCGGTGTGATACAC 1112
Db 605 ATTAAGCCTTAGCTTAGATGACAGATGGCAATTCAGAGATTCGGTGTGATACAC 546
QY 1113 AAGCAAAAGCATCTAAAGCAATCTAGTGTAGTACCAAGATAAAGATCCAAATATA 1172
Db 545 AAGCAAAAGCATCTAAAGCAATCTAGTGTAGTACCAAGATAAAGATCCAAATATA 486
QY 1173 GCAGCCCAAGAAAGATGAAGAAATGAAGGTTTGGTGAATATTCACGGT 1232
Db 485 GCAGCCCAAGAAAGATGAAGAAATGAAGGTTTGGTGAATATTCACGGT 426
QY 1233 CTCCTACATTTGATCTTTTAACTTCAAGAGATTTTATTTGGCTGATGGGTA 1292
Db 425 CTCCTACATTTGATCTTTTAACTTCAAGAGATTTTATTTGGCTGATGGGTA 366
QY 1293 AGCCAAACATTTCTATTGTTTTTACTATGTGTAGCTACTTGCAGTAAGTTCATTTGTTT 1352
Db 365 AGCCAAACATTTCTATTGTTTTTACTATGTGTAGCTACTTGCAGTAAGTTCATTTGTTT 306
QY 1353 TACTATGTCACCTGTTGAGTAATACAGATTAATCTTAGTGAATTTACTTACAAA 1412
Db 305 TACTATGTCACCTGTTGAGTAATACAGATTAATCTTAGTGAATTTACTTACAAA 246
QY 1413 GTACTTTTCAAAATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGT 1472
Db 245 GTACTTTTCAAAATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGT 186
QY 1473 TGTGAGGGAAGGCTTACACACATCTTTTGAATTTGAAAAGTGAACCAAGGCAC 1532
Db 185 TGTGAGGGAAGGCTTACACACATCTTTTGAATTTGAAAAGTGAACCAAGGCAC 127
QY 1533 AGTGGCTCACACCTGTATCCACAGCACTTAGGGAAGCAAGTCAGAGATTTGATGAAG 1592
Db 126 AGTGGCTCACACCTGTATCCACAGCACTTAGGGAAGCAAGTTAGAGATTCATGAAG 67
QY 1593 CTAGAGTTAGAGACCGCTGGGCAAGTATGAGCAATGTCTATTAATAAATAAAT 1652
Db 66 CTAGAGTTAGAGACCGCTGGGCAAGTATGAGCAATGTCTATTAATAAATAAAT 7
QY 1653 GGAATA 1658
Db 6 GGAATA 1

```

RESULT 14

BG531177 744 bp mRNA linear EST 03-APR-2001
LOCUS 602561489F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699294 5',
DEFINITION mRNA sequence.
ACCESSION BG531177
VERSION BG531177.1 GI:13522714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
NIH-MGC <http://img.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://img.lnl.gov>
Plate: L1CM1531 row: a column: 23
High quality sequence stop: 740.
Location/Qualifiers
1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4699294"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctggc); Site_2: SfiI (ggccatagc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTTGCGC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCAGCGCGCAGTGTG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC library."

ORIGIN

Query Match 35.0%; Score 648; DB 12; Length 744;
Best Local Similarity 97.2%; Pred. No. 1e-88;
Matches 723; Conservative 0; Mismatches 15; Indels 6; Gaps 6;

```

QY 705 GCAAAAAGTGAAGACAGTGAACAGATGATTAACCTAGTAAGATGTAACGAT 764
Db 1 GCAAAAAGTGAAGACAGTGAACAGATGATTAACCTAGTAAGATGTAACGAT 60
QY 765 TAAACGGAATTTGAGAA-AAGAGAGGAGACAGATTGAGGAGCAAGAGAGAAC 823
Db 61 TAAACGGAATTTGAGAA-AAGAGAGGAGACAGATTGAGGAGCAAGAGAGAAC 120
QY 824 ATCCAAAAGACCTCAGAGAACATTTTCTTTGTGACGATTAACGACCTTTTCCA 883
Db 121 ATCCAAAAGACCTCAGAGAACATTTTCTTTGTGACGATTAACGACCTTTTCCA 180
QY 884 AATTGTGAATTTCTCAATTCATGTTATGCTTTTAAATAATAGACATGTTCTAAAGT 943
Db 181 AATTGTGAATTTCTCAATTCATGTTATGCTTTTAAATAATAGACATGTTCTAAAGT 240
QY 944 AGCTGTAACTAACCAACCATCTCGATGTAGTAACTGACCTTAATGTGAACAC 1003
Db 241 AGCTGTAACTAACCAACCATCTCGATGTAGTAACTGACCTTAATGTGAACAC 300

```


AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M9732 row: n column: 21
High quality sequence stop: 638.

FEATURES
source
1..668
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3913172"
/issue_type="leiomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb."

ORIGIN

Query Match 34.4%; Score 635.2; DB 10; Length 688;
Best Local Similarity 97.9%; Pred. No. 9.1e-87;
Matches 654; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
43 GCTCTCGGGCTTTGCTCGGCGCACTCGCTTTCAGACCTCAACAGAGCTCGGACAC 102
1 GCTCTCGGGCTTTGCTCGGCGCACTCGCTTTCAGACCTCAACAGAGCTCGGACAC 60
QY 103 GGAAGGTTTCTCTTGGGAAATGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 162
DB 61 GGAAGGTTTCTCTTGGGAAATGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 120
QY 163 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 222
DB 121 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 223 GCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 282
DB 181 GCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 240
QY 283 ATCAATGATCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
DB 241 ATCAATGATCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 343 CATGACGTTTAAAGAGAGGCTGCTTCACAAAAATCTGCGAGAGATTTTCAACCA 402
DB 301 CATGACGTTTAAAGAGAGGCTGCTTCACAAAAATCTGCGAGAGATTTTCAACCA 360
QY 403 CCTGTTTCTGCTATTAACCAAGTATTAATCAAGAAAGTGTGCTTACTCATGAGAT 462
DB 361 CCTGTTTCTGCTATTAACCAAGTATTAATCAAGAAAGTGTGCTTACTCATGAGAT 420
QY 463 GGAACATTCCTTATATAAACTTCAAAAAGAGATTTTCAAGGGTACCTTTAGTGT 522
DB 421 GGAACATTCCTTATATAAACTTCAAAAAGAGATTTTCAAGGGTACCTTTAGTGT 480
QY 523 CAATCTGGGATGCTGAACAACCTGGTTAAACCTGATCAAGTTCCTGATGCTGAC 582
DB 481 CAATCTGGGATGCTGAACAACCTGGTTAAACCTGATCAAGTTCCTGATGCTGAC 540
QY 583 TGGTTTAAAGCCGAGCAATCAACAACAGCTCTAAATTTTAAAGAGATGATGAT 642
DB 541 TGGTTTAAAGCCGAGCAATCAACAACAGCTCTAAATTTTAAAGAGATGATGAT 599
QY 643 AAAGAGGTACATAAGATTAATGAATGATGCTTCAATCAAGAGAAATTAAGATAT 702

DB 600 AAAGAGGTACATAAGATTAATGAATGATGCTTCAATCAAGAGAAATTAAGAT 659
QY 703 ATGCAAAA 710
DB 660 CTGGCGAA 667

RESULT 17
CB135704/c 620 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0187980 L14CholCKO Homo sapiens cDNA clone L14CholCKO-30-F08
DEFINITION 5' mRNA sequence.
ACCESSION CB135704
VERSION CB135704.1 GI:28102652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 620)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21c Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.krdb.re.kr
Plate: 30 row: F column: 08
High quality sequence stop: 620.
Location/Qualifiers
1..620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14CholCKO-30-F08"
/sex="M"
/cell_line="Chol-CK"
/lab_host="Top10P"
/note="Organ: Liver; Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares Laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

TITLE
JOURNAL
COMMENT

FEATURES
source

ORIGIN

Query Match 33.4%; Score 616.8; DB 14; Length 620;
Best Local Similarity 99.7%; Pred. No. 5.9e-84;
Matches 618; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
711 GCAGTAGTAATACAGTAAGATGTAACAGATTAACAGAAATTTGAGAAAGAGA 790
DB 620 GCAGTAGTAATACAGTAAGATGTAACAGATTAACAGAAATTTGAGAAAGAGA 561
QY 791 GAGACAGATTCAGGCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 850
DB 560 GAGACAGATTCAGGCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 501
QY 851 TTTCTTTGTCAGGATTAAGGACCTTTTCCAAATTCGATTTCTTCATTCATGAT 910
DB 500 TTTCTTTGTCAGGATTAAGGACCTTTTCCAAATTCGATTTCTTCATTCATGAT 441
QY 911 ATGCTTTAAATATAGATGTTTCTTAAGAGTGTGATGATGATGATGATGATGAT 970
DB 440 ATGCTTTAAATATAGATGTTTCTTAAGAGTGTGATGATGATGATGATGATGAT 381

QY 971 GTAGTAGACATCTGACCTTAATGATGAGAACACACTGACATCTCGAAGCTAGTCCAGCT 1030
 Db 380 GTAGTAGACATCTGACCTTAATGATGAGAACACACTGACATCTCGAAGCTAGTCCAGCT 321
 QY 1031 AGTACACCAAAATCAATTAAGCATTAAGCCTTAGACTTAGATGACAGATGCGAATTCAG 1090
 Db 320 AGTACACCAAAATCAATTAAGCATTAAGCCTTAGACTTAGATGACAGATGCGAATTCAG 261
 QY 1091 AGATCCGCTGTTTAATACACAGACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1150
 Db 260 AGATCCGCTGTTTAATACACAGACCAATCAATCAATCAATCAATCAATCAATCAATCAAT 201
 QY 1151 CAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAAATGAAGTGAAG 1210
 Db 200 CAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAAATGAAGTGAAG 141
 QY 1211 GGTTCGTGGAATATTCAGGCTCTCTACATTTGATCCTTTAACTTACAGAGATTT 1270
 Db 140 GGTTCGTGGAATATTCAGGCTCTCTACATTTGATCCTTTAACTTACAGAGATTT 81
 QY 1271 TTTTATTTGGCTGATGAGTAAAGCCAAACATTTGATTTTACTTACTTACTTACTTACTT 1330
 Db 80 TTTTATTTGGCTGATGAGTAAAGCCAAACATTTGATTTTACTTACTTACTTACTTACTT 21
 QY 1331 TTGCAGTAAGTTCATTTGTT 1350
 Db 20 TTGCAGTAAGTTCATTTGTT 1
 RESULT 18
 LOCUS B1771321 706 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603054695F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204182 5',
 mRNA sequence.
 ACCESSION B1771321
 VERSION B1771321.1 GI:15762899
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 1 (bases 1 to 706)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1M1511 row: n column: 23
 High quality sequence stop: 703.
 Location/Qualifiers
 1..706
 location="Homo sapiens"
 mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5204182"
 /lab_host="DH10B"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung; 16 week female
 spleen, and 20-22 week male spleen. Library is oligo-dT
 primed, and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:"

ORIGIN this is a NIH_MGC Library."
 Query Match 33.3%; Score 616; DB 12; Length 706;
 Best Local Similarity 91.2%; Pred. No. 7.2e-84;
 Matches 704; Conservative 0; Mismatches 0; Indels 68; Gaps 2;
 QY 5 GCGCGCGGTGACATGAGGGGAGAGTACCTCGCGGCTGCTCGGGCTTGGCTGGC 64
 Db 1 GCGCGCGGTGACATGAGGGGAGAGTACCTCGCGGCTGCTCGGGCTTGGCTGGC 60
 QY 65 GCACTGCTTTCCAGCAGCTCAACAGGACTCGGACAGAGAGTTCTTCTTGGGAA 124
 Db 61 GCACTGCTTTCCAGCAGCTCAACAGGACTCGGACAGAGAGTTCTTCTTGGGAA 120
 QY 125 GTAAAAGTGAAGCCAGAAACAGATTTAGTTCCTCAATGATGATGTGAAGTTGT 184
 Db 121 GTAAAAGTGAAGCCAGAAACAGATTTAGTTCCTCAATGATGATGTGAAGTTGT 180
 QY 185 TATCAATGACATTCAGAAATATATTCATGCTATGAGCTTTTATTAATTC 244
 Db 181 TATCAATGACATTCAGAAATATATTCATGCTATGAGCTTTTATTAATTC 225
 QY 245 TCAGCGAGTAAATGAGCAGACCTGAGAAAAATTTATCAAAATGCAAAAAGATGTG 304
 Db 226 -----AGAAATGTG 233
 QY 305 GTAGTTGTGACAAATCCGTCGATTCAGATCAATCATGAGCTTTAGAGAGGCTG 364
 Db 234 GTAGTTGTGACAAATCCGTCGATTCAGATCAATCATGAGCTTTAGAGAGGCTG 293
 QY 365 CTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTGTGTTTCTGTAATTACA 424
 Db 294 CTTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTGTGTTTCTGTAATTACA 353
 QY 425 CCAAGTATTAACAGAAAGCTGCTACATCATGCTGGAATCTTAATTAACCT 484
 Db 354 CCAAGTATTAACAGAAAGCTGCTACATCATGCTGGAATCTTAATTAACCT 413
 QY 485 CAAAAGAGCTTTTCAACAGGATACCTTATGATGATGCCAATGCGCATGTGACAA 544
 Db 414 CAAAAGAGCTTTTCAACAGGATACCTTATGATGATGCCAATGCGCATGTGACAA 473
 QY 545 CTGGGTATTAACCTGATATAGGTCCTGATATCCAGCTGTTTACCGAGAGATCAA 604
 Db 474 CTGGGTATTAACCTGATATAGGTCCTGATATCCAGCTGTTTACCGAGAGATCAA 533
 QY 605 ACACACAGCTCTAATTTTGAAGAAGATGATCCTTAAAGAGGATACATAAGATAAT 664
 Db 534 ACACACAGCTCTAATTTTGAAGAAGATGATCCTTAAAGAGGATACATAAGATAAT 593
 QY 665 GAAATGATCTCTCATTAACAAGGAA-TTAAAGATTTATGCAAAAAGTGAAGACAG 723
 Db 594 GAAATGATCTCTCATTAACAAGGAACTTAAAGATTTATGCAAAAAGTGAAGACAG 653
 QY 724 TGAACAAGCAGTATTAAGTAAAGATGTAACAGATTTAAACGAGAA 775
 Db 654 TGAACAAGCAGTATTAAGTAAAGATGTAACAGATTTAAACGAGAA 705
 RESULT 19
 LOCUS BC043923 1597 bp mRNA linear HTC 13-JAN-2003
 DEFINITION Mus musculus, clone IMAGE:3486297, mRNA.
 ACCESSION BC043923
 VERSION BC043923.1 GI:27694065
 KEYWORDS HTC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1597)
 AUTHORS Strausberg, R.

Mon Apr 19 12:46:09 2004

us-10-063-523-21.rst

Page 18

TITLE Direct Submission
JOURNAL Submitted (10-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigrl.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, V., Haghighi, P., Hansen, N., Ho, S.-L., Karling, E., Kwong, P., Latic, P., Legaspi, R., Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCluskey, J.C., McDowell, U., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Tsungue, C., Vogt, J.D., Walker, M.A., Weethey, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX File: 85 Row: b Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: frame shifted.

FEATURES
source Location/Qualifiers
1..1597
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3486297"
/issue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
/clone_1lb="NCI CGAP_Mams"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 33.2%; Score 613.6; DB 11; Length 1597;
Best Local Similarity 72.8%; Pred. No. 1e-83;
Matches 865; Conservative 0; Mismatches 304; Indels 19; Gaps 5;
Db 194 GATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTTAACTTCAGAGCA 253
110 GATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTTAACTTCAGAGCA 169
254 GTAATGAGCAAGCACTGAAGAAATATATTCATGCTTTTAACTTCAGAGCA 313
170 GTAAAGCAACATCACTGAAGAAAGTTCTTTAACTTCAGAGCAAGCTGGG 229
314 TACAAATTCGCTGCTATTCATGATCAGATCAGCTTTTAACTTCAGAGCA 373
230 TATTAATTCGCTGCTATTCATGATCAGATCAGCTTTTAACTTCAGAGCA 289
374 AACTTGAGAGCAATTTTCAACCAAGCACTGTTTCTGCTATTAACCAAGTATA 433
290 AACTTCAGCAATCTTTCAACCAAGCACTGTTTCTGCTATTAACCAAGTATA 349
434 ATTAACAGAAAGCTGCTATTCATGATCAGATCAGCTTTTAACTTCAGAGCA 493
350 ACAACAGAAAGCTGCTATTCATGATCAGATCAGCTTTTAACTTCAGAGCA 409
494 CTTTTCAGAGGAGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 553
Db 410 CTTTTCATAGGATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 469

QY 554 AAAACGTATACAGTTCCTGATATGTCACAGTGGTTTAAAGGAGCAAGCAACAGCAGC 613
Db 470 AAAACAGAACTGCTCTGTCAGTCCATGCTCTTTAGTAGAGCTGTAGAGCAACAGT 529
QY 614 TCTAATTTTGAAGAAATGATCTTTAAAGAGGATCATTAAGATAAATGAATGAT 673
Db 530 TCTCACTTTTAAATGAATGATGATTAAGAAAGTCCATTAAGATAAATGAATGAT 589
QY 674 GCTTCTTCAAGAGAAATTA-----AAGATATGCAAAAAGGAGCAAGTAAAC 728
Db 590 GCTGCTGTCAGAAAGATTTAAAGTGAAGATATGTCAGAAAGTGAACAAAGTAAAC 649
QY 729 AAGCAGTAAATAACTAGTAAAGATGTAAGATTAACAGATTAACAGAAATGAAGAAAGGA 788
Db 650 GAGAAATAGAGAACTATGATGATGATTAACCAATTA-----AGAAATGAAGAACCC 706
QY 789 GAGAGCAAGATTCAGGAGCAAGAGAAAGAAATCCAAAGAAAGCCTCAGAGAAAC 848
Db 707 AGCAACACAGGAGTACAGAGCAGAGAGAAAGTCCAGAGAAACCAAGAGAAACA 766
QY 849 TTTTCTTGTGAGGATTAACGACCTTTTCCAAATTCGAATTTCTTATTCATTCATG 908
Db 767 TCTTCTTGTGAGGATTAACGACCTTTTCCAAATTCGAATTTCTTATTCATTCATG 826
QY 909 TTAATGCTTTAAATAATGACATGTTTCTAATAAGTACGTTACTACACCAACATCTG 968
Db 827 TTAATGCTTTAAATAATGACATGTTTCTAATAAGTACGTTACTACACCAACATCTG 886
QY 969 ATGATGAGCAATCTGACCTTATGATGATGATGATGATGATGATGATGATGATGAT 1028
Db 887 ATGATGAGCAATCTGACCTTATGATGATGATGATGATGATGATGATGATGATGAT 946
QY 1029 CTAGTACCAACCAATTCATTAAGCAATTAAGCTTAAAGCTTAAAGCTTAAAGCT 1088
Db 947 TGCCACAGCCAGCTACGTAAGCAAGGAGCTTAAACACACAGCAGCAGGAGCTGTGA 1006
QY 1089 AGAGATCGGTTGTTAGATACACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1148
Db 1007 AGAGATCGGTTGTTAGATACACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1066
QY 1149 ACCAAGTAAAGATCCAAATGATGAGAGCCAGCAAGCAAGCAAGCAAGCAAGCAAG 1208
Db 1067 ACCAAGTAAAGATCCAAATGATGAGAGCCAGCAAGCAAGCAAGCAAGCAAGCAAG 1123
QY 1209 AGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
Db 1124 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1177
QY 1269 TTTTATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1328
Db 1178 TTTTATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1236
QY 1329 ACTTGAGTAAAGTATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1376
Db 1237 TAAATCA-CAGAAAAGTTGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1283

RESULT 20
AL602519 623 bp mRNA linear EST 04-SEP-2003
LOCUS DEFNITION DKFZP866C1814.1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZP866C1814.5, mRNA sequence.
ACCESSION AL602519
VERSION AL602519.1 GI:15166025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 623)
Wambut, R., Heubner, D., Nemes, W., Weil, B. and Wiemann, S.
EST (Wambut, R., Heubner, D., Nemes, H.W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DKFZ686C1814) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ686C1814"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 32.9%; Score 608; DB 9; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-82;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CTGAGGCGCGGATGATGAGAGGAGAGTACGTCGGCGGTCTCTCGGCGTTTGCT 60
16 CTGAGGCGCGGATGATGAGAGGAGAGTACGTCGGCGGTCTCTCGGCGTTTGCT 75
61 CGGCGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
76 CGGCGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
121 GGAAGTAAAGGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 180
136 GGAAGTAAAGGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 195
181 TGTATACATTTGACATTCAGAAATATATTCATGCTATCGCTTTTGAAGTTTAA 240
196 TGTATACATTTGACATTCAGAAATATATTCATGCTATCGCTTTTGAAGTTTAA 255
241 TTCTTGAAGGAGTAAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 300
256 TTCTTGAAGGAGTAAATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 315
301 TGTGTAGTGTGTATCAAAATTCGTGTATTCAGATCAGATCAGATCAGATCAG 360
316 TGTGTAGTGTGTATCAAAATTCGTGTATTCAGATCAGATCAGATCAGATCAG 375
361 GGTGCTTCAAAAACCTTTCAGAGAGATTTTCAACCAAGACCTTGTCTCTCT 420
376 GGTGCTTCAAAAACCTTTCAGAGAGATTTTCAACCAAGACCTTGTCTCTCT 435
421 AACACCAAGTATATATACAGAAAGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
436 AACACCAAGTATATATACAGAAAGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 495
481 ACTCTAAAAAGACCTTTTTCAGAGGATCTTTTGTGTTGCAATCTGGGATCTGA 540
496 ACTCTAAAAAGACCTTTTTCAGAGGATCTTTTGTGTTGCAATCTGGGATCTGA 555
541 ACAACTGGGTTATATACTGTATCAGATTCCTGTATGCTCACTGGTTTTCAGCA 600
556 ACAACTGGGTTATATACTGTATCAGATTCCTGTATGCTCACTGGTTTTCAGCA 615
601 ACAAAACAC 608
616 ACAAAACAC 623

```

RESULT 21
CB135111 581 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0187053 L14ChoICK0 Homo sapiens cDNA clone L14ChoICK0-19-H06
DEFINITION 5', mRNA sequence.
ACCESSION CB135111
VERSION CB135111.1 GI:28101713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-335, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.kribb.re.kr
Plate: 19 row: H column: 06
High quality sequence stop: 581.
Location/Qualifiers

FEATURES

source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14ChoICK0-19-H06"
/sex="M"
/cell_line="Choi-CK"
/lab_host="top10P"
/clone_lib="L14ChoICK0"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
Laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Query Match 31.2%; Score 577.8; DB 14; Length 581;
Best Local Similarity 99.7%; Pred. No. 4.8e-78;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

770 CGAGAAATTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 829
581 CGAGAAATTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 522
830 AAAGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 889
521 AAAGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 462
890 GAATTTCTTCAATCATGTGTATGTCTTTTAAATAATGACATGTTTCTTAAAGTGT 949
461 GAATTTCTTCAATCATGTGTATGTCTTTTAAATAATGACATGTTTCTTAAAGTGT 402
950 AACTAGAACCAACATCTGATGTAGTACATCTGACCTTAAATGTAGAACACACTGAC 1009
401 AACTAGAACCAACATCTGATGTAGTACATCTGACCTTAAATGTAGAACACACTGAC 342
1010 ATTCTGAAGTACTCAGCTAGTACACCAATCACTTAAAGCTTAAAGCTTGAAGTTA 1069
341 ATTCTGAAGTACTCAGCTAGTACACCAATCACTTAAAGCTTAAAGCTTGAAGTTA 282
1070 GATGACAGATGGCAATTCAGAGATCTGGTGTATGATACACAGACCAAGCATCTAAA 1129

```

TITLE
JOURNAL
COMMENT

FEATURES

ORIGIN

100

11

(<http://www.judawig.org.br/scripts/generaCmiz.php?cd=FM9&cz=FM9-2000>)

221100-004-e10&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 44

High quality sequence stop: 597.

FEATURES

source

1. .643

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CI0084"

/note="Organ: colon; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 30.2%; Score 559.2; DB 10; Length 643;

Best Local Similarity 97.5%; Pred. No. 3e-75; Indels 2; Gaps 2;

Matches 589; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

1022 AGTCCAGCTAGTACACCAAAATCATTAGCACTTAAGCCTTAGACTAGATGACAGATGG 1081

642 AGTCCAGCTAGT-CACTCTAATCATTAGCACTTAAGCCTTAGACTAGATGACAGATGG 584

1082 CAATTCAAGAGCTCTGCTGTTAGATACACAAGACAAACGATCTTAAGCAATATCTGCT 1141

583 CAATTCAAGAGCTCTGCTGTTAGATACACAAGACAAACGATCTTAAGCAATATCTGCT 524

1142 AGTAG-TAACCAAGATTAAGCATCCAAATGAGCAGCCAGACAGATGAAGAATGA 1200

523 AGTAGTAAACCAAGATTAAGCATCCAAATGAGCAGCCAGACAGATGAAGAATGA 464

1201 AAGATGAAGGCTTGTGTAATTCACGCTCTCTACATTTGATCTTTAACTTTA 1260

463 AAGATGAAGGCTTGTGTAATTCACGCTCTCTACATTTGATCTTTAACTTTA 404

1261 CAAGAGATTTTATTTTGGCTGATGGTAAAGCAAACTTTCATTTGTTTACTAT 1320

403 CAAGAGATTTTATTTTGGCTGATGGTAAAGCAAACTTTCATTTGTTTACTAT 344

1321 GTTAGACTACTGCACTAAGTTCATTGTTTACTATGCTGCTGTTGCAATATAC 1380

343 GTTAGACTACTGCACTAAGTTCATTGTTTACTATGCTGCTGTTGCAATATAC 284

1381 AAGATTAAGTCTTAGAGCATTTACTTCAAAAGTCTTTTCAAAATCAGATGCTTTTA 1440

283 AAGATTAAGTCTTAGAGCATTTACTTCAAAAGTCTTTTCAAAATCAGATGCTTTTA 224

1441 TTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTC 1500

223 TTTCCAAACCTTTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTC 164

1501 TTTCTTGAATTTGAAAAATGAGACCAAGGCTTCAACCTTGAATTTCCGACACT 1560

163 TTTCTTGAATTTGAAAAATGAGACCAAGGCTTCAACCTTGAATTTCCGACACT 104

1561 TAGGGAAGCAAGTCTAGAGGATTTGATTAAGCTAGAGGATTAAGACCAAGCTGGGCAAC 1620

103 TAGGGAAGCAAGTCTAGAGGATTTGATTAAGCTAGAGGATTAAGACCAAGCTGGGCAAC 44

1621 GTAT 1624

43 GAAT 40

RESULT 24

BI912725/c

BI912725 778 bp mRNA linear EST 16-OCT-2001

DEFINITION 603176385F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240564 5',

mRNA sequence.

BI912725

VERSION BI912725.1 GI:16176950

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Email: cgabs-remail.nih.gov

Contact: Robert Straube, Ph.D.

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

plate: IMAGE1606 row: j column: 21

High quality sequence start: 3

High quality sequence stop: 625.

Location/Qualifiers

1. .778

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5240564"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI;

Site 2: BcoRI (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (BcoRI site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH_MGC Library."

ORIGIN

Query Match 30.1%; Score 556.4; DB 12; Length 778;

Best Local Similarity 94.1%; Pred. No. 7e-75;

Matches 698; Conservative 0; Mismatches 31; Indels 13; Gaps 11;

1099 GTTGTGATGATCAAGCAAGCAAGATCTTAA-GCAATAGTGTAGTAA--CCAGA 1155

771 GTTGTGATGATCTAGTACTTACGATTTGAATCAAGTACTGTATATATATGCGATGA 712

1156 TAAAGCATCCAAATGAGCAGCCAG--AAACAGATGAAGAAATGAAAAGATG-AAAGG 1212

711 TATAGCATCCCAATGAGCAGCCAGGTTACAGATGAAGCAATGATGATGTAAGGC 652

1213 TTTTGGTGAATATTCACGGCTCC-TACATTTGATCCCTTTTAACTTACCA-AGAGAT 1270

651 TTTTGGTGAATATTCACGGCTCCCTTACATTTGATCCCTTTTAACTTACCAAGGAGAT 592

1271 TTTTATTTGGCTGATGGGTAAAGCCAACTTCTATTTGTTTAACTATGTTGA-GCTA 1329

591 TTTTATTTGGCTGATGGGTAAAGCCCAATTTCTATTTGTTTAACTATGTTGAAGCTTA 532

1330 CTGCACTAGTCTATTTGTTTAACTATGTTTCAACCTTGGAGATATACAGAGATTAAC 1389

531 CTGCACTAGTCTATTTGTTTAACTATGTTTCAACCTTGGAGATATACAGAGATTAAC 472

1390 TCTTAGTCACTTACTTCAAAAGTACTTTTCAAAATCAGATGCTTTTATTTCCAAAC 1449

471 TCTTAGTCACTTACTTCAAC-AGTACTTTTCAAAATCAGATGCTTTTATTTCCAAAC 413

1450 CTTTATTTTCACTTACTTAACTGTTGAGGGGAAGCTTTACAGACACATTTCTTAG 1508

```

Db      412 CTTTCTTCACCTTTCCTAGCTTGTGAGGGAGAGCTTACACA-ACACATCTTTTGG 354
QY      1509 AATTGAAAAGTGAGACCGACAGTGGCTCACCTGTATCCAGCACTTGGAGG 1568
Db      353 AATTGAAAAGTGAGACCGACAGTGGCTCACCTGTATCCAGCACTTGGAGG 294
QY      1569 ACAATCGAGGAGATTGATGAACTAGAGTTAAGACCGAGCTGGGACGATTTGAG 1628
Db      233 ACAATCGAGGAGATTGATGAACTAGAGTTAAGACCGAGCTGGGACGATTTGAG 234
QY      1629 ACCATGCTATTTAAAAATTTAAAAAGCAAGATAGCTTATTTTCAAAATATGGA 1688
Db      233 ACCATGCTATTTAAAAATTTAAAAAGCAAGATAGCTTATTTTCAAAATATGGA 174
QY      1689 AAGAAATTTATATGAAAATTTATCTGAGTCATTAATAATTCCTTAAGTGATCTTTT 1748
Db      173 AAGAAATTTATATGAAAATTTATCTGAGTCATTAATAATTCCTTAAGTGATCTTTT 114
QY      1749 AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGATATCATCATTAATTTGC 1808
Db      113 AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGATATCATCATTAATTTGC 54
QY      1809 AAAACATCATCTTAAAAATTTAAA 1830
Db      53 -AAACATCATCTTAAAAATTTAAA 33

RESULT 25
AA781435/c 549 bp mRNA linear EST 31-DEC-1998
LOCUS      aj26d07.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391437 3',
DEFINITION mRNA sequence.
ACCESSION AA781435
VERSION    AA781435.1 GI:2840766
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS   NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES    National Cancer Institute, Cancer Genome Anatomy Project (CCGAP),
JOURNAL   Tumor Gene Index
COMMENT    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
www-bio.1nl.gov/bdrp/image/image.html
Insert length: 1000 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 490.
Location/Qualifiers
1..549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NHT"
/vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from CloneTech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTCAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors

```

```

ORIGIN
Query Match      29.6%; Score 547.4; DB 9; Length 549;
Best Local Similarity 99.8%; Pred. No. 28-73;
Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cc5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

QY      1289 GTAAGCCAAACATTTCTATTTGTTTACTATGTTGAGTACTTGCAGTAAGTCACTTGG 1348
Db      549 GTAAGCCAAACATTTCTATTTGTTTACTATGTTGAGTACTTGCAGTAAGTCACTTGG 490
QY      1349 TTTTACTATGTTCACTGTTTGACAGTAAATPACAGATPACTCTTATGTCATTACTTCA 1408
Db      489 TTTTACTATGTTCACTGTTTGACAGTAAATPACAGATPACTCTTATGTCATTACTTCA 430
QY      1409 CAATGATCTTTTCAAAATCATGATGCTTTTATTTTCAAAACCTTTTTCACCTTCACT 1468
Db      429 CAATGATCTTTTCAAAATCATGATGCTTTTATTTTCAAAACCTTTTTCACCTTCACT 370
QY      1469 AAGTTGTAGGGGAGAGGCTTACAGACACATTCCTTGAATTTGGAAAAGTGAACGAG 1528
Db      369 AAGTTGTAGGGGAGAGGCTTACAGACACATTCCTTGAATTTGGAAAAGTGAACGAG 310
QY      1529 GCAAGTGGCTCAACCTGTATATCCAGACATTAGGGAAGACATGTCAGAGAGTGAAT 1588
Db      309 GCAAGTGGCTCAACCTGTATATCCAGACATTAGGGAAGACATGTCAGAGAGTGAAT 250
QY      1589 GAAGCTTAGAGTATAGACACAGCTGAGGACATGTAATGACATGTCATTAATTAATTA 1648
Db      249 GAAGCTTAGAGTATAGACACAGCTGAGGACATGTAATGACATGTCATTAATTAATTA 190
QY      1649 AATGTGAAAAGCAAGATATGCTTATTTCAAAATATGAAAAGAAATTTATATGAAAAT 1708
Db      189 AATGTGAAAAGCAAGATATGCTTATTTCAAAATATGAAAAGAAATTTATATGAAAAT 130
QY      1709 TATCTGAGTATTAATAATTTCTCTTAAGTATPCTTTTAAAGATCACTTATGGCTATA 1768
Db      129 TATCTGAGTATTAATAATTTCTCTTAAGTATPCTTTTAAAGATCACTTATGGCTATA 70
QY      1769 GTTGCCAGATTAATCTGTGATATCATGCAATTAATTTCAAAACATCATCTTAATTTA 1828
Db      69 GTTGCCAGATTAATCTGTGATATCATGCAATTAATTTCAAAACATCATCTTAATTTA 10
QY      1829 AAAAAAAAA 1837
Db      9 AAAAAAAAA 1

RESULT 26
B1462610 716 bp mRNA linear EST 21-AUG-2001
LOCUS      603203033F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269087 5',
DEFINITION mRNA sequence.
ACCESSION B1462610
VERSION    B1462610.1 GI:15253266
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS   NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLES    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (BLNL)

```


DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLMT at:
<http://image.llnl.gov>
 Plate: L1AM1678 row: 0 column: 08
 High quality sequence stop: 714.
 Location/Qualifiers

FEATURES

source

1..716
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5269087"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_97"
 /note="Organ testis; Vector: pBluescript (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (pGcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTT-3', size-selected for average
 insert size 2.2 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

Query Match 29.4%; Score 543.6; DB 12; Length 716;
 Best Local Similarity 97.4%; Pred. No. 6.4e-73;
 Matches 606; Conservative 0; Mismatches 9; Indels 7; Gaps 5;

1 CTGAGGCGGCGGTAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 60
 98 CTAGGCGGCGGTAGCATGAGGCGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 157
 61 CGGCGCATCTGCTTCCAGACCTCAACGCACTGCGGACGGAAGGTTTCTTCTTGG 120
 158 CGGCGCATCTGCTTCCAGACCTCAACGCACTGCGGACGGAAGGTTTCTTCTTGG 217
 121 GGAAGTAAAGGTGAAGCCAGACAGCATTAAGTATCCCAATGATGATGTTGAAGT 180
 218 GGAAGTAAAGGTGAAGCCAGACAGCATTAAGTATCCCAATGATGATGTTGAAGT 277
 181 TGTATTACATTCAGATTCAGAAATATATTCATCTCATGCTTTTAACTTTATTA 240
 278 TGTATTACATTCAGATTCAGAAATATATTCATCTCATGCTTTTAACTTTATTA 337
 241 TTCTTCAAGCGAATGAATGAGCAAGCACTGAAGAAATATATTCATCTCATGCTTTT 300
 338 TTCTTCAAGCGAATGAATGAGCAAGCACTGAAGAAATATATTCATCTCATGCTTTT 397
 301 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCAGATCAGATCAGAT 360
 398 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCAGATCAGATCAGAT 457
 361 GCTGCTTCAAAAACCTTGAGAGGATTTTCAACCAAGACCTGTTTCTGCTAAT 420
 458 GCTGTT---CAAAAATTCAGAGAGATTTTCAACCAAGACCTGTTTCTGCTAAT 514
 421 AACACCAAGTATATACAGAAAGTGTCTTACTCATGCACTGAACATTCCTTATCAT 479
 515 AACACCAAGTATATACAGAAAGTGTCTTACTCATGCACTGAACATTCCTTATCAT 574
 480 AACCTCAAAAAGACTTTTTCACAGGATCCTTTAG-TGGTTGCCAATGCGGCAATGCT 538
 575 AAACTCAAAAAGACTTTTTCACAGGATCCTTTAG-TGGTTGCCAATGCGGCAATGCT 634
 539 GAAACAATGCGGTAT-AAAATGTATCAAGTCTCTGTATGCTCA-CTGTTTAAAGCCAG 596
 635 GAAACAATGCGGTAT-AAAATGTATCAAGTCTCTGTATGCTCA-CTGTTTAAAGCCAG 694
 597 CAGTACAAACACACAGCTCTAA 618
 695 CAGTACAAACACACAGCTCTAA 716

RESULT 27
 AU144581/c
 LOCUS
 DEFINITION
 AU144581 HEMBA1 Homo sapiens cDNA clone HEMBA1002381 3', mRNA

ACCESSION
 AU144581
 VERSION
 AU144581.1 GI:11006102
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source

1..645
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBA1002381"
 /tissue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /clone_lib="HEMBA1"
 /note="Vector: pMR18SFL3"

ORIGIN

Query Match 29.0%; Score 536.2; DB 9; Length 645;
 Best Local Similarity 94.0%; Pred. No. 8.9e-72;
 Matches 608; Conservative 0; Mismatches 34; Indels 5; Gaps 5;

996 TAGAACACATGCAATTCCTGAAGCTTGTCCAGCTATATACCAACCAATCATTAAGATA 1055
 644 TGTGAGACCCNCTGNAATTCATGAGTGCAGTATG-CGCCCAATCATTAAGATA 586
 1056 AAGCTTAGACTTGAATGACAGATGCAATTCAGAGATCTCGGTTGTAGATCACAGA 1115
 585 AACCTTAGACTTGAATGACAGATGCAATTCAGAGATCTCGGTTGTAGATCACAGA 527
 1116 ACAACGATC-TAAAGCAATCTGTGATGATACCAAGATTAAGATCAACCAATGAGC 1174
 526 CCAACCTAATTTAAAGCAATCTGTGATGATACCAAGATTAAGATCAACCAATGAGC 467
 1175 AGCCCAAGAAAGATGAAGAAATGAAGATGAAGGTTTGGTGAATTTACAGGTC- 1233
 466 AGCCCAAGAAAGATGAAGAAATGAAGATGAAGGTTTGGTGAATTTACAGGTC- 407
 1234 TCCTACATTTGATCTTTTAACTTACCTTACAGAGATTTTAACTTGGCTGATGGTAAA 1293
 406 TCCTACATTTGATCTTTTAACTTACCTTACAGAGATTTTAACTTGGCTGATGGTAAA 347
 1294 GCGAAAGATTTCTATGTTTCTTCTAGTGTGAGCTACTGACAGTATGATTTGTTT 1353
 346 GCGAAAGATTTCTATGTTTCTTCTAGTGTGAGCTACTGACAGTATGATTTGTTT 287

QY 1354 ACTAGTTCACCTGTTTGAGTAATACAGAGTAACCTTAGTGCATTACTTCAAG 1413
DB 286 ACTATGTCACCGTTTGAGTAATACAGAGTAACCTTAGTGCATTACTTCAAG 227
QY 1414 TACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGT 1473
DB 226 TACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGT 167
QY 1474 GTTAGAGGGAAGGCTTACACAGACATCTTTAGATTGGAAGTGAACAGACACA 1533
DB 166 GTTAGAGGGAAGGCTTACACA-ACACATCTTTAGATTGGAAGTGAACAGACACA 108
QY 1534 GTGGCTCACACCTGTATCCAGCACTTAGGGAAGACAAGTCAAGAGATTGTAAGC 1593
DB 107 GTGGCTCACACCTGTATCCAGCACTTAGGGAAGACAAGTCAAGAGATTGTAAGC 48
QY 1594 TAGGAGTTAGAGACCGCTGGGCAACGATTGAGCCATGCTATT 1640
DB 47 TAGGAGTTAGAGACCGCTGGGCAACGATTGAGCCATGCTATT 1

RESULT 28
BQ422301 886 bp mRNA linear EST 23-MAY-2002
LOCUS BQ422301
DEFINITION AGENCOURT_7802195 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042035
5', mRNA sequence.
BQ422301 GI:21117616
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHM3280 row: m column: 12
High quality sequence stop: 707.
Location/Qualifiers
1..886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6042035"
/issue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI. Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 28.1%; Score 519.4; DB 13; Length 886;
Best Local Similarity 96.7%; Pred. No. 2.6e-69;
Matches 556; Conservative 0; Mismatches 6; Indels 13; Gaps 2;

QY 95 TCAGACACGAGAGGTTTCTTCTGGGAGTAAGAGTGAAGCAAGACACTTACT 154
DB 245 TTGGAATTTGAGAGGTTTCTTCTGGGAGTAAGAGTGAAGCAAGACACTTACT 304
QY 155 GATTCGCAATGATGATGTTGAAGTGTATATCATATGACATTCAGAAATATATTCGA 214

DB 305 GATTCGCAATGATGATGTTGAAGTGTATATCATATGACATTCAGAAATATATTCGA 364
QY 215 TGTATACGCTTTTACCTTTTAAATCTTTCAGGAGTAATATGACAGACACTGAAG 274
DB 365 TGTATACGCTTTTACCTTTTAAATCTTTCAGGAGTAATATGACAGACACTGAAG 424
QY 275 AAATATATCAATGCAAAAGAAATGAGTGTAGTGTATCAAAATCCGCTCATTTCA 334
DB 425 AAATATATCAATGCAAAAGAAATGAGTGTAGTGTATCAAAATCCGCTCATTTCA 484
QY 335 GATCAGATCATGACGTTTAAAGAGAGCTGCTTCAAAAACCTTGACAGACATTTTCA 394
DB 485 GATCAGATCATGACGTTTAAAGAGAGAGCTGCTTCAAAAACCTTGACAGACATTTTCA 544
QY 395 AACCAAGACCTGTTTCTGCTATTACACCAAGTATATTAACAGAAAGCTGCTACT 454
DB 545 AACCAAGACCTGTTTCTGCTATTACACCAAGTATATTAACAGAAAGCTGCTACT 604
QY 455 CATGACTGGAACATTCCTTATATAACTCAAAAAGACTTTTTCAGAGTACTTTA 514
DB 605 CATGACTGGAACATTCCTTATATAACTCAAAAAGACTTTTTCAGAGTACTTTA 652
QY 515 GTGGTGGCAATCTGGGCAATGCTGGAACCACTGGGTTATATACTGATCAGGTCCTGT 574
DB 653 GTGGTGGCAATCTGGGCAATGCTGGAACCACTGGGTTATATACTGATCAGGTCCTGT 712
QY 575 ATGTCACTGGTTTTACCGAGAGTACAAACACACAGCTCTAATTTTGAAGAGAT 634
DB 713 ATGTCACTGGTTTTACCGAGAGTACAAACACACAGCTCTAATTTTGAAGAGAT 772
QY 635 GGAT-CCTTAAAGAGGTATCATTAATATGAA 668
DB 773 GGATCCCTTAAAGAGGTATCATTAATATGAA 807

RESULT 29
B1664110 886 bp mRNA linear EST 21-AUG-2001
LOCUS B1664110
DEFINITION 603202891P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5268502 5',
mRNA sequence.
B1664110 GI:15254766
EST.
ACCESSION B1664110.1 GI:15254766
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Tohiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHM11677 row: f column: 23
High quality sequence stop: 715.
Location/Qualifiers
1..886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5268502"
/lab_host="DH10B"
/clone_id="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified

FEATURES
SOURCE

```

1      .967
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3830405G04"
/sex="female"
/tissue_type="placenta and extra embryonic tissue"
/idv_stage="18 days pregnant, adult"
/lab_host="DH0B"
/clone_id="Riken full-length enriched, 18 days pregnant, placenta and extra embryonic tissue"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genetic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGGAGAAGAAAGATCCACAGAGCTCTTTTTTTTTTTTTN 3']. cDNA was prepared by using triphase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGGAGAAGATTCCTCGCATTAATAAATTAAATGCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamH sites. Vector: a modified pBluescript KS(+) after blunt excision from Lambda

```

ORIGIN	FLC 1"
Query Match	26.9%; Score 498; DB 13; Length 967;
Best Local Similarity	83.3%; Pred. No. 4,26-66;
Matches	578; Conservative 0; Mismatches 115; Indels 1; Gaps 1;
QY	6 GCGCGGTACGATGAGAGGGAGAGTACGTGCGCGGTCTCTCGAGGCTTGTGCTCGCG 65
DB	35 GAGCGCGGAGATGAGAGGGGAGAG-CACGTGTGGGGGTGCTGTCTGCGTCTGCTCGCG 93
QY	66 CACTCGCTTTCAGCACTTCAACGGAATCTCGACAGAAAGGTTTCTTCTTGGGAG 125
DB	94 CGCTCACCTTTCATCATCTCAACACACACTCAGACAGAAAGGTTTCTCTCGGTGAA 153
QY	126 TAAAGGTGAAGCCAAAGACGACTACTGATTCGCAAGAGATGATGTTGAATGTTT 185
DB	154 TGAAGGTGAAGCCAAAGATAGCTTACTGATTCAGATGAGACAGTTTAAATGTTT 213
QY	186 ATACAAATTGACATTCAGAAATATATTCATGCTATACAGCTTTTATGCTTTTAAATCTT 245
DB	214 ATACAAATTGACATTCAGAAATATATTCATGCTATACAGCTTTTATGCTTTTAAATCTT 273
QY	246 CAGCGGAGATTAAGACAGCACTGAAAGAAATATTAACAAGTCAAAAGAAATGCG 305
DB	274 TAGGTGAAGTAAAGAACATGCACTGAAAGAGTTCTTCAAATGTCAGAAAGACTGCG 333
QY	306 TAGGTGGTACAAATTCCTGCTGATTCAGATCAGATCATGACGTTTAAAGAGAGCTGC 365
DB	334 TGGGTGGTAAATTCCTGCTGATTCAGATCAGATCATGACGTTTAAAGAGAGCTGC 393
QY	366 TTCAAAAACCTGCGAGAGCATTTTTCACCAAGACCTGTTTCTGCTATTAACAC 425
DB	394 TCACAGAAATTAACAGACATCTTTCAGACCTGAGCTGTTTCTGTTGTTAAACAC 453
QY	426 CAACTATTAATTAAGAAAGCTGCTCTACTCATGCACTGGAACATTCTTATATAACCTC 485
DB	454 CGAGTATTAACAGAAAGCTGCTCTACTCATGCTGGAACAGCTTATATAACCTC 513
QY	486 AAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGGCCATCTGGGCACTGTCTGAACAC 545
DB	514 AAAAGGGGCTTTTTCATAGGGTACCATTTGGTGGTTACCAACTGGGAATGTCTATCAAC 573
QY	546 TGGTATTAATAACCTGATACGGTCTCTGATATGCACTGTTTACCGGACAGTACAA 605
DB	574 TGGTATTAATAACGAACTGCTCTCTGATATGCACTGTTTATAGTACCTGTGAGGA 633
QY	606 CACAAGCTCAAAATTTTTCAGAGAGATGATCTTAAAGAGAGTACATTAAGATAATG 665
DB	634 CACAAGCTCAAAATTTTTCAGAGAGATGATCTTAAAGAGAGTACATTAAGATAATG 693
QY	666 AAATGATGCTTCAATTAAGAGAAATTAAGAG 699
DB	694 AAATGATGCTTCAATTAAGAGAAATTAAGAG 727
RESULT 33	
LOCUS	BB600568 641 bp mRNA linear EST 26-OCT-2001
DEFINITION	BB600568 RIKEN full-length cDNA clone D230004N03 5', mRNA sequence.
ACCESSION	BB600568
VERSION	BB600568.2 GI:16450473
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 641)
AUTHORS	Aikawa,T., Garincsi,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiromoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Konda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, K., and Hayashiaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Dec 1, 2000 this sequence version replaced gi:11509169.

Sanjo, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arikawa, T., et al. 2001)

Unpublished (2001)

On Dec 1, 2000 this sequence version replaced gi:11509169.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagii, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1577-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamahata, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences *Mamm. Genome*, 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

1. .641

```

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D23004N03"
/tissue_type="eyeball"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, 12 days embryo
eyeball"
/notes="Site 1: Salt. Site 2: Bantl; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 5'
GAGGAGAGACCGCCGCCCACTGAGATTTTTTTTTTTTNN 3', cDNA was
prepared by using rTetraase thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence 15'
GAGGAGAGGATTCGGATTAAATTAATTAATTCGGCCCCCCCCC 3'. cDNA
was cleaved with Bantl and XhoI. Vector: a modified
bluescript KS(+) after bulk excision from Lambda FLX I."

```

25.1%; Score 464; DB 10; Length 641;

[illegible]

RESULT 34	AM978690/c	487 bp	mRNA	linear	EST 02-JUN-2000
LOCUS	AM978690/c				
DEFINITION	EST390799	MAGE	resequences,	MAGEF	Homo sapiens CDNA, mRNA sequence.
ACCESSION	AM978690				
VERSION	AM978690.1	GI:8169962			
KEYWORDS	EST.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	1 (bases 1 to 487)				
	Hedge, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,				
	Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Vestman, T. J. and				
	Quackenbush, J.				
TITLE	Assessment of gene expression patterns in a model of colon tumor				
	metastasis using a 19,200 element cDNA microarray				
	Unpublished (2000)				
JOURNAL	Contact: John Quackenbush				
COMMENT	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850, USA				
	Tel: 301 838 3528				
	Fax: 301 838 0208				
	Email: johnqc@icgr.org				
	Plate: 396				

Seq primer: Forward.
Location/Qualifiers
1. .487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1lb="MAGE Resequences, MAGE"
/note="Vector: pBluescriptSKm"

ORIGIN

Query Match 25.1%; Score 463.8; DB 10; Length 487;
Best Local Similarity 98.5%; Pred. No. 9.4e-61;
Matches 468; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1345 TTGTGTTTACTATGTTACCTGTTGACGATATACAGATATACCTTATGTCATTAC 1404
DB 475 TTGTTTCTATATGTTACCTGTTTGCAGTATACAGATATACCTTATGTCATTAC 416
QY 1405 TTCACAAAGTACTTTTCAACATGATGCTTTTATTTCCAAACCTTTTTCACCTT 1464
DB 415 TTCACAAAGTACTTTTCAACATGATGCTTTTATTTCCAAACCTTTTTCACCTT 356
QY 1465 CACTAAGTTGTTGAGGGGAAAGCTTACACACACATTTTGAATTGAAAAGTGAGA 1524
DB 355 CACTAAGTTGTTGAGGGGAAAGCTTACACACACATTTTGAATTGAAAAGTGAGA 296
QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACCTTAGGAAACAAGTCAGAGGATT 1584
DB 295 CCAGGACAGTGGCTCACACCTGTATCCAGACCTTAGGAAACAAGTCAGAGGATT 236
QY 1585 GATTGAAGCTAGAGAGTTAGAGACCAAGCTGGGCAAGTATGAGACCATGTCTATTA 1644
DB 235 GATTGAAGCTAGAGAGTTAGAGACCAAGCTGGGCAAGTATGAGACCATGTCTATTA 176
QY 1645 AATTAATGGAAGAGAGATATGCTTATTTTCAAAATATGAAAAGAAATTTATTA 1704
DB 175 AATTAATGGAAGAGAGATATGCTTATTTTCAAAATATGAAAAGAAATTTATTA 116
QY 1705 AATTATCTGAGCTATTAATAATCTCTTAACTGATGATCTTTTGAAGTACATTATG 1764
DB 115 AATTATCTGAGCTATTAATAATCTCTTAACTGATGATCTTTTGAAGTACATTATG 56
QY 1765 TAGAGTGGCAAGTAAATGCTGATATCATGAATTAATTTGCCAAACATCATC 1819
DB 55 TAGAGTGGCAAGTAAATGCTGATATCATGAATTAATTTGCCAAACATCATC 1

RESULT 35
BU258945 812 bp mRNA 1linear EST 26-NOV-2002
LOCUS BU258945 603412839F1 CSECHN38 Gallus gallus cDNA clone Chest332n 5', mRNA
DEFINITION sequence.
ACCESSION BU258945
VERSION BU258945.1 GI:25523420
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Archaeopteryx; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianidae; Gallus.
1 (bases 1 to 812)
Boardman, P. E., Sanz-izquierro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.,
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335354
12445392
JOURNAL MEDLINE
PUBMED
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930

Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .812
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="Chest332n5"
/dev_stage="36"
/lab_host="DH10B"
/clone_1lb="CSECHN38"
/note="Organ: Limbs; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 25.0%; Score 463; DB 13; Length 812;
Best Local Similarity 75.2%; Pred. No. 9.2e-61;
Matches 577; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 23 GGGAGAGTACGTCGCGGCTGCTCTCGGCTTGTGCTCGCGCACTGCTTCCAGCAC 82
DB 1 GGGAGAGAGAGTACGTCGCTGCTCTCGGCTTGTGCTCGCGCCCTCGCTTCCAGCAC 60
QY 83 CTCACACGAGCTGAGACAGGAAAGTTTCTTCTTGGGAAATGAAGTGAAGCCAG 142
DB 61 CTCACACGAGCTGAGACAGGAAAGTTTCTTCTTGGGAAATGAAGTGAAGCCAG 120
QY 143 AACGACATTCGATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 202
DB 121 AACGACATTCGATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 203 AATATATTCATGCTATGACCTTTTATGCTTTTATATTTCTTCCAGGCGAATGATGAG 262
DB 181 AATATATTCATGCTATGACCTTTTATGCTTTTATATTTCTTCCAGGCGAATGATGAG 240
QY 263 CAAGCACTGAAAGAAATATATCAAAATGCAAAAGAAATGATGATGATGATGATGATGAT 322
DB 241 CAAGCACTGAAAGAAATATATCAAAATGCAAAAGAAATGATGATGATGATGATGATGAT 300
QY 323 CGTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 382
DB 301 CGTGTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 383 GAGCATTTTCAACCAAGCAAGCTTTTCTCTGCTATTAACCAAGATATATTAACAGAA 442
DB 361 GAGCATTTTCAACCAAGCAAGCTTTTCTCTGCTATTAACCAAGATATATTAACAGAA 420
QY 443 AGCTGCTTCACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 502
DB 421 AGCTGCTTCACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 503 AGGATACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 562
DB 481 AGGATACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 563 TCAGGTTCTGATATGTCACCTGTTTATGAGCGAGAGTACAAACACACAGCTTAAATTT 622
DB 541 TCAGGTTCTGATATGTCACCTGTTTATGAGCGAGAGTACAAACACACAGCTTAAATTT 600
QY 623 TTGAAGAAAGTGAATCTTAAAGAGAGTACATTAAGTAAATGATGATGATGATGATGAT 682

Accession	Sequence	Position
Db	601 TTTTAAGAAAGATGGATCCCTACCAAGGTTCAACAGTAATAGATGTATGCCACCTTG	660
QY	683 CAAGAGAAATTAAAGATATATGCAAAAAAGTGAAGCAGTGAAACAGCATGATATAA	742
Db	661 CAGAGAGAGCTACAGAAAATATGCTCTGATGTAGAGAGCAGTGAAACATCTGTAGAGAAAG	720
QY	743 CTAGTAAAGATGTAAACAGATTAAAGAGAAATTGAGAAAAGAG	789
Db	721 CTCTTAACAGAGGTGAGCCAAATTGAAGAGAGCATCAATTGAAAAG	767

RESULT	36			
LOCUS	AM977201/c			
DEFINITION	AM977201	472 bp	mRNA	linear
ACCESSION	EST389310	MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.		
VERSION	AM977201			
KEYWORDS	AM977201.1	GT:816844		
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			

REFERENCE
AUTHORS
1 (bases 1 to 472)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,

TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
-------	--

COMMENT
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528

Seq primer: Forward.

```
FEATURES
source
location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
/cdate_lib="MAGB resequences"
/cnote_lib="MAGB resequences"
/cnote="Vector: pBluscriptSkm"
```

Query Match	25.0%;	Score 462.4;	DB 10;	Length 472;
Best Local Similarity	98.7%;	Pred. No. 1.6e-60;		
Matches 466; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1219	GGAAATATCAGGTCCTCTACATTTTGAATCCCTTTAACTTACCTTACAGAGAGATTTTTTTT	1278
Db	472	TGAATATTCAGGTCCTCTACATTTTGAATCCCTTTAACTTACAGAGAGATTTTTTTT	413
QY	1279	TGCTGATGGGTAAAGCCAAATTTCTATTGTTTTTTACTATGTTGACTTACTGCAGTA	1338
Db	412	GGGCTGAAGGGTAAAGCCAAATTTCTATTGTTTTTTACTATGTTGACTTACTGCAGTA	353
QY	1339	AGTTCATTGTTTTTACTATGTTTCCCTGTTTGCAATAACAGATTAATCTTTAGTC	1398
Db	352	AGTTCATTGTTTTTACTATGTTTCCCTGTTTGCAATAACAGATTAATCTTTAGTC	293
QY	1399	ATTACTCTACAAAGTACTTTTTCAAATCATGATGCTTTTATTTCCAAACCTTTTTTC	1458
Db	292	ATTACTCTCCAAAGTACTTTTTCAAATCATGATGCTTTTATTTCCAAACCTTTTTTC	233
QY	1459	ACCTTTCATCTAGTGTGTGAGGGGAGGCTTACACAGACACTTCTTTAGATTGGAAA	1518
Db	232	ACCTTTCATCTAGTGTGTGAGGGGAGGCTTACACAGACACTTCTTTAGATTGGAAA	173
QY	1519	GTGAGACCAAGCAGTGGCTCACACTGTAAATCCAGCACTTAGGGAAGACATGTCAG	1578

Db	172	GTGAGCACGAGCAGTGGCTCAACCTGTATCCAGCCCTTTGAGGAGAAACAATGAG	113
Qy	1579	AGGATTTATTTGAACCTTGGAGGTTGAGACCGACGCTGGGCAACGATTTAGACCATGTCTA	1638
Db	112	AGGATTTATTTGAACCTTGGAGGTTGAGACCGACGCTGGGCAACGATTTAGACCATGTCTA	53
Qy	1639	TTTAAAAATTAAATGCGAAAAGCAAGATAGCTTATTTCAAATTATGAGAA	1690
Db	52	TTTAAAAATTAAATGCGAAAAGCAAGATAGCTTATTTCAAATTATGAGAA	1

RESULT	37
AIR820814/c	
LOCUS	523 bp mRNA linear EST 24-OCT-2000
DEFINITION	YPI6A2.Y5 Scores breast 3mbHst Homo sapiens cDNA clone
	IMAGE187582.5', similar to TR:Q5018 Q5018 ORF', RNA sequence.
ACCESSION	AIR820814
VERSION	AIR820814.1
KEYWORDS	GI:5439893
SOURCE	EST
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Homo sapiens

REFERENCE
Mammalia; Eutheria; Primates; Catarrhini; Homnadae; Homo.
1 (bases 1 to 523)
NOT CON http://www.ncbi.nlm.nih.gov/ncbi/ncbi

Tumor Gene Index
Journal
Unpublished (1997)
 Other items: 191637 x5

Email: cgapbs-romail.nih.gov
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
IMAGE Consortium is a non-profit organization dedicated to the
provision of a repository of a previously frozen human clone

information
This 5' resequenced clone has no previous 5' data to verify this
and need a control

```

new read against
Putative full length read
The vector to vector length is 706
Possible reversed clone: similarity on wrong strand
Insert length: 780 Std Error: 0.00
Seq primer: -40bp from Gibco
High quality sequence stop: 441.

```

FEATURES	Location/Qualifiers
source	1. 523 /cervarium, rhino, caracorell

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib=" Soares breast 3nBbSt"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATGCTGAATGGAGGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fátima
Bonaldo."

```

Query Match	24.1%	Score 446	DB 9	Length 523
Best Local Similarity	92.7%	Pred. No. 4.5e-58		
Matches 492	Conservative	0	Mismatches 31	Indels 8
			Gaps 2	
109	TTTTTCTTTGGGAGTAAAGGCGAAGCAGCATTAAGTCCCAATGGA	168		

Db 523 TGTCTCTTCTTAAGAGTAAAGATGAGGCAAGAAATAGCATTTACTGATTCGCAATGGA 464
QY 169 TGAATGTGAAGTGTGTTATPACAAATTGACATTCAGAAATATATTCATGCTGATGACTTTT 228
Db 463 TGAATGTGAAGTGTGTTATPACAAATTGACATTCAGAAATATATTCATGCTGATGACTTTT 409
QY 229 TACCTTTTATTAATCTTCAAGGCAAGTAATGAGCAAGCATGAGAAATATTTTCAAA 288
Db 408 TACCTTTTATTAATCTTCAAGGCAAGTAATGAGCAAGCATGAGAAATATTTTCAAA 349
QY 289 TGTCAAAAAGATGTGTAGTGTGTGACAAATTCCTGCTCATTTGATGATGATGATGAC 348
Db 348 TGTCAAAAAGATGTGTAGTGTGTGACAAATTCCTGCTCATTTGATGATGATGATGAC 289
QY 349 GTTTAAGAGAGGCTGCTTCAAAAAGTTCAGAGGCAATTTTTCACCAAGACCTTGT 408
Db 288 GTTTAAGAGAGGCTGCTTCAAAAAGTTCAGAGGCAATTTTTCACCAAGACCTTGT 229
QY 409 TTTTCTGCTATTACACCAAGTATTAATAACAGAAAGCTGCTCATGCTGATGCTGGAACA 468
Db 228 TTTTCTGCTATTACACCAAGTATTAATAACAGAAAGCTGCTCATGCTGATGCTGGAACA 169
QY 469 TTTCTTATATTAACCTTCAAAAAGGACTTTTTCACAGGGTACCTTTATGTGTGCTGATCT 528
Db 168 TGTCTT---GAAACCTCAAGAGAGGACTTTTTCACAGGGTACCTTTATGTGTGCTGATCT 112
QY 529 GGGCATGTCTGAACCACTGGGCTTATTAATACTGATGAGGTTCTGCTGATGCTGATGCTT 588
Db 111 GGTATTTCTGAAACCACTGATGATTAATACTGATGAGGTTCTGCTGATGCTGATGCTT 52

RESULT 38
Bg087655
LOCUS H3144D04-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
DEFINITION H3144D04 5', mRNA sequence.
ACCESSION Bg087655
VERSION Bg087655.2 GI:40106963
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Dol,H.,
1 (bases 1 to 602)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Genomic-wide expression profiling of mid-gestation placenta and
JOURNAL embryo using a 15,000 mouse development cDNA microarray
MEDLINE 20381348
PUBMED 10922068
COMMENT On Jan 26, 2001 this sequence version replaced gi:12570307.
Other_BESTs: H3144D04-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://igsun.grc.nia.nih.gov/cdna/15k.html> for details.
Place: H3144 row: D column: 04
Seq primer: -21M13 Reverse
High quality sequence stop: 602
POLYA=No.

FEATURES

Location/Qualifiers
1..602
/organism="Mus musculus"
/mol_type="mRNA"

/strain="CS7BL/6J"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="H3144D04"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"
/clone_id="NIA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 Kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development cDNA microarray, 2000, Proc Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the r-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

Query Match 23.9%; Score 442; DB 12; Length 602;
Best Local Similarity 84.0%; Pred. No. 1.e-57;
Matches 499; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 6 GCGCGGTAGCAGTGAAGAGAGTACGTCGCGGCTCTGCGGCTTGTCTGCGCG 65
Db 8 GAGCGGAGATGAGAGGCGAGAGCAGTGGGCGGCTGCTGCTGCTGCTGCGCG 67
QY 66 CACTGCTTTCAGACACCTGACACGAGTCTGACACGAGAGGTTTCTTGGGAG 125
Db 68 CGCTCATTTTCATCATCTCAACACAGACTCAGACAGGAGTTTCTCTCGGTGAAA 127
QY 126 TAAAGGTGAAGCCAAAGACATTTCTATTTCCCAAAGATGATGATGATGATG 185
Db 128 TGAAGGTGAAGCCAAAGACATTTCTATTTCCCAAAGATGATGATGATGATG 187
QY 186 ATCAATTGACATTCAGAAATATATTCATGATGATGATGATGATGATGATGATG 245
Db 188 ATCAATTGACATTCAGAAATATATTCATGATGATGATGATGATGATGATGATG 247
QY 246 CAGCGGAGTGAATGAGACACGCTGAGAAATATTTTCAATGTCAAAAAGATG 305
Db 248 TAGGTGAAGTGAAGACACGCTGAGAAATATTTTCAATGTCAAAAAGATG 307
QY 306 TAGGTGTCAAAATTCCTGCTCATTCATGATGATGATGATGATGATGATGATG 365
Db 308 TGGGTGTCAAAATTCCTGCTCATTCATGATGATGATGATGATGATGATGATG 367
QY 366 TTCAAAAAGTTCAGAGACATTTTCAACCAAGACCTGTTTCTGCTATTAAC 425
Db 368 TCCACAGAAATTCAGAGACATTTTCAACCAAGACCTGTTTCTGCTATTAAC 427
QY 426 CAAGTATTAATACAGAAAGTGTCTACTGATGATGATGATGATGATGATGATGATG 485
Db 428 CGAGTATTAATACAGAAAGTGTCTACTGATGATGATGATGATGATGATGATGATG 487
QY 486 AAAAGGACTTTTTCAGAGGCTTCTTATGTTGCTGATGATGATGATGATGATG 545
Db 488 AAAAGGACTTTTTCAGAGGCTTCTTATGTTGCTGATGATGATGATGATGATG 547
QY 546 TGGGTATTAATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 599
Db 548 TGGGTATTAATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 601

Best Local Similarity 97.6%; Pred. No. 2.2e-56;
Matches 452; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1222 ATATTCACGGCTCTCCATATTTGATTCCTTTACCTTACAGAGATTTTATTTG 1281
465 ATATTCACGGCTCTCCATATTTGATTCCTTTACCTTACAGAGATTTTATTTG 406
QY 1282 CTGATGGGTAAGCCAAATTTCTATTTTCTATGTGAGCTACTTGCAATG 1341
405 CTGATGGGTAAGCCAAATTTCTATTTTCTATGTGAGCTACTTGCAATG 346
QY 1342 TCATTTGTTTACTATGTTCACCTGTTTGACAGTAAACAGATTAAGCTTATG 1401
345 TCATTTGTTTACTATGTTCACCTGTTTGACAGTAAACAGATTAAGCTTATG 286
QY 1402 TACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTTTCAC 1461
285 TACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTTTCAC 226
QY 1462 TTTCACTAGTTGTGAGGGGAAAGGCTTACAGACACATCTTTTATGATTTGAAAAGT 1521
225 TTTCACTAGTTGTGAGGGGAAAGGCTTACACACATCTTTTATGATTTGAAAAGT 167
QY 1522 AAGCCAGGACAGTGGCTCACACCTGTATCCAGACTTTAGGAAAGCAAGTCAGAG 1581
166 AAGCCAGGACAGTGGCTCACACCTGTATCCAGACTTTAGGAAAGCAAGTCAGAG 107
QY 1582 ATTGATTAAGCTAGAGATTAGAGACAGCCTGGGCAAGTATGAGCAATGCTATTA 1641
106 ATTGATTAAGCTAGAGATTAGAGACAGCCTGGGCAAGTATGAGCAATGCTATTA 47
QY 1642 AAAAATTAATGAAAAAGCAAGATAGCCTTATTTTCAAAATA 1684
46 AAAAATTAATGAAAAAGCAAGATAGCCTTATTTTCAAAATA 4

RESULT 41
BG922020 634 bp mRNA linear EST 05-JUN-2001
LOCUS 602821921F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:495098 5',
DEFINITION mRNA sequence.
ACCESSION BG922020
VERSION BG922020.1 GI:14302496
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10906 row: 1 column: 05
High quality sequence stop: 632.
Location/Qualifiers

FEATURES
source
1..634
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:495098"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"

/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt;
Site 2: Not; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Query Match 23.4%; Score 433.4; DB 12; Length 634;
Best Local Similarity 83.8%; Pred. No. 3.2e-56;
Matches 502; Conservative 0; Mismatches 96; Indels 1; Gaps 1;
QY 3 GAGGCGGCGTAGCATGAGGGGAGAGTACGTGGGCGGTCTC-GGGCTTTGTGCTC 61
18 GAGGCGGCGCATGATGAGGGGAGAGACAGCTGGGGGCGTCTGTGGCTTCGCTC 77
QY 62 GCGGCACTGCTTTCCAGACCTTCAACAGCGACTCGGACAGGAGGTTTCTTGG 121
78 GCGGCGCTCACTTTCCATCATCTCAACAGACTCAGACAGGAGGTTTCTCCTCGT 137
QY 122 GAAGTAAAGTGAAGCCAGAAACAGCATTAAGTCCCAATGATGTTGAAGT 181
138 GAAGTAAAGTGAAGCCAGAAATAGCATTAAGTTCACAGATGACAAAGTTAA 197
QY 182 GTTATACAAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAT 241
198 GTTATACAAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAT 257
QY 242 TCTTCAGGCGAAGTAATGCAAGCACTGGAAGAAATATATCAATGTCAAAAGAT 301
258 TCTTCAGGCGAAGTAATGCAAGCACTGGAAGAGTTCTTTCATATGTCAGAAAG 317
QY 302 GTGCTAGGTTGTAACAATTCGCTGCTATTCATGATGATGATGATGATGATG 351
318 GTGCTAGGTTGTAACAATTCGCTGCTATTCATGATGATGATGATGATGATG 377
QY 362 CTGCTTACAAAACTTGCGAGGACATTTTTCAGAACCAACCTTTTTCGCTATTA 421
378 TTACTCCACAGAACTTACAGACACATCTTTCAGGCTGATGCTTTTCCGTGTTA 437
QY 422 ACACCAAGTAAATTAACAAGAGGCTGCTACTATCATGACATGCAATTCCTTATTA 481
438 ACACCAAGTAAATTAACAAGAGGCTGCTACTATCATGACATGCAATTCCTTATTA 497
QY 482 CTGCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTTCGATTCGGGCAATGCGAA 541
498 CTTCAAAAGGGGCTTTTTCATAGGGTACATGCTGTATCAATCTGGAAATGCTGAT 557
QY 542 CAATGGGTTATTAACAAGTATCAGGTTCTGTATGTCACATGATTTAGCCAGCAGT 600
558 CAATGGGTTATTAACAAGGAACTGCTTCTGTATGTCACATGCTTATTAAGGCTGT 616

RESULT 42
AA831922/c 437 bp mRNA linear EST 18-MAR-1998
LOCUS OC90404.81 NCI_CGAP_Homo sapiens cDNA clone IMAGE:1356942 3',
DEFINITION mRNA sequence.
ACCESSION AA831922
VERSION AA831922.1 GI:2905021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/ncicgap/
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLM at:
 www-bio.llnl.gov/bbip/image/image.html
 Insert Length: 1809 Std Error: 0.00
 Seq primer: -40m3 fwd. Et from Amersham
 High quality sequence stop: 427.
 Location/Qualifiers

FEATURES

1. 437
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1356942"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_1lb="NCI CGAP GCBI"
 /note="Vector: p773D-Pac (pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 23.4%; Score 432.2; DB 9; Length 437;
 Best Local Similarity 99.3%; Pred. No. 6.1e-56;
 Matches 434; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

1398 CATTACTTACAAAGTACTTTTCAACATGATGCTTTATTTCCAAACCTTTT 1457
 437 CATTACTTACAAAGTACTTTTCAACATGATGCTTTATTTCCAAACCTTTT 378
 1458 CACCTTCTCAATGTTGAGGGGAGGCTTACAGACATTTCTTTAGATTGAAA 1517
 377 CACCTTCTCAATGTTGAGGGGAGGCTTACAGACATTTCTTTAGATTGAAA 318
 1518 AGTGAAGCAGGACAGTGGCTCACACCTGTAATCCACACTTGAAGGAAAGTCTG 1577
 317 AGTGAAGCAGGACAGTGGCTCACACCTGTAATCCACACTTGAAGGAAAGTCTG 258
 1578 GAGGATGATTGAAGCTGAGATTGAGACCAAGCTGGGCAAGTATGAGCAATGCT 1637
 257 GAGGATGATTGAAGCTGAGATTGAGACCAAGCTGGGCAAGTATGAGCAATGCT 198
 1638 ATTAAAAAATTAATGAAAGCAAGATGAGCTTTATTTTCAAAATGAAAGAAATT 1697
 197 ATTAAAAAATTAATGAAAGCAAGATGAGCTTTATTTTCAAAATGAAAGAAATT 138
 1698 ATTAAAAAATTAATGAGTCAATTAATTTCTCTTAAGTATGATCTTTTGAAGTACA 1757
 137 ATTAAAAAATTAATGAGTCAATTAATTTCTCTTAAGTATGATCTTTTGAAGTACA 78
 1758 TTATGCTAGAGTCCAGATTAATGCTGATATCATGCAATTAATTTGCAAAACATCA 1817
 77 TTATGCTAGAGTCCAGATTAATGCTGATATCATGCAATTAATTTGCAAAACATCA 18
 1818 TCTAAAAATTTAAAAAA 1834
 17 TCTAAAAATTTAAAAAA 1

RESULT 43

BB638750
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

TITLE
 JOURNAL
 COMMENT

BB638750 618 bp mRNA linear EST 31-AUG-2001
 BB638750 RIKEN full-length enriched, 3 days neonate thymus Mus
 musculus cDNA clone A630051L12 5', mRNA sequence.
 BB638750.1 GI:15401242
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 618)
 Hara,A., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Kono,H., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takanashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshinide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 yhl.http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
 Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y., and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
 Arakawa,T., Ishii,Y., and Hayashizaki,Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Func. Genomics 2 pre, L72-L86 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1. 618
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A630051L12"
 /tissue_type="thymus"
 /dev_stage="3 days neonate"
 /lab_host="DH10B"
 /clone_1lb="RIKEN full-length enriched, 3 days neonate
 thymus"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'

ORIGIN

/dev stage="13 days pregnant adult"
/clone.lib="RIKEN full-length enriched, 13 days pregnant
adult Female placenta"

Query Match 23.2%; Score 429; DB 13; Length 622;
Best Local Similarity 83.2%; Pred. No. 1.5e-55;
Matches 486; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 6 GCGGGGAGAGATGAGGGGGAGAGTACGTGGGGCTGCTCGGGCTTTGTCTGGCG 65
DB 39 GAGGGGCGAGATGAGGGGGCGAGAGACGTTGGGGGTCTGTGGCTTCGTCTGGCG 98
QY 66 CACTGCTTTCCAGACCTCAACAGGACTGGACAGGAGTTTCTTCTGGGAG 125
DB 99 CGCTCACTTTCATCATCTCAACAGACTCAGACAGGAGTTTCTCTCGGTGAA 158
QY 126 TAAAGGTGAAGCCAGAGACGATTAAGTATCCCAATGAGATGATGAGTTGTT 185
DB 159 TGAAGGTGAAGCCAGAGATGATTAAGTATCCCAATGAGATGAGTTGTT 218
QY 186 ATACAATTGACATTCAGAAATATATTCATGCTATGCTTATGCTTTATATCTT 245
DB 219 ATACATTTGACATTCAGAAATATATTCATGCTATGCTTATGCTTTATATCTT 278
QY 246 CAGGCGAATTAATGAGCAGACGATGAGAAATTTATCAATGTCAGAAAGATGAG 305
DB 279 TAGGTGAGTAAACGAAATGACATGCAAGAAAGTTCTTCAATGTCAGAAAGATGAG 338
QY 306 TAGGTGATCAAAATCCGTGCTCATTCAGATCATGATCATGATGATGAGAGGCTGC 365
DB 339 TGGGTGATTAATTTCCGTGCTCATTCAGATCATGATCATGATGATGAGAGGCTGC 398
QY 366 TTCACAAAATCTTCAGAGACATTTTCAACCAAGACCTGTTTCTGCTATTAAC 425
DB 399 TCACAGAAATTCAGAGACATTTTCAAGCCCTGAGCTGTTTCTGTTTAAAC 458
QY 426 CAAGTATTAATCAGAAAGCTGCTCATTCAGATCATGATCATGATGATGAGAGGCTGC 485
DB 459 CGAGTATTAACAGAAAGCTGCTCATTCAGATCATGATCATGATGATGAGAGGCTGC 518
QY 486 AAAAGAGATTTTCAAGGATCTTTAGTGTGCTTCCATGTCGATGTCGATGAC 545
DB 519 AAGGGGGCTTTTCAAGGATCTTTAGTGTGCTTCCATGTCGATGTCGATGAC 578
QY 546 TGGGTATTAATTAAGTATGAGGTTCTGATGTCGATGTCGATGTCGATGTC 589
DB 579 TGGGTATTAATTAAGTATGAGGTTCTGATGTCGATGTCGATGTCGATGTC 622

RESULT 45 798 bp mRNA linear EST 24-OCT-2000
BF139015 601782740F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4010744 5',
LOCUS
DEFINITION
RNA sequence.
BF139015
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (base 1 to 798) http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Straube, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LHM9248 row: p column: 09
High quality sequence stop: 648.
Location/Qualifiers

FEATURES

source

1.798
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4010744"
/issue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/notes="Toban: lung; Vector: PCMV-SPORE6; Site 1: NotI;
Site 2: SalI; Transgenic model MNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: 0.19g
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 23.1%; Score 427.4; DB 10; Length 798;
Best Local Similarity 80.9%; Pred. No. 2.2e-55;
Matches 596; Conservative 0; Mismatches 131; Indels 10; Gaps 8;

QY 15 GCATGGAGGGGAGAGTACGTCGCGGCTGCTCGGGCTTTGTCTCGGCGACCTGCTT 74
DB 1 GTATGAGGGCGAGACAGACGTTGGGGGTCTGCTCGGCTCGGCGGCTCACTT 60
QY 75 TCAGACCTCAACACGAGCTCGGACACGGAAGTTTCTTCTGGGAGAAAGAG 134
DB 61 TCATCATCTCAACACAGACTCAGACAGGAGTTTCTCTCGGTGAATGAAG 120
QY 135 AAGCAAGAACAGCATTAATGATTCCTCAATGATGATGATGATGATGATGATGATG 194
DB 121 AAGCCAGAAATACATTAATGATTCATGATTCATGATTCATGATTCATGATTCATG 179
QY 195 ACATTCAGAAATTAATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 254
DB 180 ACATTCAGAAATTAATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 239
QY 255 TAAATGAGCAGACGAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 314
DB 240 TAAATGAGCAGACGAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 298
QY 315 ACAATTCGCTGCTCATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 374
DB 299 ATAAATTCGCTGCTCATTCATGATTCATGATTCATGATTCATGATTCATGATTCATG 358
QY 375 ACTTCAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGATTA 434
DB 359 ACTTCAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGATTA 418
QY 435 TAAAGAGAGCTGCTTCAATGATTCATGATTCATGATTCATGATTCATGATTCATGATTC 494
DB 419 CAACAGAAAGCTGCTCACTCACTGCTGGAACACGCTTATTAACCTCAAGGGGGC 478
QY 495 TTTTTCAGAGGATCCTTTAGGTTGGTGC-AATCGGCGATGCTGCAACACTGGTTAT 553
DB 479 TTTTTCAGAGGATCCTTTAGGTTGGTGC-AATCGGCGATGCTGCAACACTGGTTAT 538
QY 614 TCTAATTTTGA-AAGATGATCCTTA-AAGAGTACATPAAT--AATGAAT 669
DB 599 TCTAATTTTGA-AAGATGATCCTTA-AAGAGTACATPAAT--AATGAAT 658
QY 670 GTATGCTTC-ATTAAGAGGATTAAGATATTAAGAGTATTAAGAGTATTAAGAGTATTA 728
DB 659 GTATGCTTC-ATTAAGAGGATTAAGATATTAAGAGTATTAAGAGTATTAAGAGTATTA 716

/db_xref="taxon:10090"
 /clone="IMAGE:3062673"
 /tissue_type="upper Head"
 /dev_stage="9.5 and 10.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1lb="NH BMAP H10"
 /note="Organ: Head; Vector: pyx-asc; Site_1: Ecor I;
 Site_2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pyx-asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAAGTGAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH)."

ORIGIN

Query Match 22.6%; Score 418.6; DB 14; Length 577;
 Best Local Similarity 82.8%; Pred. No. 5.9e-54;
 Matches 478; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 102 CGGAGGTTTCTTCTTGGGGAAGTAAAGTGAAGCCAAAGCAGTACTTATCC 161
 1 CGGAGGTTTCTTCTTGGGGAAGTAAAGTGAAGCCAAAGTGAAGTACTTATCC 60
 DB 162 AATGATGATGTAAGTGTATATACATGACATCAGAAATATATTCATCTATC 221
 61 AGATGACACAGCTTAAAGTGTATATACATGACATCAGAAATATATTCATCTAC 120
 QY 222 AGCTTTTAACTTTTAAATTTCTTCAGCGGAAGTAAATAGCAAGCACTGAAGAAATAT 281
 121 GGCTTTTAACTTTTAAATTTCTTCAGCGGAAGTAAATAGCAAGCACTGAAGAAATAT 180
 DB 282 TATCAATGTCAAAAGAAATGTGTAGTGTGATCAAAATCCGTGCTATTCAGATCAGA 341
 181 TTTCAATGTCAAAAGAAATGTGTAGTGTGATCAAAATCCGTGCTATTCAGATCAGA 240
 QY 342 TCATGACGTTTAGAGAGAGGCTGCTTCACAAAAACCTTGAGAGCAATTTTCAAAACGAG 401
 241 TCATGACATTTAGAGAGAGGCTTCTCAAGAAATTTAGACACATCTTCAAGCCCTG 300
 DB 402 ACCTGTTTCTTCTGCTATTTACACCAAGTATATACAGAAAGCTGCTCTACTCATCAGC 461
 301 AGCTGTTTCTTCTGCTATTTACACCAAGTATATACAGAAAGCTGCTCTACTCATCAGC 360
 QY 462 TGGAACTCTCTTATATTAACCTCAAAAAGAACTTTTCAAGGCTACCTTTAGTGTTG 521
 361 TGGAACTCTCTTATATTAACCTCAAAAAGAACTTTTCAAGGCTACCTTTAGTGTTG 420
 DB 522 CCAATCTGGGCAATGTCTGAACAACTGGGTTATTAACCTGATATAGGTTCTGTATGCTCA 581
 421 CCAATCTGGGCAATGTCTGAACAACTGGGTTATTAACCTGATATAGGTTCTGTATGCTCA 480
 QY 582 CTGGTTTAAAGCGAGAGTCAAAACACAGCTCTAAATTTTGAAGAAGATGATCTCT 641
 481 CTGGTTTAAAGCGAGAGTCAAAACACAGCTCTAAATTTTGAAGAAGATGATCTCT 540
 DB 642 TAAAGAGGTACATTAAGATTAATGATATGATGCTTC 678
 541 TAAAGAGGTACATTAAGATTAATGATATGATGCTGC 577

RESULT 48
 CAS51388 570 bp mRNA linear EST 19-NOV-2002
 LOCUS C0842F06-5N NIA Mouse Blastocyst cDNA Library (Long) Mus musculus
 DEFINITION cDNA clone NIA: C0842F06 IMAGE:30029057 5', mRNA sequence.
 ACCESSION CAS51388

FEATURES

source

VERSION CAS51388.1 GI:25095532
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 570)
 AUTHORS Piao, Y., Kargul, G.-J., Dudekula, D.B., Qian, Y., Tanaka, T., Luo, A. and
 Ko, M.-S. H.
 TITLE Systematic Analyses of NIA Mouse Blastocyst cDNA Library (Long)
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: C0842F06-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@nigun.grc.nia.nih.gov
 Plate: C0842 row: F column: 06
 Seq primer: M13 Reverse
 High quality sequence stop: 570
 POLYA=No.

Location/Qualifiers

1..570
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="tasest:C0842F06-5N"
 /db_xref="taxon:10090"
 /clone="NIA: C0842F06 IMAGE:30029057"
 /tissue_type="Blastocyst"
 /dev_stage="3.5-dpc"
 /lab_host="DH10B"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://nigun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). (PMID: 11544199)). Total RNAs were
 extracted from a pool of 20 Blastocysts. Double-stranded
 cDNAs were synthesized with an Oligo(dT) primer
 [Invitrogen]:
 5'-pGACTTCTTATGATCGGAGCGGCGCCCTTTTCTTTT-3' from
 0.2 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lone-linker IL-SalI, purified by phenol/chloroform, and
 separated from free linkers by centrifugation 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer SalI-S. The
 products were purified by phenol/chloroform and centrifuged
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.2 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Query Match 22.6%; Score 418.2; DB 14; Length 570;
 Best Local Similarity 84.3%; Pred. No. 6.8e-54;
 Matches 471; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 6 GCGGCGTACATGATGAGGAGAGAGTACGTCGCGGCTCTCGGGCTTTGCTGCGCG 65
 11 GAGGCGGAGATATGAGGCGAGAGACGTTGGGGGCTCTGCGCTGCTGCGCG 70
 DB 66 CACTGCTTTTCAAGCACTCAACACGACTCGGACAGGAAAGTTTCTTGGGGAAG 125
 71 CGCTCACTTTTCAATCATCTCAACACGACTCGGACAGGAAAGTTTCTTGGGGAAG 130
 QY 126 TAAAGGTGAAGCCAAAGACATTAAGTATCCCAATGATGATGATGATGATGATG 185
 131 TGAAGGTGAAGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATG 190

Db 37 TCACAGAAATCTACAGACACATCTTTCAAGCCCTGACCTGGTTTCTGTGTAAAC 436

Qy 426 CAAGTATATATACAGAAAGCTGCTCTACTCATGCACCTGGAAATTCTCTATATAAACCTC 465

Db 437 CGGTTATACACAGAAAGCTGCTGCATCTCATCTGCTGTGGAACAGCCCTTATATAAACCTC 466

Qy 486 AAAAGACCTTTTTCACAGGTACTCTTATAGTGTGGCAATCTGGGCACTGTGAACAC 545

Db 497 AAAAGGGGCTTTTTCATAGGGCAACATTTGGCGGTTTACCAAACTGTGAATGCGGTATCAC 556

Qy 546 TGGGTTATATAACTGTATCAGGTTCCGTATATCC 580

Db 557 TGGGTTATATAACAGAACCCGCTCTCTGTAGCTCC 591

RESULT 50					
W51769/c					
LOCUS	422 bp	mrna	linear	EST 11-OCT-1996	
DEFINITION	W51769				
	z337807.s1 Soares senescent fibroblasts NDHSF Homo sapiens cDNA				

ACCESSION	W51.769
VERSION	W51.769.1
KEYWORDS	GI.1349836
SOURCE	EST.
ORGANISM	Homo sapiens (human)

REFERENCE
AUTHORS
1 (Pages 1 to 422)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaca, E., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaschik, E., Waterson, R., Williamson, A., Woldmann, P. and Wilson, R.
Wiley-Interscience, New York, 1992

TITLE The Masbu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LIND ; contact the
 IMAGE Consortium (info@image.lindl.gov) for further information.
 Insert Length: 848 Std Error: 0.00
 Seq primer: mcb.REGA+ET
 High quality sequence stop: 360.

FEATURES	Location/Qualifiers
source	1. .422

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:155981"
/db_xref="taxon:9606"
/clone="IMAG:324469"
/tissue_type="senescent fibroblast"
/lab_host="DH10 (ampicillin resistant)"
/clone_1b="Scars senescent fibroblasts NBHSP"
/notes="Vector: pRT3D (pharmacia) with a modified
polylinker V type: phagemid; site 1: Not I; site 2: Eco
RI; strand cdna was primed with a Not I - oligo (nr)
primer 5'
TGTACCAATCTGAATGAGAGCGGCCGATTTTTTTTTTTT 31'
double-stranded cdna was digested, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI site of a modified pRT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Scars and M. Fatima Bonaldo."

```

ORIGIN

Query Match	22.1%	Score 408;	DB 14;	Length 422;
Best Local Similarity	99.8%;	Pred. No. 2.8e-52;		
Matches 419; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

QY	1409	CAAAGTCTTTTCAAAACATCAGATGGTTTTATTTCCAAACCTTTTTCACCTTCACT	1468
Db	420	CAAGTACTTTTTCAAAACATCAGATGGTTTTATTTCCAAACCTTTTTCACCTTCACT	361
QY	1469	AAAGTTGTTAGGGGAAGGCTTTCACAGACACATCTCTTTAGATTGGAAAAGTGAACCG	1528
Db	360	AAAGTTGTTAGGGGAAGGCTTTCACAGACACATCTCTTTAGATTGGAAAAGTGAACCG	301
QY	1529	GCAATAGTGGCTTCACACTGTATATCCCGACCTTAGGGAAAGCAAGTACGAGGATTGATT	1588
Db	300	GCAATAGTGGCTTCACACTGTATATCCCGACCTTAGGGAAAGCAAGTACGAGGATTGATT	241
QY	1589	GAACTTAGGAGTTAGAGACCAAGCCTCGGGCAACGTATTGAGACCAATGCTATTATTAATAATA	1648
Db	240	GAACTTAGGAGTTAGAGACCAAGCCTCGGGCAACGTATTGAGACCAATGCTATTATTAATAATA	181
QY	1649	AAATGGAAAAGCAAGAAATAGCTTTATTTTC-AAAATATGAAAGAAATTTATATGAAGAT	1707
Db	180	AAATGGAAAAGCAAGAAATAGCTTTATTTTCGAAAATATGAAAGAAATTTTATATGAAGAT	121
QY	1708	TTATCTGAGTCATTAAATATTCCTCTTAAGATATCTTTTATAGAAAGTACATATAGGCTAG	1767
Db	120	TTATCTGAGTCATTAAATATTCCTCTTAAGATATCTTTTATAGAAAGTACATATAGGCTAG	61
QY	1768	AGTTGCCAGATPAAATAGCTGATATCATGACATATTAATTTGCAAAACATCATCTAAATTT	1827
Db	60	AGTTGCCAGATPAAATAGCTGATATCATGACATATTAATTTGCAAAACATCATCTAAATTT	1

Search completed: April 18, 2004, 02:13:16
Job time : 4913 secs

Mon Apr 19 12:46:07 2004

us-10-063-523-21.olig10.rst

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 19:03:43 / Search time 4881 Seconds
(without alignments)
11312.266 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849
Sequence: 1 ctgagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 27513289 segs, 14931090276 residues

Word size: 10

Total number of hits satisfying chosen parameters: 37366543

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: EST:
1: em.estba:*
2: em.esthum:*
3: em.estin:*
4: em.estmu:*
5: em.estov:*
6: em.estpl:*
7: em.estiro:*
8: em.hic:*
9: gb.est1:*
10: gb.est2:*
11: gb.hic:*
12: gb.est3:*
13: gb.est4:*
14: gb.est5:*
15: em.estfun:*
16: em.estom:*
17: em.gss.hum:*
18: em.gss.inu:*
19: em.gss.pln:*
20: em.gss.vit:*
21: em.gss.fun:*
22: em.gss.mam:*
23: em.gss.mus:*
24: em.gss.prc:*
25: em.gss.pod:*
26: em.gss.phg:*
27: em.gss.vit1:*
28: gb.gss1:*
29: gb.gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	744	40.2	883	13	BQ921560 AGENCOURT
2	704	38.1	1018	12	BM479419 AGENCOURT
3	652	35.3	703	13	BM479419 AGENCOURT
4	643	34.8	665	14	CA429280 UI-H-PH1-CA429280

5	636	34.4	789	13	BQ221128 AGENCOURT
6	634	34.3	1078	13	BQ216065 AGENCOURT
7	608	32.9	623	9	AL602519 DFE2P686C
8	570	30.8	688	10	BE888265 601511787
9	549	29.7	736	9	AU125653 AU125653
10	525	28.4	549	9	AA781435 AA781435
11	518	28.0	620	14	CB135704 CB135704
12	479	25.9	581	12	CA135111 CA135111
13	469	25.4	778	12	BS70593 BS70593
14	431	23.3	487	10	AM978690 AM978690
15	427	23.1	437	9	AA831922 AA831922
16	405	21.9	509	9	A1830957 A1830957
17	400	21.6	665	12	BQ199837 BQ199837
18	395	21.4	706	12	BT771321 BT771321
19	390	21.1	886	13	BQ422301 BQ422301
20	378	20.4	886	12	BI464110 BI464110
21	364	19.7	400	12	BC943348 BC943348
22	364	19.7	716	12	BI462810 BI462810
23	360	19.5	360	9	A1472709 A1472709
24	352	19.1	643	10	BR812538 BR812538
25	351	19.0	744	12	BG531177 BG531177
26	328	17.7	328	9	AA774511 AA774511
27	324	17.5	465	10	AA667496 AA667496
28	321	17.4	848	14	CB959880 CB959880
29	319	17.3	370	9	AA456838 AA456838
30	316	17.0	778	12	BI912725 BI912725
31	314	17.0	668	9	AU139555 AU139555
32	301	16.3	701	12	BI909258 BI909258
33	299	16.2	422	14	WS1769 WS1769
34	294	15.9	316	9	A1014808 A1014808
35	292	15.8	652	9	AA905493 AA905493
36	284	15.4	563	9	AU144027 AU144027
37	275	14.9	645	9	AU144581 AU144581
38	260	14.1	472	10	AM977201 AM977201
39	213	11.5	264	13	CO1486 CO1486
40	209	11.3	209	9	AA280141 AA280141
41	174	9.4	350	10	BF826597 BF826597
42	165	8.9	977	13	BQ431082 BQ431082
43	156	8.4	857	10	BF218805 BF218805
44	140	7.6	869	10	BF240591 BF240591
45	138	7.5	948	10	BE894160 BE894160
46	135	7.3	221	10	BF736047 BF736047
47	132	7.1	900	10	BG030242 BQ030242
48	121	6.5	346	14	FO8936 FO8936
49	117	6.3	534	12	BG494352 BG494352
50	104	5.6	472	9	AL559192 AL559192
51	88	4.8	480	9	A1024776 A1024776
52	80	4.3	225	9	AA089592 AA089592
53	79	4.3	347	14	R83667 R83667
54	79	4.3	508	9	A1820815 A1820815
55	79	4.3	523	9	A1820814 A1820814
56	79	4.3	526	9	A1821443 A1821443
57	73	3.9	469	14	R83653 R83653
58	73	3.9	505	9	A1821445 A1821445
59	73	3.9	521	14	R83668 R83668
60	69	3.7	379	10	BF742611 BF742611
61	68	3.7	316	10	BE465988 BE465988
62	61	3.6	124	10	BF171490 BF171490
63	53	2.9	300	9	A1627970 A1627970
64	50	2.7	377	14	R83736 R83736
65	49	2.7	466	12	BM089787 BM089787
66	49	2.7	472	12	BM254410 BM254410
67	43	2.3	467	9	AA847559 AA847559
68	42	2.3	79	9	AA744439 AA744439
69	42	2.3	449	13	BA482424 BA482424
70	40	2.2	280	9	AV755170 AV755170
71	40	2.2	295	12	BG388112 BG388112
72	40	2.2	441	9	A1623152 A1623152
73	40	2.2	591	28	AQ285508 AQ285508
74	39	2.1	339	10	BF846262 BF846262
75	39	2.1	423	12	BG884390 BG884390
76	39	2.1	485	10	BE298406 BE298406
77	39	2.1	493	28	AQ181916 AQ181916

78	C	151	37	2.0	400	9	A134861.1	A134861.1 Q030H02.X
79	C	152	37	2.0	400	14	H033398	H033398 Y148D04.S1
80	C	153	37	2.0	401	14	T52553	T52553 Y021902.S1
81	C	154	37	2.0	402	9	AA669224	AA669224 AC16C10.S
82	C	155	37	2.0	403	10	BG012246	BG012246 RC2-GN026
83	C	156	37	2.0	404	9	AA947812	AA947812 C087E08.S
84	C	157	37	2.0	405	9	AA808048	AA808048 C038G10.S
85	C	158	37	2.0	406	9	AA894920	AA894920 AM62B02.S
86	C	159	37	2.0	409	28	AQJ11597	AQJ11597 RC1-HSP-216
87	C	160	37	2.0	411	13	B313646	B313646 B33830
88	C	161	37	2.0	412	9	AA736425	AA736425 ZH31A04.S
89	C	162	37	2.0	413	9	A1538852	A1538852 CP74E04.X
90	C	163	37	2.0	416	9	A1587213	A1587213 CT54G10.X
91	C	164	37	2.0	416	14	M38437	M38437 ZC78502.S1
92	C	165	37	2.0	417	10	A1610376	A1610376 PD19B08.X
93	C	166	37	2.0	417	9	B6992129	B6992129 QV3-GN020
94	C	167	37	2.0	419	14	H03415	H03415 Y148I04.S1
95	C	168	37	2.0	419	28	B69995	B69995 CIT-HSP-206
96	C	169	37	2.0	420	9	A1760835	A1760835 WH96E11.X
97	C	170	37	2.0	425	10	AM513946	AM513946 XT83A12.X
98	C	171	37	2.0	427	14	W44827	W44827 ZC78502.S1
99	C	172	37	2.0	429	29	HS4535717	HS4535717 Homo SADI
100	C	173	37	2.0	430	12	BM16448	BM16448 UI-E-DW0-
101	C	174	37	2.0	431	9	AA721582	AA721582 NV72A07.F
102	C	175	37	2.0	431	28	AO546735	AO546735 CITBI-EL-
103	C	176	37	2.0	432	10	ACQ08513	ACQ08513 CIT-HSP-2
104	C	177	37	2.0	432	14	H02532	H02532 Y140F10.S1
105	C	178	37	2.0	433	14	H87153	H87153 YW15A08.S1
106	C	179	37	2.0	439	28	BL700926	BL700926 DKFZP6860
107	C	180	37	2.0	442	28	B2604437	B2604437 WHA2M67TR
108	C	181	37	2.0	443	13	BK495782	BK495782 DKFZP7790
109	C	182	37	2.0	444	9	A1085270	A1085270 OY71D06.X
110	C	183	37	2.0	444	12	BC998288	BC998288 PM4-HT130
111	C	184	37	2.0	445	28	ACQ60764	ACQ60764 CITBI-EL-
112	C	185	37	2.0	449	13	BU963252	BU963252 AGENCOURT
113	C	186	37	2.0	452	28	AOJ16000	AOJ16000 RPTC11-56
114	C	187	37	2.0	458	13	BU428854	BU428854 UI-HF-BNO
115	C	188	37	2.0	460	28	AOQ62758	AOQ62758 CITBI-EL-
116	C	189	37	2.0	464	14	H20669	H20669 YH3B09.F1
117	C	190	37	2.0	464	28	B36455	B36455 HS-1040-B2-
118	C	191	37	2.0	466	28	AZ521648	AZ521648 RPTC1-11-2
119	C	192	37	2.0	466	28	AOQ25181	AOQ25181 HS 2017.A
120	C	193	37	2.0	466	28	AO601303	AO601303 HS 5373.A
121	C	194	37	2.0	468	10	BE062118	BE062118 RCI-BT05
122	C	195	37	2.0	468	10	BE301754	BE301754 bb78A07.X
123	C	196	37	2.0	472	10	BE301754	BE301754 HS 5207.A
124	C	197	37	2.0	473	9	AA564570	AA564570 H125D01.S
125	C	198	37	2.0	475	28	B41627	B41627 HS-1054-A1-
126	C	199	37	2.0	476	28	AO553532	AO553532 RPTC1-11-3
127	C	200	37	2.0	480	10	BE062219	BE062219 RCI-BT05
128	C	201	37	2.0	481	13	BU735221	BU735221 UI-E-DW0-
129	C	202	37	2.0	484	28	AO462870	AO462870 HS 5207.A
130	C	203	37	2.0	488	9	AA723017	AA723017 ZH30F04.S
131	C	204	37	2.0	488	9	AL771876	AL771876 DKFZP686H
132	C	205	37	2.0	491	9	AV741743	AV741743 AV741.S
133	C	206	37	2.0	493	9	AA601460	AA601460 H071D03.S
134	C	207	37	2.0	495	28	AOQ20774	AOQ20774 HS 3026.B
135	C	208	37	2.0	496	28	AO487338	AO487338 RPTC1-11-2
136	C	209	37	2.0	497	28	AA446782	AA446782 ZW89E02.X
137	C	210	37	2.0	500	13	AOQ02240	AOQ02240 HS 2111.B
138	C	211	37	2.0	500	13	BU659555	BU659555 C149C01-2
139	C	212	37	2.0	500	29	AG029036	AG029036 Homo SADI
140	C	213	37	2.0	501	28	B82414	B82414 RPTC11-1511
141	C	214	37	2.0	503	10	BF896590	BF896590 QV1-MT022
142	C	215	37	2.0	511	9	AA939273	AA939273 QG11D07.S
143	C	216	37	2.0	513	28	BF220211	BF220211 601296766
144	C	217	37	2.0	517	13	BK564073	BK564073 DKFZP686K
145	C	218	37	2.0	522	28	AOQ020197	AOQ020197 CIT-HSP-2
146	C	219	37	2.0	525	28	AO189342	AO189342 HS 3199.F
147	C	220	37	2.0	527	9	AL698810	AL698810 DKFZP686L
148	C	221	37	2.0	529	9	AA984187	AA984187 am82B02.S
149	C	222	37	2.0	530	28	AO534232	AO534232 RPTC1-11-3
150	C	223	37	2.0	530	28	AO534232	AO534232 RPTC1-11-3

224	37	2.0	533	10	BF915467	MR3-JT0012	297	37	2.0	700	13	BE507211	DKFZp799E
C 225	37	2.0	537	28	BG006707	CIV4-GN012	298	37	2.0	701	29	AG163678	AG163678 Pan trogl
C 226	37	2.0	537	28	AQ390925	CITBI-E1-	C 299	37	2.0	704	28	BZ611052	BZ611052
C 227	37	2.0	538	14	CD516226	AGENCOURT	300	37	2.0	705	9	AL118573	AL118573 DKFZp761B
C 228	37	2.0	539	13	EX492535	DKFZp781K	301	37	2.0	709	12	BQ004673	BQ004673 UI-H-E10-
C 229	37	2.0	541	10	BF750213	MR0-BN011	302	37	2.0	710	29	AG046139	AG046139 Pan trogl
C 230	37	2.0	547	28	BS9747	CIT-HSP-344	C 303	37	2.0	712	13	EX509855	EX509855 DKFZp686F
C 231	37	2.0	552	9	AUI58442	AUI58442	C 304	37	2.0	716	29	CD103528	CD103528 Homo sapi
C 232	37	2.0	553	13	BU070387	im09a02.x	C 305	37	2.0	716	29	AG013358	AG013358
C 233	37	2.0	561	9	AA532512	njs4d04.s	C 306	37	2.0	720	14	CB962874	CB962874 AGENCOURT
C 234	37	2.0	561	10	AM973876	EST386099	C 307	37	2.0	722	11	BC022423	BC022423 Homo sapi
C 235	37	2.0	562	10	BE789139	601476253	C 308	37	2.0	748	12	BI870175	BI870175 AGENCOURT
C 236	37	2.0	562	28	AQ697272	HS-5531_B	C 309	37	2.0	749	14	CB962143	CB962143 AGENCOURT
C 237	37	2.0	568	9	AUI47979	AUI47979	C 310	37	2.0	762	13	BU943294	BU943294 AGENCOURT
C 238	37	2.0	569	9	AL710527	DKFZp686J	C 311	37	2.0	762	29	AG107420	AG107420 Pan trogl
C 239	37	2.0	572	9	AL698800	DKFZp686X	C 312	37	2.0	764	28	AO550972	AO550972
C 240	37	2.0	574	28	AQ820118	HS-3289_A	C 313	37	2.0	775	28	BZ600570	BZ600570 WHAAN66TF
C 241	37	2.0	577	13	BU728638	UI-E-CQ1-	C 314	37	2.0	786	29	AG111428	AG111428 Pan trogl
C 242	37	2.0	578	10	AM970887	EST382970	C 315	37	2.0	797	28	AQ898769	AQ898769 HS-3130_A
C 243	37	2.0	583	13	BU949010	1i72c08.Y	C 316	37	2.0	801	10	BF969660	BF969660 602272038
C 244	37	2.0	583	14	CB164646	K-EST0225	C 317	37	2.0	821	13	BU668967	BU668967 AGENCOURT
C 245	37	2.0	583	28	AQ537858	RPCI-11-3	C 318	37	2.0	822	14	CB988992	CB988992 AGENCOURT
C 246	37	2.0	588	12	BG562655	602581439	C 319	37	2.0	828	13	BU153681	BU153681
C 247	37	2.0	588	13	EX481755	DKFZp686I	C 320	37	2.0	839	13	CD109867	CD109867 AGENCOURT
C 248	37	2.0	590	14	CD370042	UI-H-FT1-	C 321	37	2.0	846	13	BU146870	BU146870 AGENCOURT
C 249	37	2.0	592	14	CA390427	CB10d09.x	C 322	37	2.0	847	13	BU539739	BU539739 AGENCOURT
C 250	37	2.0	594	13	EX476279	DKFZp686E	C 323	37	2.0	859	12	BG165856	BG165856 602344329
C 251	37	2.0	595	12	BT711238	1d93g11.x	C 324	37	2.0	862	13	BU166581	BU166581
C 252	37	2.0	596	28	AQ606501	HS-5396_B	C 325	37	2.0	866	12	BG565625	BG565625 602583234
C 253	37	2.0	599	28	AQ393335	CITBI-E1-	C 326	37	2.0	878	10	BF687764	BF687764 602066813
C 254	37	2.0	605	28	AQ597289	HS-5300_B	C 327	37	2.0	882	13	EX454875	EX454875
C 255	37	2.0	606	14	CB154403	K-EST0212	C 328	37	2.0	891	10	BE504333	BE504333
C 256	37	2.0	606	28	B89478	RPCI11-2701	C 329	37	2.0	896	13	BU501990	BU501990 AGENCOURT
C 257	37	2.0	611	13	EX482534	DKFZp686F	C 330	37	2.0	919	13	BU854791	BU854791
C 258	37	2.0	613	12	BM009120	603629488	C 331	37	2.0	920	13	EX411468	EX411468
C 259	37	2.0	613	12	BM663006	UI-E-C10-	C 332	37	2.0	936	13	BO672356	BO672356 AGENCOURT
C 260	37	2.0	618	9	AL041398	DKFZp434C	C 333	37	2.0	937	13	BO709314	BO709314 AGENCOURT
C 261	37	2.0	621	10	AM372037	RC2-BT031	C 334	37	2.0	939	13	BO990436	BO990436 AGENCOURT
C 262	37	2.0	622	13	EX508889	DKFZp686E	C 335	37	2.0	978	12	BM564927	BM564927 AGENCOURT
C 263	37	2.0	624	28	BH609679	H1V19D08	C 336	37	2.0	1006	12	BM556037	BM556037 AGENCOURT
C 264	37	2.0	624	29	AG020440	Homo sapi	C 337	37	2.0	1019	12	BM915174	BM915174 AGENCOURT
C 265	37	2.0	625	9	AV729885	AV729885	C 338	37	2.0	1062	12	BM807223	BM807223
C 266	37	2.0	626	13	EX484482	DKFZp686C	C 339	37	2.0	1066	10	BF685026	BF685026 602142889
C 267	37	2.0	631	28	AQ548567	CITBI-E1-	C 340	37	2.0	1135	12	BM809105	BM809105
C 268	37	2.0	636	28	AQ266645	RPCI11-74	C 341	37	2.0	1200	13	EX404747	EX404747
C 269	37	2.0	642	12	BM767402	K-EST0049	C 342	37	2.0	1201	13	EX440322	EX440322
C 270	37	2.0	651	13	EX507212	DKFZp779E	C 343	37	2.0	1224	12	BM925065	BM925065 AGENCOURT
C 271	37	2.0	652	29	AG093883	Pan trogl	C 344	37	2.0	1358	12	BM564410	BM564410 AGENCOURT
C 272	37	2.0	653	29	AG020439	Homo sapi	C 345	37	2.0	14767	11	BC041345	BC041345 Homo sapi
C 273	37	2.0	654	12	BG122285	602350250	C 346	36	1.9	237	10	BF747357	BF747357 RC3-BT033
C 274	37	2.0	655	29	AG051619	Pan trogl	C 347	36	1.9	244	10	BF858528	BF858528 RCL-FT019
C 275	37	2.0	659	29	AG052135	Pan trogl	C 348	36	1.9	279	10	BF876189	BF876189 CM4-BT003
C 276	37	2.0	663	9	AUI22266	AUI22266	C 349	36	1.9	286	10	BF746674	BF746674
C 277	37	2.0	665	14	CD704268	EST20795	C 350	36	1.9	345	28	B85266	B85266
C 278	37	2.0	668	9	AV752750	AV752750	C 351	36	1.9	366	28	AQ066169	AQ066169 HS-2245_A
C 279	37	2.0	669	29	AG157252	Pan trogl	C 352	36	1.9	386	9	AA214093	AA214093
C 280	37	2.0	673	29	AG119029	Pan trogl	C 353	36	1.9	393	9	AV754944	AV754944
C 281	37	2.0	673	29	AG128869	Pan trogl	C 354	36	1.9	404	10	AM848833	AM848833 IL3-C7021
C 282	37	2.0	674	14	CA389624	CA389624	C 355	36	1.9	413	9	AI335387	AI335387
C 283	37	2.0	675	29	AG124531	Pan trogl	C 356	36	1.9	413	12	BQ024624	BQ024624 UI-I-BBPD
C 284	37	2.0	680	13	EX507966	DKFZp686O	C 357	36	1.9	415	9	AA579061	AA579061 nF27a12.6
C 285	37	2.0	680	28	AQ780044	HS-3169_A	C 358	36	1.9	415	28	B60261	B60261
C 286	37	2.0	680	29	AG040386	Pan trogl	C 359	36	1.9	421	28	AQ468607	AQ468607 HS-2006_B
C 287	37	2.0	681	12	BI461494	603026372	C 360	36	1.9	426	28	AQ215219	AQ215219 HS-2004_B
C 288	37	2.0	681	29	AG121146	Pan trogl	C 361	36	1.9	451	12	BI763955	BI763955 603049835
C 289	37	2.0	684	28	AG166450	Pan trogl	C 362	36	1.9	472	28	B32886	B32886
C 290	37	2.0	687	29	AG162684	Pan trogl	C 363	36	1.9	506	28	AG676033	AG676033 HS-2162_A
C 291	37	2.0	690	29	AG155968	Pan trogl	C 364	36	1.9	513	28	AG784510	AG784510 HS-3168_A
C 292	37	2.0	692	9	AL709348	DKFZp686H	C 365	36	1.9	524	28	AQ663998	AQ663998 HS-3277_B
C 293	37	2.0	692	10	AM955712	EST367782	C 366	36	1.9	527	28	AO151931	AO151931 HS-2215_B
C 294	37	2.0	694	29	AG173809	Pan trogl	C 367	36	1.9	527	28	AO194349	AO194349 RPCI11-61
C 295	37	2.0	694	28	BE7121	CIT-HSP-201	C 368	36	1.9	545	28	AQ544758	AQ544758 CITBI-E1-
C 296	37	2.0	699	10	AM979152	EST391262	C 369	36	1.9	570	13	EX470732	EX470732 DKFZp686H

```

370 36 603 28 A0600058 HS_5354_B
371 36 613 28 A0474559 CITBI-EI-
372 36 621 28 A0474559 CITBI-EI-
373 36 641 28 A0474559 CITBI-EI-
374 36 641 28 A0474559 CITBI-EI-
375 36 641 28 A0474559 CITBI-EI-
376 36 641 28 A0474559 CITBI-EI-
377 36 641 28 A0474559 CITBI-EI-
378 36 641 28 A0474559 CITBI-EI-
379 36 641 28 A0474559 CITBI-EI-
380 36 641 28 A0474559 CITBI-EI-
381 36 641 28 A0474559 CITBI-EI-
382 36 641 28 A0474559 CITBI-EI-
383 36 641 28 A0474559 CITBI-EI-
384 36 641 28 A0474559 CITBI-EI-
385 36 641 28 A0474559 CITBI-EI-
386 36 641 28 A0474559 CITBI-EI-
387 36 641 28 A0474559 CITBI-EI-
388 36 641 28 A0474559 CITBI-EI-
389 36 641 28 A0474559 CITBI-EI-
390 36 641 28 A0474559 CITBI-EI-
391 36 641 28 A0474559 CITBI-EI-
392 36 641 28 A0474559 CITBI-EI-
393 36 641 28 A0474559 CITBI-EI-
394 36 641 28 A0474559 CITBI-EI-
395 36 641 28 A0474559 CITBI-EI-
396 36 641 28 A0474559 CITBI-EI-
397 36 641 28 A0474559 CITBI-EI-
398 36 641 28 A0474559 CITBI-EI-
399 36 641 28 A0474559 CITBI-EI-
400 36 641 28 A0474559 CITBI-EI-
401 36 641 28 A0474559 CITBI-EI-
402 36 641 28 A0474559 CITBI-EI-
403 36 641 28 A0474559 CITBI-EI-
404 36 641 28 A0474559 CITBI-EI-
405 36 641 28 A0474559 CITBI-EI-
406 36 641 28 A0474559 CITBI-EI-
407 36 641 28 A0474559 CITBI-EI-
408 36 641 28 A0474559 CITBI-EI-
409 36 641 28 A0474559 CITBI-EI-
410 36 641 28 A0474559 CITBI-EI-
411 36 641 28 A0474559 CITBI-EI-
412 36 641 28 A0474559 CITBI-EI-
413 36 641 28 A0474559 CITBI-EI-
414 36 641 28 A0474559 CITBI-EI-
415 36 641 28 A0474559 CITBI-EI-
416 36 641 28 A0474559 CITBI-EI-
417 36 641 28 A0474559 CITBI-EI-
418 36 641 28 A0474559 CITBI-EI-
419 36 641 28 A0474559 CITBI-EI-
420 36 641 28 A0474559 CITBI-EI-
421 36 641 28 A0474559 CITBI-EI-
422 36 641 28 A0474559 CITBI-EI-
423 36 641 28 A0474559 CITBI-EI-
424 36 641 28 A0474559 CITBI-EI-
425 36 641 28 A0474559 CITBI-EI-
426 36 641 28 A0474559 CITBI-EI-
427 36 641 28 A0474559 CITBI-EI-
428 36 641 28 A0474559 CITBI-EI-
429 36 641 28 A0474559 CITBI-EI-
430 36 641 28 A0474559 CITBI-EI-
431 36 641 28 A0474559 CITBI-EI-
432 36 641 28 A0474559 CITBI-EI-
433 36 641 28 A0474559 CITBI-EI-
434 36 641 28 A0474559 CITBI-EI-
435 36 641 28 A0474559 CITBI-EI-
436 36 641 28 A0474559 CITBI-EI-
437 36 641 28 A0474559 CITBI-EI-
438 36 641 28 A0474559 CITBI-EI-
439 36 641 28 A0474559 CITBI-EI-
440 36 641 28 A0474559 CITBI-EI-
441 36 641 28 A0474559 CITBI-EI-
442 36 641 28 A0474559 CITBI-EI-

```

```

443 34 165 12 B1038371
444 34 173 12 A0278517
445 34 179 12 CB856780
446 34 179 12 CB856781
447 34 179 12 CB856781
448 34 179 12 CB856781
449 34 179 12 CB856781
450 34 179 12 CB856781
451 34 179 12 CB856781
452 34 179 12 CB856781
453 34 179 12 CB856781
454 34 179 12 CB856781
455 34 179 12 CB856781
456 34 179 12 CB856781
457 34 179 12 CB856781
458 34 179 12 CB856781
459 34 179 12 CB856781
460 34 179 12 CB856781
461 34 179 12 CB856781
462 34 179 12 CB856781
463 34 179 12 CB856781
464 34 179 12 CB856781
465 34 179 12 CB856781
466 34 179 12 CB856781
467 34 179 12 CB856781
468 34 179 12 CB856781
469 34 179 12 CB856781
470 34 179 12 CB856781
471 34 179 12 CB856781
472 34 179 12 CB856781
473 34 179 12 CB856781
474 34 179 12 CB856781
475 34 179 12 CB856781
476 34 179 12 CB856781
477 34 179 12 CB856781
478 34 179 12 CB856781
479 34 179 12 CB856781
480 34 179 12 CB856781
481 34 179 12 CB856781
482 34 179 12 CB856781
483 34 179 12 CB856781
484 34 179 12 CB856781
485 34 179 12 CB856781
486 34 179 12 CB856781
487 34 179 12 CB856781
488 34 179 12 CB856781
489 34 179 12 CB856781
490 34 179 12 CB856781
491 34 179 12 CB856781
492 34 179 12 CB856781
493 34 179 12 CB856781
494 34 179 12 CB856781
495 34 179 12 CB856781
496 34 179 12 CB856781
497 34 179 12 CB856781
498 34 179 12 CB856781
499 34 179 12 CB856781
500 34 179 12 CB856781

```

ALIGNMENTS

```

RESULT 1
LOCUS B0921560
DEFINITION B0921560
ACCESSION B0921560
VERSION B0921560.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 883)
NIN-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

ORIGIN

Query Match	40.2%;	Score 744;	DB 13;	Length 883;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 744;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	239	AAAGATGAGGTAAGTGGTAAACAATTCGGTCGTCATCGATCGATCGATCGATCGATCG	354
Db	1	AAAGATGAGTGAAGTGGTAAACAATTCGGTCGTCATCGATCGATCGATCGATCGATCG	60
QY	355	AGAGAGGCTGCTTCCACAAAACTTGCAGAGACATTTTCCAAACCAAGACTGTGTTTTCT	414
Db	61	AGAGAGGCTGCTTCCACAAAACTTGCAGAGACATTTTCCAAACCAAGACTGTGTTTTCT	120
QY	415	GCATTAACACCAAGTATATATACAGAAAGCTGCTACTCATCGACTGAGACATTCCTT	474
Db	121	GCATTAACACCAAGTATATATACAGAAAGCTGCTACTCATCGACTGAGACATTCCTT	180
QY	475	ATATAAAGCTCAAAAAGGACTTTTTCACAGGGTACCTTATAGTGTGTCACATCTGGGAC	534
Db	181	ATATAAAGCTCAAAAAGGACTTTTTCACAGGGTACCTTATAGTGTGTCACATCTGGGAC	240
QY	535	GTGTGAACAACCTGGGTATATAAAACGTATACAGGTTCTGTATGTCCACTGTGTTTAGCG	594
Db	241	GTGTGAACAACCTGGGTATATAAAACGTATACAGGTTCTGTATGTCCACTGTGTTTAGCG	300
QY	595	AGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGAATCCTTAAGAAGGTACA	654
Db	301	AGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGAATCCTTAAGAAGGTACA	360
QY	655	TAAAGTAAATGAATGTATGTTCTTATCAAGAGGAAATTAAGAGTATATGCAAAAAAGT	714
Db	361	TAAAGTAAATGAATGTATGTTCTTATCAAGAGGAAATTAAGAGTATATGCAAAAAAGT	420
QY	715	GGAAGCACTGTAACAAGCAGTGTGATTAACCTGTAAAGATGTAAACAGATTAATAAGAGA	774
Db	421	GGAAGCACTGTAACAAGCAGTGTGATTAACCTGTAAAGATGTAAACAGATTAATAAGAGA	480
QY	775	AATTGAGAAAAGAGAGGAGCACAGATTCAAGCAGCAAGAGAGAGACATCCAAAAAGA	834
Db	481	AATTGAGAAAAGAGAGGAGCACAGATTCAAGCAGCAAGAGAGAGACATCCAAAAAGA	540
QY	835	CCCTCAGAGAAACATTTTCTTTGTGACGACATTACGACCTTTTTCGAAATTTGTAAT	894

	541	600
D5	CCCTCAGSAGAACTTTTTCCTTTCAGGCATTAGAACCTTTTCCAAATTCGAAAT	600
Q5	TCTTCATTCAATGCTGTTATGCTCTTTAAAAAATAGACATGTTCTTAAAAAGTAGCTGTAACTA	954
D6	TCTTCATTCAATGCTGTTATGCTCTTTAAAAAATAGACATGTTCTTAAAAAGTAGCTGTAACTA	660
Q6	CAACCACCATTCGATGATGATGAGACATCTGACCTTAAATGTTAAACAACATGACATTC	1012
D7	CAACACCATTCGATGATGATGAGACATCTGACCTTAAATGTTAAACAACATGACATTC	720
Q7	TGAAGTAGTCCAGCTAGTACACC	1038
D8	TGAAGTAGTCCAGCTAGTACACC	744

[illegible]

ORIGIN

Query Match	38.1%	Score 704	DB 12	Length 1018
Best Local Similarity	100.0%	Pred. No. 0		
Matches 704	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	20	GAGGGGGAGAGTACGTGGCGGTGCTCCGGGCTTTGCTGGCGCACTCGCTTTCAG	79
Db	1	GAGGGGGAGTACGTGGCGGTGCTCCGGGCTTTGCTGGCGCACTCGCTTTCAG	60
Qy	80	CACCTCAACGGGCTCGACACGGAAAGTTTCTTTGGGGAAGTAAAGGGAAGCC	139
Db	61	CACCTCAACGGGCTCGACACGGAAAGTTTCTTTGGGGAAGTAAAGGGAAGCC	120
Qy	140	AAGAACGAGTTTACTGATTTCCCAAATGAGATGTTGAATGTTTATACATGACATT	199
Db	121	AAGAACGAGTTTACTGATTTCCCAAATGAGATGTTGAATGTTTATACATGACATT	180

QY	200	CAGAAATCATCATGGTATCAGGCTTTTGTGCTTTTAATCTTCAGGGGAAAT	259
Db	181	CAGAAATATATCCATGCTATCAGCTTTTGTGCTTTTAATCTTCAGGGGAAAT	240
QY	260	GAGCAAGCACTGAAAGAAAATATATCAATGTCAAAAAGATGTGTGTGTTGTCAAA	319
Db	241	GAGCAAGCACTGAAAGAAAATATATCAATGTCAAAAAGATGTGTGTGTTGTCAAA	300
QY	320	TTCCGTGCTACATTCAGATCAGATCTGAAGCTTTAGAGAGGCTCTTCAAAAACCTTG	379
Db	301	TTCCGTGCTACATTCAGATCAGATCTGAAGCTTTAGAGAGGCTCTTCAAAAACCTTG	360
QY	380	CAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGTATTACCAAGTATATACA	439
Db	361	CAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGTATTACCAAGTATATATACA	420
QY	440	GAAAGCTCTCTACCTCATCGATCGAATTCCTATATTAACCTCAAAAAGGACTTTT	499
Db	421	GAAAGCTCTCTACCTCATCGATCGAATTCCTATATTAACCTCAAAAAGGACTTTT	480
QY	500	CACAGGTAACCTTTAGTGTGTGCCAATCTGGCACTGTCTGAACCACTGGGTATTAAACT	559
Db	481	CACAGGTAACCTTTAGTGTGTGCCAATCTGGCACTGTCTGAACCACTGGGTATTAAACT	540
QY	560	GATACAGGTCCTGATATGTCCACTGAGTTTATAGCCAGAGTACCAACACACAGCTCTAAA	619
Db	541	GATACAGGTCCTGATATGTCCACTGAGTTTATAGCCAGAGTACCAACACACAGCTCTAAA	600
QY	620	TTTTTTGAAGAGATGATTCCTTAAAGAGGTACATAAGATTAATGAATGTATCTTCA	679
Db	601	TTTTTTGAAGAGATGATTCCTTAAAGAGGTACATAAGATTAATGAATGTATCTTCA	660
QY	680	TTACAGAGAGATTTAAAGATTTATGCAAAAAGGGAAGACAG 723	
Db	661	TTACAGAGAGATTTAAAGATTTATGCAAAAAGGGAAGACAG 704	

RESULT 3					
EX089041					
LOCUS	703 bp	mRNA	linear	EST 23-JAN-2001	
DEFINITION	EX089041 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1391457, mRNA sequence.			IMAGE1391457	

ACCESSION	EX089041
VERSION	EX089041.1
KEYWORDS	EST. GI:27823633
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Eumalacostraca; Euteleostomi; Primates; Carnivora; Homnidae; Homo. 1 (bases 1 to 703)
AUTHORS	Ebert,U., Hell,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE	Human Unigeneset - RZP3
JOURNAL	Unpublished (2003)
COMMENT	Contact: Ina Rolfs

RZPD Deutsches Ressort-Zentrum für Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp98BN143513.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.de/ClonedCards/cgi-
bin/showlib.pl.cgi?response=libno=972](http://www.rzpd.de/ClonedCards/cgi-bin/showlib.pl.cgi?response=libno=972) Contact: Ina Rofe
RZPD Deutsches Ressort-Zentrum für Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel.: +49 30 32659 101
Fax: +49 30 32659 111

```

www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer
M13r, Primer sequence: TTTCACACAGAGAAACACCTATGAC.
location/Qualifiers
1..703
/organism="Homo sapiens"
FEATURES
source
```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998N143513 ; IMAGE:1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTTACCACATCTGAAGTGGAGGAGCGGCCCAATTTTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to C0t5 and was
constructed by Bento Soares and M. Fatima Bonaldo. "

```

Query Match	35.3%	Score 652;	DB 13;	Length 703;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches	702;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;
QY	915	CTTTAAAAATAGCATGTTTCTTAAAGTAGCTGTACTACACACACATCTCGATGTAG	974	
Db	1	CTTTAAAAATAGCAAGTTCTTAAAGTAGCTGTACTACACACACATCTCGATGTAG	60	
QY	975	TAGCAATCTGACCTTATATGGTAGACACACTGACATCTCCGAAAGCTACAGCTAGTA	1034	
Db	61	TAGCAATCTGACCTTATATGGTAGACACACTGACATCTCCGAAAGCTACAGCTAGTA	120	
QY	1035	CACCAACAATCTTAAGCATTAAGCCTTGAAGCTTGAAGTACAGATGGCAATTCAGAGAT	1094	
Db	121	CACCAACAATCTTAAGCATTAAGCCTTGAAGCTTGAAGTACAGATGGCAATTCAGAGAT	180	
QY	1095	CTCGGTTGATAGTACACAGACAAAGATCTAAGAAATATCTGTAGTATGTAACCAAG	1154	
Db	181	CTCGGTTGATAGTACACAGACAAAGATCTAAGAAATATCTGTAGTATGTAACCAAG	240	
QY	1155	ATTAAGCATCCAAATATGACGAGCCGAGAAACAGATGAAGAAATGAAAGGTT	1214	
Db	241	ATTAAGCATCCAAATATGACGAGCCGAGAAACAGATGAAGAAATGAAAGGTT	300	
QY	1215	TTGGAGATATTCACGGGCTCCATCTTATGATCCTTTAACCCTTACAGAGAGATTTTT	1274	
Db	301	TTGGAGATATTCACGGGCTCCATCTTATGATCCTTTAACCCTTACAGAGAGATTTTT	360	
QY	1275	TATTTGGCTGATGGATGAAGCCAAACATTTCTATTTGTTTACTATGTTGAGCTACTTGC	1333	
Db	361	TATTTGGCTGATGGATGAAGCCAAACATTTCTATTTGTTTACTATGTTGAGCTACTTGC	420	
QY	1335	AGTAGATTCATTTGTTTCTATATGTCACCTGTTTGAGTAATACACAGATATCTCTTA	1394	
Db	421	AGTAGATTCATTTGTTTCTATATGTCACCTGTTTGAGTAATACACAGATATCTCTTA	480	
QY	1395	GTGCATTTACTCTCAAAAGTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTT	1455	
Db	481	GTGCATTTACTCTCAAAAGTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTT	540	
QY	1455	TTTCAACCTTCACTAAGTGTGTGAGGGAAGGCTACACAGACATCTTTAGAAATGG	1511	
Db	541	TTTCAACCTTCACTAAGTGTGTGAGGGAAGGCTTACACAGACATCTTTAGAAATGG	600	
QY	1515	AAAAATGAGACAGGACAGTGGCTCACACTGTATCTCCAGACATTAGGGAAGCAAGT	1577	
Db	601	AAAAATGAGACAGGACAGTGGCTCACACTGTATCTCCAGACATTAGGGAAGCAAGT	660	
QY	1575	CAGAGGATGTATGAAGCTGAGAAATTGAGACCGACGCTGGGC	1617	
Db	661	CAGAGGATGTATGAAGCTGAGAAATTGAGACCGACGCTGGGC	703	

RESULT 4

CA429280/c
LOCUS CA429280 665 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-FHL-bfl-n-12-0-UI.s1 NCI CGAP_FHL Homo sapiens CDNA clone
ACCESSION CA429280
VERSION CA429280.1 GI:24792006
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA
sequence: 188-316, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes

FEATURES
source
1.665
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FHL-bfl-n-12-0-UI"
/tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="MD10B (Life Technologies)"
/clone_lib="NCI CGAP_FHL"
/note="Organ: Chondrosarcoma; Vector: pTT73-Pac
(pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP_FHL is a normalized CDNA library
obtained from a cell line derived from grade I
chondrosarcoma tissue. The library was constructed and
normalized according to Bonaldi, Lemon and Soares, Genome
Research, 6:791-806, 1996. First strand CDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded CDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pTT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand CDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGATCCGGC. The cell line was provided by Dr. James Martin
from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Cell Line C58 - Grade 1
Chondrosarcoma
TAG LIB=UI-H-FHL
TAG_SEQ=AGATCCGGC"

ORIGIN
Query Match 34.8%; Score 643; DB 14; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 CAGCCCAAGAAAGATGAAGATGAAGGTTTGGTGAATATTCACGGTC 1233
DB 665 CAGCCCAAGAAAGATGAAGATGAAGGTTTGGTGAATATTCACGGTC 606
QY 1234 TCTTCAATTTGATCCTTTAACTTACAGAGATTTTATTTGGCTAGGGTAA 1293
DB 605 TCTTCAATTTGATCCTTTAACTTACAGAGATTTTATTTGGCTAGGGTAA 546
QY 1294 GCCAAACATTTCTATTTTACATAGTGTAGACTTGCATAGTCAATTTGTTT 1353

DB 545 GCCAAACATTTCTATTTGTTTACTATGTTAGACATCTGCAGTAAGTCTATTTT 486
QY 1354 ACTATGTTCACTGTTTGAAGTAATACAGATTAAGTCTTATTTGCTTACCAAG 1413
DB 485 ACTATGTTCACTGTTTGAAGTAATACAGATTAAGTCTTATTTGCTTACCAAG 426
QY 1414 TACTTTTCAACATGATGATGCTTTATTTCCAAACCTTTTTCCTTCACTAAGT 1473
DB 425 TACTTTTCAACATGATGATGCTTTATTTCCAAACCTTTTTCCTTCACTAAGT 366
QY 1474 GTTAGAGGGAAGGCTTACACAGACATTTCTTTAGAAATTTGAAAGTACAGGAC 1533
DB 365 GTTAGAGGGAAGGCTTACACAGACATTTCTTTAGAAATTTGAAAGTACAGGAC 306
QY 1534 GTGAGTCAACCTGTTATCCACGACTTGGGGAAGCAAGTACAGAGATTTGAAGC 1593
DB 305 GTGAGTCAACCTGTTATCCACGACTTGGGGAAGCAAGTACAGAGATTTGAAGC 246
QY 1594 TAGAGTTAGAGACAGCCTGGGCAACGATTTAGACATGCTTATTAATAAATG 1653
DB 245 TAGAGTTAGAGACAGCCTGGGCAACGATTTAGACATGCTTATTAATAAATG 186
QY 1654 GAAAGCAGAAATAGCTTATTTTCAAAATATGAAAGAAATTTATGAAATTTATCT 1713
DB 185 GAAAGCAGAAATAGCTTATTTTCAAAATATGAAAGAAATTTATGAAATTTATCT 126
QY 1714 GAGTCAATTAATTTCTCTTAAGTATGATCTTTTGAAGTACATATGCTAGAGTTC 1773
DB 125 GAGTCAATTAATTTCTCTTAAGTATGATCTTTTGAAGTACATATGCTAGAGTTC 66
QY 1774 CAGATTAATGCTGATATCATGCAATTAATTTGCAAAACATC 1816
DB 65 CAGATTAATGCTGATATCATGCAATTAATTTGCAAAACATC 23

RESULT 5
BQ221128 789 bp mRNA linear EST 02-MAY-2002
LOCUS BQ221128
DEFINITION AGENCOURT_7558634 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:6045433
5', mRNA sequence.
ACCESSION BQ221128
VERSION BQ221128.1 GI:20402528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS NIH-MGC <http://img.ncbi.nlm.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1AM13289 row: k column: 02
High quality sequence scop: 546.
Location/Qualifiers
1.789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6045433"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;

FEATURES
source

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.4%; Score 636; DB 13; Length 789;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 CGGCGGTAGCATGAGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCGGCCG 66
DB 1 CGGCGGTAGCATGAGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCGGCCG 60
QY 67 ACTGCTTTCCAGCACTCTCAACAGGACCTGGACAGGAGGTTTCTTCTGGGGAAGT 126
DB 61 ACTGCTTTCCAGCACTCTCAACAGGACCTGGACAGGAGGTTTCTTCTGGGGAAGT 120
QY 127 AAAAGGTGAAGCCAAAGAACAGCATTACTGATTCGCAAAATGATGATGTAAGTTGTTA 186
DB 121 AAAAGGTGAAGCCAAAGAACAGCATTACTGATTCGCAAAATGATGATGTAAGTTGTTA 180
QY 187 TACAAATTGACATTCAGAAATATATTCATGCTATGATGCTTTTACCTTTAATTCCTC 246
DB 181 TACAAATTGACATTCAGAAATATATTCATGCTATGATGCTTTTACCTTTAATTCCTC 240
QY 247 AGCGCAAGTAATGAGCAAGCACTGAGAAATATTCATCAATGTCAAAAGAAATGTGGT 306
DB 241 AGCGCAAGTAATGAGCAAGCACTGAGAAATATTCATCAATGTCAAAAGAAATGTGGT 300
QY 307 AGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAAGAGAGGCTGCT 366
DB 301 AGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAAGAGAGGCTGCT 360
QY 367 TCACAAAACCTTGAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAAACAC 426
DB 361 TCACAAAACCTTGAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAAACAC 420
QY 427 AAGTATTAATACAGAAAGCTGCTTACTCATGCTGAAACCTTCTTATATTAACCTCA 486
DB 421 AAGTATTAATACAGAAAGCTGCTTACTCATGCTGAAACCTTCTTATATTAACCTCA 480
QY 487 AAAAGGACTTTTTCAGAGGTAACCTTGAAGTGGCAATGCGCATGCTGAACAAC 546
DB 481 AAAAGGACTTTTTCAGAGGTAACCTTGAAGTGGCAATGCGCATGCTGAACAAC 540
QY 547 GGGTTATAAACCTGTATCAGGTTCTGTATGTCACACTGGTTTTCAGGAGCATCAAC 606
DB 541 GGGTTATAAACCTGTATCAGGTTCTGTATGTCACACTGGTTTTCAGGAGCATCAAC 600
QY 607 ACACAGCTCTAAATTTTGAAGAAGATGATGCTT 642
DB 601 ACACAGCTCTAAATTTTGAAGAAGATGATGCTT 636

```

RESULT 6
LOCUS B0216065 1078 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7595259 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042359
5' mRNA sequence.
ACCESSION B0216065
VERSION B0216065.1 GI:20397465
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Contact: cgapds-remail.nih.gov
Email: cgapds-remail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13281 row: j column: 24
High quality sequence stop: 494.
Location/Qualifiers
1. 1078
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6042359"
/issue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: Not;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 34.3%; Score 634; DB 13; Length 1078;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 CGGCGGTAGCATGAGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCGGCCG 66
DB 1 CGGCGGTAGCATGAGGGGAGAGTACGTGGCGGTCTCTCGGGCTTTGTCGGCCG 60
QY 67 ACTGCTTTCCAGCACTCTCAACAGGACCTGGACAGGAGGTTTCTTCTGGGGAAGT 126
DB 61 ACTGCTTTCCAGCACTCTCAACAGGACCTGGACAGGAGGTTTCTTCTGGGGAAGT 120
QY 127 AAAAGGTGAAGCCAAAGAACAGCATTACTGATTCGCAAAATGATGATGTAAGTTGTTA 186
DB 121 AAAAGGTGAAGCCAAAGAACAGCATTACTGATTCGCAAAATGATGATGTAAGTTGTTA 180
QY 187 TACAAATTGACATTCAGAAATATATTCATGCTATGATGCTTTTACCTTTAATTCCTC 246
DB 181 TACAAATTGACATTCAGAAATATATTCATGCTATGATGCTTTTACCTTTAATTCCTC 240
QY 247 AGCGCAAGTAATGAGCAAGCACTGAGAAATATTCATCAATGTCAAAAGAAATGTGGT 306
DB 241 AGCGCAAGTAATGAGCAAGCACTGAGAAATATTCATCAATGTCAAAAGAAATGTGGT 300
QY 307 AGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAAGAGAGGCTGCT 366
DB 301 AGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAAGAGAGGCTGCT 360
QY 367 TCACAAAACCTTGAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAAACAC 426
DB 361 TCACAAAACCTTGAGAGGACATTTTCAACCAAGACCTGTTTCTGCTATTAAACAC 420
QY 427 AAGTATTAATACAGAAAGCTGCTTACTCATGCTGAAACCTTCTTATATTAACCTCA 486
DB 421 AAGTATTAATACAGAAAGCTGCTTACTCATGCTGAAACCTTCTTATATTAACCTCA 480
QY 487 AAAAGGACTTTTTCAGAGGTAACCTTGAAGTGGCAATGCGCATGCTGAACAAC 546
DB 481 AAAAGGACTTTTTCAGAGGTAACCTTGAAGTGGCAATGCGCATGCTGAACAAC 540
QY 547 GGGTTATAAACCTGTATCAGGTTCTGTATGTCACACTGGTTTTCAGGAGCATCAAC 606
DB 541 GGGTTATAAACCTGTATCAGGTTCTGTATGTCACACTGGTTTTCAGGAGCATCAAC 600
QY 607 ACACAGCTCTAAATTTTGAAGAAGATGATGCTT 640
DB 601 ACACAGCTCTAAATTTTGAAGAAGATGATGCTT 634

```

RESULT 7
AL602519 623 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZP686C1814.5, mRNA sequence.
DEFINITION DKFZP686C1814.5, mRNA sequence.
ACCESSION AL602519
VERSION AL602519.1 GI:15166025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS Wamburt, R., Heubner, D., Mewes, W., Weill, B. and Wiemann, S.
TITLE EST (Wamburt, R., Heubner, D., Mewes, W., Weill, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZP686C1814) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source
1..623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686C1814"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/note="Vector: pTRIPlex2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"

ORIGIN

Query Match 32.9%; Score 608; DB 9; Length 623;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGGTAGCATGAGGAGAGTACGTGCGCGGTGCTCGGCGTTGTGCT 60
DB 16 CTGAGCGCGCGGTAGCATGAGGAGAGTACGTGCGCGGTGCTCGGCGTTGTGCT 75
QY 61 CGGCGCACTCGCTTTCCAGACCTCAACACGAGCTCGAACAAGGTTTCTTTGG 120
DB 76 CGGCGCACTCGCTTTCCAGACCTCAACACGAGCTCGAACAAGGTTTCTTTGG 135
QY 121 GGAAGTAAAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 136 GGAAGTAAAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 195
QY 181 TGTATTATACATTCATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 240
DB 196 TGTATTATACATTCATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 255
QY 241 TTTCTCAGCGGAGTAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 256 TTTCTCAGCGGAGTAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315
QY 301 TGTGTAGGTGATCAAAATTCGTCATTCAGATCAGATCAGATCAGATCAGATCAG 360
DB 316 TGTGTAGGTGATCAAAATTCGTCATTCAGATCAGATCAGATCAGATCAGATCAG 375
QY 361 GGTGCTTCAAAAAGTTCAGAGAGATTTTCAACCAAGGCTTTTCTGCTAT 420
DB 376 GGTGCTTCAAAAAGTTCAGAGAGATTTTCAACCAAGGCTTTTCTGCTAT 435

QY 421 AACACCAAGTATATACAGAAAGCTGCTCTACTCATCATGGAACATTCTTATATA 480
DB 436 AACACCAAGTATATACAGAAAGCTGCTCTACTCATCATGGAACATTCTTATATA 495
QY 481 ACCTCAAAAAGGCTTTTCCAGAGGAGTACCTTTAGGTGGTGGCATGCTGTA 540
DB 496 ACCTCAAAAAGGCTTTTCCAGAGGAGTACCTTTAGGTGGTGGCATGCTGTA 555
QY 541 ACAAGTGGTTATATAAAGTATCAGTTCCTGTATGTCACATGCTTTTACCCAGCAGT 600
DB 556 ACAAGTGGTTATATAAAGTATCAGTTCCTGTATGTCACATGCTTTTACCCAGCAGT 615
QY 601 ACAACAC 608
DB 616 ACAACAC 623

RESULT 8
BE888265 688 bp mRNA linear EST 20-OCT-2000
LOCUS 601511787F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913172.5,
DEFINITION mRNA sequence.
ACCESSION BE888265
VERSION BE888265.1 GI:10344394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M732 row: n column: 21
High quality sequence stop: 638.

FEATURES

source
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3913172"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Query Match 30.8%; Score 570; DB 10; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCTCTGGGCTTGTCTGTGCGCGGCGGCGGCTTCCAGACCTCAACAGGAGCTGGAC 102
DB 1 GCTCTGGGCTTGTGCTGTGCGCGGCGGCGGCTTCCAGACCTCAACAGGAGCTGGAC 60
QY 103 GGAAGTTTCTTCTTGGGAGTAAAGGTGAAGCAAGACAGATTAAGTATCCCA 162
DB 61 GGAAGTTTCTTCTTGGGAGTAAAGGTGAAGCAAGACAGATTAAGTATCCCA 120
QY 163 AATGATGATGTTGAAGTGTATTATCAATTGACATTCGAAATATATTCATGCTATCA 222

Db 121 AATGATGATGTTGAAGTTGTTTATACATTGACATTGAGAAATATATTCATGCTATCA 180
QY 223 GCTTTTAGCTTTTATTAATCTCTTACGCGAAGTAATGACAGACCTGAAAGAAATATT 282
Db 181 GCTTTTAGCTTTTATTAATCTCTTACGCGAAGTAATGACAGACCTGAAAGAAATATT 240
QY 283 ATCAATATGCAAAAAGAAATGTTAGTTGTTGATCAATTCGCTCATTCATGATCAAT 342
Db 241 ATCAATATGCAAAAAGAAATGTTAGTTGTTGATCAATTCGCTCATTCATGATCAAT 300
QY 343 CATGACGTTTGAAGAGAGGCTGCTTACAAAACTTTCAGAGACATTTTCAAAACAGA 402
Db 301 CATGACGTTTGAAGAGAGGCTGCTTACAAAACTTTCAGAGACATTTTCAAAACAGA 360
QY 403 CTTTGTCTTCTGCTATTATACACCAAGTATATAACAGAAAGCTGCTTACTCATCGACT 462
Db 361 CTTTGTCTTCTGCTATTATACACCAAGTATATAACAGAAAGCTGCTTACTCATCGACT 420
QY 463 GGAACATTCCTTATATATAAAGCTCAAAAAGAACTTTTCAAGGGTACCTTTAGTGTGC 522
Db 421 GGAACATTCCTTATATATAAAGCTCAAAAAGAACTTTTCAAGGGTACCTTTAGTGTGC 480
QY 523 CATCTGGGCGATGCTGAAACAATGGGTTATATAAATCTGATCAAGTTCTGTTATGTCAC 582
Db 481 CATCTGGGCGATGCTGAAACAATGGGTTATATAAATCTGATCAAGTTCTGTTATGTCAC 540
QY 583 TGGTTTACCGAGAGCTACAAACACACAG 612
Db 541 TGGTTTACCGAGAGCTACAAACACACAG 570

RESULT 9
AUI25653 736 bp mRNA linear EST 01-AUG-2002
LOCUS AUI25653 NT2RM4 Homo sapiens cDNA clone NT2RM401965 5', mRNA
DEFINITION AUI25653 NT2RM4 Homo sapiens cDNA clone NT2RM401965 5', mRNA
ACCESSION AUI25653
VERSION AUI25653.1 GI:10950369
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 736)
Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
Isozaki, T.
HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T.,
Suzuki, Y., Sugano, S., Isozaki, T.)
Unpublished (2000)
COMMENT Contact: Takao Isozaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
LOCATION/Qualifiers
1. 736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4001965"
/cell_type="leukocarcinoma"
/cell_line="NT2"
/clone_id="NT2RM4"
/note="Vector: DME18SFU3; mRNA from uninduced NT2 neuronal
precursor cells"

FEATURES
source

ORIGIN

Query Match 29.7%; Score 549; DB 9; Length 736;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGAGCGCGCGGTAGCATGAGGAGAGAGTACGTGCGGCTGCTCGGCGCTTGTGCT 60
Db 36 CTGAGCGCGCGGTAGCATGAGGAGAGAGTACGTGCGGCTGCTCGGCGCTTGTGCT 95
QY 61 CGGCGCACTCGCTTTCACACCTCAACCGAGCTTCGACAGGAGGTTTCTTCTTG 120
Db 96 CGGCGCACTCGCTTTCACACCTCAACCGAGCTTCGACAGGAGGTTTCTTCTTG 155
QY 121 GGAAGTAAAGGTGAAGCAAGCAAGCACTGATTCGAAATGATGATGTTGAAGT 180
Db 156 GGAAGTAAAGGTGAAGCAAGCAAGCACTGATTCGAAATGATGATGTTGAAGT 215
QY 181 TGTATTATACATTGACATTGACAAATATATTCATGCTATCAAGTTTATGCTTATTA 240
Db 216 TGTATTATACATTGACATTGACAAATATATTCATGCTATCAAGTTTATGCTTATTA 275
QY 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAAGAAATATTTATCAATGTCAAAAGAA 300
Db 276 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAAGAAATATTTATCAATGTCAAAAGAA 335
QY 301 TGTGTAGGTGGTGAACAAATTCCTGCTGATTCAGATCAATCAAGCTTTTGAAGAG 360
Db 336 TGTGTAGGTGGTGAACAAATTCCTGCTGATTCAGATCAATCAAGCTTTTGAAGAG 395
QY 361 GCTGCTTCAAAAAGCTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATT 420
Db 396 GCTGCTTCAAAAAGCTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATT 455
QY 421 AACACCAAGTATATTAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTATATA 480
Db 456 AACACCAAGTATATTAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTATATA 515
QY 481 ACCCTCAAAAAGACTTTTTCACAGGGTACCTTAGAGTTGCGCAATCGGCGATGCTGA 540
Db 516 ACCCTCAAAAAGACTTTTTCACAGGGTACCTTAGAGTTGCGCAATCGGCGATGCTGA 575
QY 541 ACAAGCTGGTTATATAAATCTGATCAAGTTCTGATGTCATGCTGTTTACCGGACAGT 600
Db 576 ACAAGCTGGTTATATAAATCTGATCAAGTTCTGATGTCATGCTGTTTACCGGACAGT 635
QY 601 ACAACCAACAGCTCTTAATTTTTCAGAGAGATGATCTTAAAGAGAGT 651
Db 636 ACAACCAACAGCTCTTAATTTTTCAGAGAGATGATCTTAAAGAGAGT 686

RESULT 10
AA781435/c 549 bp mRNA linear EST 31-DEC-1998
LOCUS AA781435 aJ26d07.81 Soares_testis_NHT Homo sapiens cDNA clone 1391437 3',
DEFINITION AA781435
ACCESSION AA781435
VERSION AA781435.1 GI:2840766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 549)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
cDNA library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 490.

FEATURES

source
1. 549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NMT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo (dT)
primer [5',
TGTTTCAATCTGAAAGTGGAGCGGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 28.4%; Score 525; DB 9; Length 549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1313 TTCTACATCTTGAGCTACTTGACAGTAAGTCACTTTGTTTCTACTATGTTACCTGTTGC 1372
DB 525 TTCTACATCTTGAGCTACTTGAGTAAGTCACTTTGTTTCTACTATGTTACCTGTTGC 466
QY 1373 AGTAATACACAGATACTCTAGTGCACTTCACTTCAAAAGTACTTTTCAAAATCAGA 1432
DB 465 AGTAATACACAGATACTCTAGTGCACTTCACTTCAAAAGTACTTTTCAAAATCAGA 406
QY 1433 TGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTGTGAGGGGAAAGCTTACA 1492
DB 405 TGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTGTGAGGGGAAAGCTTACA 346
QY 1493 CAGACACATCTCTTAGAATTGGAAAAGTGAGACACAGACAGTGGCTCACAACCTTAATC 1552
DB 345 CAGACACATCTCTTAGAATTGGAAAAGTGAGACACAGACAGTGGCTCACAACCTTAATC 286
QY 1553 CCAGCACTTAGGGAAGACAGTCAAGAGGATTGATTGAAGCTAGAGATTAGACACAGCC 1612
DB 285 CCAGCACTTAGGGAAGACAGTCAAGAGGATTGATTGAAGCTAGAGATTAGACACAGCC 226
QY 1613 TGGGCAACGATTTGAGACATGCTCTTAAATAATTAATGAAAAGCAAGATAGCCTT 1672
DB 225 TGGGCAACGATTTGAGACATGCTCTTAAATAATTAATGAAAAGCAAGATAGCCTT 166
QY 1673 ATTTGCAAAATATGGAAGAAATTTATGAAATTTATCTGAGTCAATTAATTTCTCT 1732
DB 165 ATTTGCAAAATATGGAAGAAATTTATGAAATTTATCTGAGTCAATTAATTTCTCT 106
QY 1733 TAAGTATATCTTTTGAAGATGATTAAGCTAGAGTGGCAAGTAAATGCTGGATAT 1792
DB 105 TAAGTATATCTTTTGAAGATGATTAAGCTAGAGTGGCAAGTAAATGCTGGATAT 46
QY 1793 CATGCATATAATTTGCAAAACATCATCTAAATTTTAAAAAATAA 1837
DB 45 CATGCATATAATTTGCAAAACATCATCTAAATTTTAAAAAATAA 1
```

RESULT 11
CB135704/c CB135704 620 bp mRNA linear EST 29-JAN-2003
LOCUS

DEFINITION K-EST0197980 L14ChoICK0 Homo sapiens cDNA clone L14ChoICK0-30-F08
5', mRNA sequence.
ACCESSION CB135704
VERSION CB135704.1 GI:28102652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,C.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krdb.re.kr
Plate: 30 row: F column: 08
High quality sequence stop: 620.
Location/Qualifiers
1. 620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14ChoICK0-30-F08"
/sex="M"
/cell_line="Choi-CX"
/lab_host="Top10P"
/clone_lib="L14ChoICK0"
/note="Organ: Liver; Vector: pT73-Pac; Site 1: BclRI;
Site 2: NotI; The library was contributed by the Soares
Laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

FEATURES

source

ORIGIN

Query Match 28.0%; Score 518; DB 14; Length 620;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 618; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 731 GCAGTAGATAAATAGTAAGATGTAAACAGATTAAACGAGAAATTGAGAAAGAGA 790
DB 620 GCAGTAGATAAATAGTAAGATGTAAACAGATTAAACGAGAAATTGAGAAAGAGA 561
QY 791 GAGACACAGATTACGAGCAGAGAGAGAGAAACATCCAAAAAGACCTCGAGAAATTT 850
DB 560 GAGACACAGATTACGAGCAGAGAGAGAGAGAAACATCCAAAAAGACCTCGAGAAATTT 501
QY 851 TTCTTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTTCTTCATTCATGTGT 910
DB 500 TTCTTTGTGAGGATTAAGGACCTTTTCCAAATTCGAATTTCTTCATTCATGTGT 441
QY 911 ATGTCTTTAAAAATAGACATGTTTCTTAAAGTAGCTGTAACCAACCAATTCGAT 970
DB 440 ATGTCTTTAAAAATAGACATGTTTCTTAAAGTAGCTGTAACCAACCAATTCGAT 381
QY 971 GTAGTAGACATCTGACCTTAATGTGAGAACACACTGACATTCCTGAGCTAGTCCAGCT 1030
DB 380 GTAGTAGACATCTGACCTTAATGTGAGAACACACTGACATTCCTGAGCTAGTCCAGCT 321
QY 1031 AGTACACACAAATCATTAAGCATTAAGCCTTAAGCTTAAGATGACAGATGGCAATTCAG 1090
DB 320 AGTACACACAAATCATTAAGCATTAAGCCTTAAGCTTAAGATGACAGATGGCAATTCAG 261
QY 1091 AGATCTGGTGTGTAAGTATACAAAGCAACGATCTAAAGCAATCTGTAAGTATAC 1150
DB 260 AGATCTGGTGTGTAAGTATACAAAGCAACGATCTAAAGCAATCTGTAAGTATAC 201
```

DB	Accession	Source	Organism	Reference Authors	Title	Journal	Comment
Oy	1151	CAAAGTAAAGCATCCAAATAGCAGCCCAAGAAACAGATGAAGAAATGAAAGTGAAG	1210				
Db	200	CAAGTAAAGCATCCAAATAGCAGCCCAAGAAACAGATGAAGAAATGAAAGTGAAG	141				
Oy	1211	GGTTTGGTGAATATATCACGGTCTCTTCATATTGATGCTCTTAACTTACAGAGACAT	12707				
Db	140	GGTTTGGTGAATATATCACGGTCTCTTCATATTGATGCTCTTAACTTACAGAGACAT	81				
Oy	1271	TTTTTATTTGGCTGATGGGTAAAGCCAAACATTTGATTTTACTATGTGGAGCTAC	1330				
Db	80	TTTTTATTTGGCTGATGGGTAAAGCCAAACATTTGATTTTACTATGTGGAGCTAC	21				
Oy	1331	TTGCAGTAAAGTTCATTGTT	1350				
Db	20	TTGCAGTAAAGTTCATTGTT	1				
RESULT 12							
LOCUS	CB135111/c						
DEFINITION	K-EST0187053 LI4cho1CK0 Homo sapiens cDNA clone LI4cho1CK0-19-H06						
ACCESSION	CB135111						
VERSION	CB135111.1						
KEYWORDS	5', mRNA sequence.						
SOURCE	EST.						
ORGANISM	Homo sapiens (human)						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
	1 (bases 1 to 581)						
	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,						
	Oh,K.U., Cheong,Y.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and						
	Kim,Y.S.						
	21C Frontier Korean EST Project 2001						
	Unpublished (2002)						
	Contact: Kim YS						

ORIGIN

Query Match	25.9%	Score 479;	DB 14;	Length 581;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 579; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	DB	QY
770	CGAGAAATTCAGAAAAGAGAGGAGACACGATTTCTGCGAGAGCAAGAGGAGAGAAATATCCA	829
581	CGAGAAATTCAGAAAAGAGAGGACGACGATTCAGCGACGACAGAGAGAGAAATATCCA	522
830	AAAGACCCCTAGAGAAACATTTTCTTGTCAAGCATTAAGGACCTTTTTCCAATTCT	889

Db	521	AAAGACCCCTCAGGAGAAACATTTTCTCTGTCAAGCAATTACGGACCTTTTTCACAAATTC	462
Qy	890	GAATTCCTTCAATCAGTGTATGCTCTTTAAAAAATGACATAGTCTTAAAGTAGCTG	949
Db	461	GAATTCCTTCAATCAGTGTATGCTTTTAAAAAATGACATAGTCTTTAAAGTAGCTGT	402
Qy	950	AACACACACACACATCTCGATGTATGACACATCTGACCTTAAATGTAGAACACACTGAC	1009
Db	401	AACACACACACACATCTCGATGTATGACACATCTGACCTTAAATGTAGAACACACTGAC	342
Qy	1010	ATTCTTAAGCTAGTCCAGCTATGACACCAATCATTTAAGCATTAAGCCTTAGACTTA	1069
Db	341	ATTCTTAAGCTAGTCCAGCTATGACACCAATCATTTAAGCATTAAGCCTTAGACTTA	282
Qy	1070	GATGACAGATGGCAATCAAGAGATCTCGGTGTATGATACACAGACAAACGATCTTAA	1129
Db	281	GATGACAGATGGCAATCAAGAGATCTCGGTGTATGATACACAGACAAACGATCTTAA	222
Qy	1130	GCAAAATACGGTAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCCGAAGACGAT	1189
Db	221	GCAATATCTGGTAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCCGAAGACGAT	162
Qy	1190	GAAAGAAATGAAAAGATGAAGGGGTTTGGGAATATTCACGGTCTCTACATTTTGATCC	1249
Db	161	GAAAGAAATGAAAAGATGAAGGGGTTTGGGAATATTCACGGTCTCTACATTTTGATCC	102
Qy	1250	TTTTAACCTTACAAGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTAT	1308
Db	101	TTTTAACCTTACAAGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTAT	42
Qy	1310	GTTTTACTATGTTAGACTACTGACAGTAAGTGAATGTT	1350
Db	41	GTTTTACTATGTTAGACTACTGACAGTAAGTGAATGTT 1	

FEATURES
Source

```

RESULT 13
BG570593
LOCUS
DEFINITION
602591278F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717987 5',
mRNA sequence.
ACCESSION
BG570593
VERSION
BG570593.1
KEYWORDS
GI:13578246
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 778)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM1568 row: 1 column: 20
High quality sequence stop: 673.
Location/Qualifiers
1..778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4717987"
/lab host="DH10B (T1 phage-resistant)"
/clone_1b="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1;
SfiI (ggccgctcgagc); Site 2: SfiI (ggccatcagcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor

```

sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCCGACATG-dt (30)BN-3' (where B = A,
 C or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.4%; Score 469; DB 12; Length 778;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 TGGTCAATTCCTGCTGATTCAGATCAGATCAGTTAGAGAGGCTGCTTAC 370
 Db 117 TGGTCAATTCCTGCTGATTCAGATCAGATCAGTTAGAGAGGCTGCTTAC 176
 QY 371 AAAAAGCTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATTAAACCAAGT 430
 Db 177 AAAAAGCTGAGAGAGATTTTCAACCAAGACCTGTTTCTGCTATTAAACCAAGT 236
 QY 431 ATATATACGAAAGCTGCTTCTACTCATGCACTGGAACATCTCTTATATTAACCTCAAAA 490
 Db 237 ATATATACGAAAGCTGCTTCTACTCATGCACTGGAACATCTCTTATATTAACCTCAAAA 296
 QY 491 GGACTTTTCAAGAGGATCCTTAGTGTGTCATCTGGGATGCTGAAACAATGAGT 550
 Db 297 GGACTTTTCAAGAGGATCCTTAGTGTGTCATCTGGGATGCTGAAACAATGAGT 356
 QY 551 TATTAAGCTGATACAGTCTCTGATATGTCACGTGTTTACCGAGAGATCAACACAC 610
 Db 357 TATTAAGCTGATACAGTCTCTGATATGTCACGTGTTTACCGAGAGATCAACACAC 416
 QY 611 AGCTCTAATTTTGTGAAGAGATGATCCTTAAGAGAGATCATTAAGTAAATG 670
 Db 417 AGCTCTAATTTTGTGAAGAGATGATCCTTAAGAGAGATCATTAAGTAAATG 476
 QY 671 TATGCTTCATTAACAAGAGATTTAAAGATATATGCAAAAAAGTGAAGACAGTGAACA 730
 Db 477 TATGCTTCATTAACAAGAGATTTAAAGATATATGCAAAAAAGTGAAGACAGTGAACA 536
 QY 731 GCAATGATTAATCTAGTAAAGATGTAACAGATTTAAACGGAATG 779
 Db 537 GCAATGATTAATCTAGTAAAGATGTAACAGATTTAAACGGAATG 585

RESULT 14
 AA978690/c 487 bp mRNA linear EST 02-JUN-2000
 LOCUS
 DEFINITION EST190799 MAGE resequencences, MAGP Homo sapiens cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 487)
 Hedge, P., Qi, R., Abernathy, K., Dhar, S., Gaspard, R., Gay, C.,
 Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeaman, T. J. and
 Quackenbush, J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 Unpublished (2000)
 CONTACT: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Place: 396
 Seq primer: Forward.
 Location/Qualifiers

FEATURES

source 1.487
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_id="MAGE resequencences, MAGP"
 /note="Vector: pBluescriptSKm"

ORIGIN

Query Match 23.3%; Score 431; DB 10; Length 487;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1389 CTCTTAGGATTTACTTCAAGAGATCTTTTCAAGATCAGATGCTTTTATTTCCAAA 1448
 Db 431 CTCTTAGGATTTACTTCAAGAGATCTTTTCAAGATCAGATGCTTTTATTTCCAAA 372
 QY 1449 CTTTTTTTCACTTCACTAAGTTGTGAGGGGAAAGCTTACACAGACATTTCTTAG 1508
 Db 371 CTTTTTTTCACTTCACTAAGTTGTGAGGGGAAAGCTTACACAGACATTTCTTAG 312
 QY 1509 AATTGAAAAGTGAACAGGACACAGTGTCTCACCTGTAATCCAGACCTTAGGGAAG 1568
 Db 311 AATTGAAAAGTGAACAGGACACAGTGTCTCACCTGTAATCCAGACCTTAGGGAAG 252
 QY 1569 ACAAGTCAGAGGATGATTGAAGCTAGAGATTAGAGACCAAGCTGGGCAAGCTATTGAG 1628
 Db 251 ACAAGTCAGAGGATGATTGAAGCTAGAGATTAGAGACCAAGCTGGGCAAGCTATTGAG 192
 QY 1629 ACCATGCTATTTAAATATTAATGGAAGCAAGATAGCTTATTTTCAAAATATGGA 1688
 Db 191 ACCATGCTATTTAAATATTAATGGAAGCAAGATAGCTTATTTTCAAAATATGGA 132
 QY 1689 AAGAAATTTATGAAATTTATCTGAGTCAATTAATCTCTTAAGTATCTTTTT 1748
 Db 131 AAGAAATTTATGAAATTTATCTGAGTCAATTAATCTCTTAAGTATCTTTTT 72
 QY 1749 AGAAGTACATTATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAATTAATTTGC 1808
 Db 71 AGAAGTACATTATGCTAGAGTGGCCAGATTAATGCTGATATCATGCAATTAATTTGC 12
 QY 1809 AAAACATCATC 1819
 Db 11 AAAACATCATC 1

RESULT 15
 AA831922/c 437 bp mRNA linear EST 18-MAR-1998
 LOCUS
 DEFINITION OC90404.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE1356942 3',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 437)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Warr, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
 www-bio.llnl.gov/bdnp/image/image.html

Insert Length: 1809 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers

FEATURES

source

1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1356942"
/issue_type="germinal center B cell"
/lab_host="DH10B"
/clone_1ib="NCI CGAP GCH1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CEBR). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTCACATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Benito Soares and M. Fatima Bonaldo."

ORIGIN

Query Match

23.1%; Score 427; DB 9; Length 437;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1398 CATTACTTCACAAAGACTTTTTCACACATGATGCTTTTTCACAACTTTT 1457
DB 437 CATTACTTCACAAAGACTTTTTCACACATGATGCTTTTTCACAACTTTT 378
QY 1458 CACCTTTCACAAAGACTTTTTCACACATGATGCTTTTTCACAACTTTT 1517
DB 377 CACCTTTCACAAAGACTTTTTCACACATGATGCTTTTTCACAACTTTT 318
QY 1518 AGTAGAGCCAGGACCACTGCTCAACCTGTAATCCAGACCTTAGAGAAACAAGTACG 1577
DB 317 AGTAGAGCCAGGACCACTGCTCAACCTGTAATCCAGACCTTAGAGAAACAAGTACG 258
QY 1578 GAGGATGATTGAAGCTAGAGATTAGAGACCACTGCTGAGCAAGTATGAGACATGCT 1637
DB 257 GAGGATGATTGAAGCTAGAGATTAGAGACCACTGCTGAGCAAGTATGAGACATGCT 198
QY 1638 ATTAAAAATTAATGGAAGCAAGATAGCCTTTTTCAAAATATGGAAGAAATT 1697
DB 197 ATTAAAAATTAATGGAAGCAAGATAGCCTTTTTCAAAATATGGAAGAAATT 138
QY 1698 ATATGAAATTTATCTGAGTCATTAAATTCCTCTTAAGTATCTTTTTCAGATGAC 1757
DB 137 ATATGAAATTTATCTGAGTCATTAAATTCCTCTTAAGTATCTTTTTCAGATGAC 78
QY 1758 TTATGCGTAGAGTTCAGATTAATATGCTGATATCTGCAATTAATTTGCAAAATCA 1817
DB 77 TTATGCGTAGAGTTCAGATTAATATGCTGATATCTGCAATTAATTTGCAAAATCA 18
QY 1818 TCTAAAA 1824
DB 17 TCTAAAA 11

RESULT 16
A1830957/c 509 bp mRNA 1linear EST 21-DEC-1999
LOCUS W180d02.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409123 3',
DEFINITION mRNA sequence.
ACCESSION A1830957
VERSION A1830957.1 GI:5451628
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 509)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 1221 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
Location/Qualifiers

FEATURES

source

1. 509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2409123"
/issue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/clone_1ib="NCI CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 Kb. Life Technologies
catalog #: 11547-015"

ORIGIN

Query Match

21.9%; Score 405; DB 9; Length 509;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;

Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 897 TTCATTCATGCTGATGCTTTTAAAAATAGACATGTTCTTAAAGTAGCTTAAC 956
DB 509 TTCATTCATGCTGATGCTTTTAAAAATAGACATGTTCTTAAAGTAGCTTAAC 450
QY 957 ACCACATCTGAGTATGATGACAAATGCTAATAGTAGAACAACATGACATTCCTG 1016
DB 449 ACCACATCTGAGTATGATGACAAATGCTAATAGTAGAACAACATGACATTCCTG 390
QY 1017 AAGCTAGTCCAGTAGTACACCAAAATCAATTAGCAATAAGCCTTAGACTTAGATACA 1076
DB 389 AAGCTAGTCCAGTAGTACACCAAAATCAATTAGCAATAAGCCTTAGACTTAGATACA 330
QY 1077 GATGGCAATTTAAGAGATCTGGTGTGTAATACAAAGCAACAAAGTCTTAAGCAATA 1136
DB 329 GATGGCAATTTAAGAGATCTGGTGTGTAATACAAAGCAACAAAGTCTTAAGCAATA 270
QY 1137 CTGTAGTAGTAACCAAGATTAAGCATCAAAATAGACAGCCAGAAACAGATGAGAAA 1196
DB 269 CTGTAGTAGTAACCAAGATTAAGCATCAAAATAGACAGCCAGAAACAGATGAGAAA 210
QY 1197 TTGAAGAATGAGAGGTTTGGTGAATATTCAGCGCTCTCTTACATTTTGAACCTTTTAC 1256
DB 209 TTGAAGAATGAGAGGTTTGGTGAATATTCAGCGCTCTCTTACATTTTGAACCTTTTAC 150
QY 1257 CTTACAGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTT 1316
DB 149 CTTACAGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTT 90
QY 1317 CTATTTAGAGTACTTGAAGTAAAGTCAATTTGTTTAACTATGTTACCTGTTGACGTA 1376
DB 89 CTATTTAGAGTACTTGAAGTAAAGTCAATTTGTTTAACTATGTTACCTGTTGACGTA 30
QY 1377 ATACAGATTAATCTTATGATGATTTA 1403
DB 29 ATACAGATTAATCTTATGATGATTTA 3

RESULT 17
BQ019837/c 665 bp mRNA linear EST 27-MAR-2002
LOCUS UI-H-ED0-axe-c-16-0-UI.s1 NCI CGAP_ED0 Homo sapiens cDNA clone
DEFINITION IMAGE:5827527 3', mRNA sequence.
ACCESSION BQ019837
VERSION BQ019837.1 GI:19755114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 665)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 8-136, >Alu (matched complement)
Seq primer: M13 FORWARD
POLY-A=yes.
FEATURES
Location/Qualifiers
1..665
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5827527"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED0"
/note="Organ: Left Public Bone; Vector: pTZ19-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED0 is a cDNA library containing
the following tissue(s): Chondrosarcoma cell line C5. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTZ19-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCTCAAGCTT.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-ED0
TAG_SEQ=GCTCAAGCTT"
ORIGIN
Query Match 21.6%; Score 400; DB 12; Length 665;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 993 TGGTGAACACACTGATTCCTGGAAGCTAGTCCAGTAGTACACCAAAATCATTAGC 1052
DB 665 TGGTGAACACACTGATTCCTGGAAGCTAGTCCAGTAGTACACCAAAATCATTAGC 606
QY 1053 ATTAAGCCTTAGACTTGAAGTGAAGATGGCAATTCAGAGATCTGGTTGTTAGTACAC 1112
DB 605 ATTAAGCCTTAGACTTGAAGTGAAGATGGCAATTCAGAGATCTGGTTGTTAGTACAC 546
QY 1113 AGAGCAAGAGTCTAAGCAAAATCTGTAAGTGAACCAAGATAAAGATCCAAAATGA 1172

DB 545 AAGCAAGAGTCTAAGCAAAATCTGTAAGTGAACCAAGATAAAGATCCAAAATGA 486
QY 1173 GCAGCCGAGAAACAGATGAAGAAATTTGAAGATGAAGGGTTTGGTGAATATTCACGGT 1232
DB 485 GCAGCCGAGAAACAGATGAAGAAATTTGAAGATGAAGGGTTTGGTGAATATTCACGGT 426
QY 1233 CTCCTACATTTGATCCTTTTAACTTACCTTACAGAGATTTTATTTGGTGATGGTAA 1292
DB 425 CTCCTACATTTGATCCTTTTAACTTACCTTACAGAGATTTTATTTGGTGATGGTAA 366
QY 1293 AGCCAAACATTTGATTTGTTTAACTTACATGTTGAGTCTTACAGTAAGTCAATTTGTTT 1352
DB 365 AGCCAAACATTTGATTTGTTTAACTTACATGTTGAGTCTTACAGTAAGTCAATTTGTTT 306
QY 1353 TACTAGTTCACCTGTTTGAGTAATACACAGATACCTGTTAGTATTAATTCACCAAA 1412
DB 305 TACTAGTTCACCTGTTTGAGTAATACACAGATACCTGTTAGTATTAATTCACCAAA 246
QY 1413 GTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGT 1472
DB 245 GTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGT 186
QY 1473 TGTGAGGGGAGAGGCTTACCA 1494
DB 185 TGTGAGGGGAGAGGCTTACCA 164
RESULT 18
B1771321 706 bp mRNA linear EST 25-SEP-2001
LOCUS B1771321
DEFINITION 603054695F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204182 5',
mRNA sequence.
ACCESSION B1771321
VERSION B1771321.1 GI:15762899
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 706)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHM1511 row: n column: 23
High quality sequence stop: 703.
Location/Qualifiers
1..706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5204182"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); 16 week female
anonymous pool of 24 week female lung; RNA source
spleen, and 20-22 week male spleen; library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 21.4%; Score 395; DB 12; Length 706;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 AGAATGTGTAGTGTGTACAAATTCCTGTCATTCAGATCAGATCAGTTCAGAG 356
Db AGAATGTGTAGTGTGTGTACAAATTCCTGTCATTCAGATCAGATCAGTTCAGAG 285

QY 357 AAGAGCTGCTTACAAAACCTTGCGAGACATTTTTCACCAACACCTTGTTCGCG 416
Db AAGAGCTGCTTACAAAACCTTGCGAGACATTTTTCACCAACACCTTGTTCGCG 345

QY 417 TATTACACCAAGTATATATACAGAAAGCTGCTACTCATGAGTGGACATTCCTAT 476
Db TATTACACCAAGTATATATACAGAAAGCTGCTACTCATGAGTGGACATTCCTAT 405

QY 477 ATAAACCTCAAAAAGGACTTTTTCAGAGGTAACCTTTAGTGTGCAATCTGGGCAATG 536
Db ATAAACCTCAAAAAGGACTTTTTCAGAGGTAACCTTTAGTGTGCAATCTGGGCAATG 465

QY 537 CTGAACAACTGGGTATATAAAGTATGATGCTGTCATGTCATGCTGTTTACCCAG 596
Db CTGAACAACTGGGTATATAAAGTATGATGCTGTCATGTCATGCTGTTTACCCAG 525

QY 597 CAGTACAAACACACAGCTCTAAATTTTTCAGAAAGATGATCTTAAAGAGTACATA 656
Db CAGTACAAACACACAGCTCTAAATTTTTCAGAAAGATGATCTTAAAGAGTACATA 585

QY 657 AGATAAATGAATGTATGCTTCTCATTCAGAGGAA 691
Db AGATAAATGAATGTATGCTTCTCATTCAGAGGAA 620

RESULT 19

BQ422301 886 bp mRNA linear EST 23-MAY-2002
LOCUS BQ422301
DEFINITION AGENCOURT_7802195 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042035
5', mRNA sequence.
BQ422301.1 GI:21117616
EST.
VERSION BQ422301.1 GI:21117616
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM13280 row: m column: 12
High quality sequence stop: 707.
Location/Qualifiers

FEATURES
source

1. .886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6042035"
/issue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Nct1;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed."

ORIGIN

Query Match 21.1%; Score 390; DB 13; Length 886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GGAAGTTTCTCTTGGGAGTAATAAGTGAAGCAAGAAACAGCATTAATTCCTCA 162
Db GGAAGTTTCTCTTGGGAGTAATAAGTGAAGCAAGAAACAGCATTAATTCCTCA 312

QY 163 AATGATGATGTGAAAGTGTATTATCATTTGACATTCAGAAATATATCCATGCTATA 222
Db AATGATGATGTGAAAGTGTATTATCAATGACATTCAGAAATATATCCATGCTATA 372

QY 223 GCTTTTAGCTTTATATATCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAATATT 282
Db GCTTTTAGCTTTATATATCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAATATT 432

QY 283 ATCAATGTCAAAAAGATGTGTAGTGTGTAATTCCTGTCATTCAGATCAGAT 342
Db ATCAATGTCAAAAAGATGTGTAGTGTGTAATTCCTGTCATTCAGATCAGAT 492

QY 433 ATCAATGTCAAAAAGATGTGTAGTGTGTAATTCCTGTCATTCAGATCAGAT 492
Db ATCAATGTCAAAAAGATGTGTAGTGTGTAATTCCTGTCATTCAGATCAGAT 492

QY 493 CATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGAGAGCATTTTCAACCAAG 552
Db CATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGAGAGCATTTTCAACCAAG 552

QY 403 CTTGTTTTTCTGCTATTAACACCAAGTATATACAGAAAGTCTCTACTATGACT 462
Db CTTGTTTTTCTGCTATTAACACCAAGTATATACAGAAAGTCTCTACTATGACT 612

QY 553 CTTGTTTTTCTGCTATTAACACCAAGTATATACAGAAAGTCTCTACTATGACT 612
Db CTTGTTTTTCTGCTATTAACACCAAGTATATACAGAAAGTCTCTACTATGACT 612

QY 463 GGAACATTCCTTATATTAACCTCAAAAAG 492
Db GGAACATTCCTTATATTAACCTCAAAAAG 642

RESULT 20

B1464110 886 bp mRNA linear EST 21-AUG-2001
LOCUS B1464110
DEFINITION 603202891.F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5268502 5',
mRNA sequence.
B1464110.1 GI:15254766
EST.
VERSION B1464110.1 GI:15254766
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shireki
Tohiyuki and Piero Carninci (RIKEN)

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1677 row: f column: 23
High quality sequence stop: 715.
Location/Qualifiers

FEATURES
source

1. .886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5268502"
/lab_host="DH10B"

ACCESSION BI462610
VERSION BI462610.1 GI:15253266
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 716)
NIH-MGC <http://mhc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM11678 row: 0 column: 08
High quality sequence stop: 714.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269087"
/lab_host="DH10B"
/clone_lib="NIH-MGC 97"
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gscag); Oligo-dT primed using primer: 5'-TTTTTTTTTTTTTTN-3', size-selected for average insert size 2.2 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

ORIGIN
Query Match 19.7%; Score 364; DB 12; Length 716;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGAGCGCGCGGTAGCATGAGGAGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 60
98 CTGAGCGCGCGGTAGCATGAGGAGGAGAGTACGTGCGGCTCTCGGGCTTTGTGCT 157
61 CGGCGGACTCGCTTCCAGACCTCAACGCACTCGACAGGAGTTTCTTCTTG 120
158 CGGCGGACTCGCTTCCAGACCTCAACGCACTCGACAGGAGTTTCTTCTTG 217
121 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATCCCAATGAGATGTTGAAT 180
218 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATCCCAATGAGATGTTGAAT 277
181 TGTATTACATGACATTCAGAAATATATTCAGATCACTTTAGCTTTTAA 240
278 TGTATTACATGACATTCAGAAATATATTCAGATCACTTTAGCTTTTAA 337
241 TTCTTACGCGAAGTAAATGAGCACTGAAGAAATATTTCAATATGTAAGAA 300
338 TTCTTACGCGAAGTAAATGAGCACTGAAGAAATATTTCAATATGTAAGAA 397
301 TGTGTGATGTTGTTACAAATTCGGTGTATTCAGATCAGATATAGCTTTAGAGAG 360
398 TGTGTGATGTTGTTACAAATTCGGTGTATTCAGATCAGATATAGCTTTAGAGAG 457
361 GCTG 364

Db 458 GCTG 461

RESULT 23
LOCUS A1472709/c 360 bp mRNA linear EST 09-MAR-1999
DEFINITION tcl4f06.x1 NCI-CGAP Lym5 Homo sapiens cDNA clone IMAGE:2044067 3'
similar to contigins Alu repetitive element, mRNA sequence.
ACCESSION A1472709
VERSION A1472709.1 GI:4325754
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 360)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Mark Ratfield, M.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/dbip/image/image.html
Seq primer: -40UP from G1bco
High quality sequence stop: 356.
Location/Qualifiers
1..360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2044067"
/tissue_type="follicular lymphoma"
/lab_host="SOLR (Stratagene, Kanamycin resistant)"
/clone_lib="NCI CGAP Lym5"
/note="Organ: lymph node; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Non-amplified library. ~5' adaptor sequence: 5' GAATTCGGCAGG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN
Query Match 19.5%; Score 360; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1281 GCTGATGGTAAAGCCCAATTTCTATTTTCTACTAGTGGATCTTGAGTAAG 1340
360 GCTGATGGTAAAGCCCAATTTCTATTTTCTACTAGTGGATCTTGAGTAAG 301
1341 TTCAATTTGTTTACTATGTTTCACTGTTTGCAGTAAATACAGATTAAGTGCAT 1400
300 TTCAATTTGTTTACTATGTTTCACTGTTTGCAGTAAATACAGATTAAGTGCAT 241
1401 TTACTCAAAAGTACTTTTCAAAATCAAGATGCTTTTATTTTCAAACTTTTTCAC 1460
240 TTACTCAAAAGTACTTTTCAAAATCAAGATGCTTTTATTTTCAAACTTTTTCAC 181
1461 CTTCACATAGTTGTTGAGGGAAGGCTTCAAGACACATCTTTTGAATGGAAAGT 1520
180 CTTCACATAGTTGTTGAGGGAAGGCTTCAAGACACATCTTTTGAATGGAAAGT 121
1521 GAGACACGACACAGTGGCTCACCTGTAATCCAGACCTTTAGGGAAGCAAGTCAGAG 1580
120 GAGACACGACACAGTGGCTCACCTGTAATCCAGACCTTTAGGGAAGCAAGTCAGAG 61
1581 GATTGATTGAAGCTAGAGAGTTAGAGCAGCTGGGCAAGTATTGAGACATGCTATT 1640

Db 60 GATTGATGAGAGCTAGAGGTTAGAGACCAAGCTGGGCAACGTTATTGAGACCATGTCTATT 1

RESULT 24
LOCUS BF812538/c 643 bp mRNA linear EST 12-JAN-2001
DEFINITION PM4-C10084-221100-004-e10 C10084 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF812538
VERSION BF812538.1 GI:12142423
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 643)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.U., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.U.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.U.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPBSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=C10084-221100-004-e10&t=2000-11-22&t=1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 597.
Location/Qualifiers
1..643
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="C10084"
/note="Organ: colon; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 19.1%; Score 353; DB 10; Length 643;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1167 AATGAGCAGCCAGAAAGATGAAGATGAAGAGGTTTGGTGAATTT 1226
1168 |||||
1169 |||||
1170 |||||
1171 |||||
1172 |||||
1173 |||||
1174 |||||
1175 |||||
1176 |||||
1177 |||||
1178 |||||
1179 |||||
1180 |||||
1181 |||||
1182 |||||
1183 |||||
1184 |||||
1185 |||||
1186 |||||
1187 |||||
1188 |||||
1189 |||||
1190 |||||
1191 |||||
1192 |||||
1193 |||||
1194 |||||
1195 |||||
1196 |||||
1197 |||||
1198 |||||
1199 |||||
1200 |||||
1201 |||||
1202 |||||
1203 |||||
1204 |||||
1205 |||||
1206 |||||
1207 |||||
1208 |||||
1209 |||||
1210 |||||
1211 |||||
1212 |||||
1213 |||||
1214 |||||
1215 |||||
1216 |||||
1217 |||||
1218 |||||
1219 |||||
1220 |||||
1221 |||||
1222 CACGGTCTCTCATTTGATCCTTTTAACTTACAGAGATTTTATTGGCTGAT 1286
1223 |||||
1224 |||||
1225 |||||
1226 |||||
1227 |||||
1228 |||||
1229 |||||
1230 |||||
1231 |||||
1232 |||||
1233 |||||
1234 |||||
1235 |||||
1236 |||||
1237 |||||
1238 |||||
1239 |||||
1240 |||||
1241 |||||
1242 |||||
1243 CACGGTCTCTCATTTGATCCTTTTAACTTACAGAGATTTTATTGGCTGAT 1378
1244 |||||
1245 |||||
1246 |||||
1247 |||||
1248 |||||
1249 |||||
1250 |||||
1251 |||||
1252 |||||
1253 |||||
1254 |||||
1255 |||||
1256 |||||
1257 |||||
1258 |||||
1259 |||||
1260 |||||
1261 |||||
1262 |||||
1263 |||||
1264 |||||
1265 |||||
1266 |||||
1267 |||||
1268 |||||
1269 |||||
1270 |||||
1271 |||||
1272 |||||
1273 |||||
1274 |||||
1275 |||||
1276 |||||
1277 |||||
1278 |||||
1279 |||||
1280 |||||
1281 |||||
1282 |||||
1283 |||||
1284 |||||
1285 |||||
1286 |||||
1287 GGGTAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTTGAGTAAGTTCAAT 1346
1288 |||||
1289 |||||
1290 |||||
1291 |||||
1292 |||||
1293 |||||
1294 |||||
1295 |||||
1296 |||||
1297 |||||
1298 |||||
1299 |||||
1300 |||||
1301 |||||
1302 |||||
1303 |||||
1304 |||||
1305 |||||
1306 |||||
1307 |||||
1308 |||||
1309 |||||
1310 |||||
1311 |||||
1312 |||||
1313 |||||
1314 |||||
1315 |||||
1316 |||||
1317 GGGTAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTTGAGTAAGTTCAAT 318
1318 |||||

QY 1347 TGTATTACTATGTTGACCTGTTTGAGTAATACAGATTAAGCTTTAGTGAATTTACTTT 1406
Db 317 TGTATTACTATGTTGACCTGTTTGAGTAATACAGATTAAGCTTTAGTGAATTTACTTT 258
QY 1407 CACAAGTACTTTTCAACATCAGATGCTTTATTTCACAAACCTTTTTCACCTTTCA 1466
Db 257 CACAAGTACTTTTCAACATCAGATGCTTTATTTCACAAACCTTTTTCACCTTTCA 1498
QY 1467 CTAAGTTGTTAGAGGGAAGGCTTACACAGACATTTCTTAGAATTTGAAAAGTGAAC 1526
Db 197 CTAAGTTGTTAGAGGGAAGGCTTACACAGACATTTCTTAGAATTTGAAAAGTGAAC 138
QY 1527 AGGCACAGTGGCTCACACCTGTAATCCAGCACTTGGGGAAGGCAAGTGAAGTTGA 1586
Db 137 AGGCACAGTGGCTCACACCTGTAATCCAGCACTTGGGGAAGGCAAGTGAAGTTGA 78
QY 1587 TTGAAGCTAGAGCTTAGAGACCAAGCTGGGCAAG 1621
Db 77 TTGAAGCTAGAGCTTAGAGACCAAGCTGGGCAAG 43

RESULT 25
Bg531177 744 bp mRNA linear EST 03-APR-2001
LOCUS 602561489F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:469294 5',
DEFINITION mRNA sequence.
ACCESSION Bg531177
VERSION Bg531177.1 GI:13522714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaubs-remail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1531 row: a column: 23
High quality sequence stop: 740.
Location/Qualifiers
1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:469294"
/issue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH MGC 61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:
SmaI (ggccatcgagc); Site:2: SmaI (ggccatcgagc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTTGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGGAGCGGCGCAGATG-dT(30)BN-3',
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."

ORIGIN
Query Match 19.0%; Score 351; DB 12; Length 744;
Best Local Similarity 99.8%; Pred. No. 0;

```

FEATURES
source
location/Qualifiers
1. .328
/organism="Homo sapiens"
/mol_type="cRNA"
/db_xref="GDB:1307092"
/db_xref="taxon:9606"
/clone="IMAGE:399269"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_Retel_Heart_NBH19W"
/note="Organ: heart; Vector: pTVT3D (Pharmacia) with a

```

OY		1314	TTACTATGTTAGCTACTTGGACGTAAAGTCATTGTTGTTTTTACTATATGTTCCACTGTTGCCA	13783
Db		328	TTACTATGTTGAAGCTACTTGCGAGTAAGTTCAATTTGTTTACTATGTTCCACTGTTGCCA	269
OY		1374	GTAATPACAAGATACTACTCTTAGTGCATTTACTCACAAAGTACTTTTCAAACATCAGAT	14338
Db		268	GTAATPACAAGATACTACTCTTAGTGCATTTACTCACAAAGTACTTTTCAAACATCAGAT	209
OY		1434	GCTTTTATTTCCAAACCTTTTTTTTCCACTTTCACTAAAGTTGTAAGGGGAAGGCTTACAC	14933
Db		208	GCTTTTATTTCCAAACCTTTTTTTTCCACTTTCACTAAAGTTGTAAGGGGAAGGCTTACAC	149
OY		1494	AGAACACATCTCTTGAATTTGGAAAAGTGAGCCAGGACACAGTGGCTCCACCTGTAATCC	15533
Db		148	AGAACACATCTCTTGAATTTGGAAAAGTGAGCCAGGACACAGTGGCTCCACCTGTAATCC	89
OY		1554	CAGCATCTTAGGGAAGAACAAGTCAGAGAGATTGATTTGAAGCTTAGAGAGTGAACACAGCT	16133
Db		88	CAGCATCTTAGGGAAGAACAAGTCAGAGAGATTGATTTGAAGCTTAGAGAGTGAACACAGCT	29
OY		1614	GGGCACGTAATTGAGACCATGTCTATTTA	1641
Db		28	GGGCACGTAATTGAGACCATGTCTATTTA	1
RESULT 27				
LOCUS	AM467496/c			
DEFINITION	hej9d11.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919477 3'			
ACCESSION	AM467496	465 bp	mRNA	linear EST 24-FEB-2000
VERSION	AM467496			
KEYWORDS	AM467496.1 GI:7037602			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	1 (bases 1 to 465)			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgsdpbs-remail.nih.gov			
	Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,			
	Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life			
	Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The			
	I.M.A.G.E. Consortium DNA Sequencing by: Washington University			
	Genome Sequencing Center			
	Clone distribution: NCI-CGAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLW at:			
	www.bio.lnl.gov/bbrp/image/image.html			
	Seq primer: -40UP from Gldco			
	High quality sequence atop: 419.			
FEATURES	Location/Qualifiers			

source 1. 465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2919477"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lab_host="DH10B"
/clone_lib="NCI CGAP CML1"
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site: 1; SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies."

ORIGIN

Query Match 17.5%; Score 324; DB 10; Length 465;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 444; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1222 ATATTCACGGCTCCTACATTTTGATCCTTTTAACCTTACAAAGAGATTTTATTTGG 1281
DB 465 ATATTCACGGCTCCTACATTTTGATCCTTTTAACCTTACAAAGAGATTTTATTTGG 406
QY 1282 CTGATGGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTGCAATAGT 1341
DB 405 CTGATGGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTGCAATAGT 346
QY 1342 TCATTGTTTGTACTATGTTTACCTGTTTGACAGTATACAGATTAACCTTAGTCAAT 1401
DB 345 TCATTGTTTGTACTATGTTTACCTGTTTGACAGTATACAGATTAACCTTAGTCAAT 286
QY 1402 TACTTCACAAGTACTTTTTCACATCAGATGCTTTTATTTCCAAACCTTTTTCACC 1461
DB 285 TACTTCACAAGTACTTTTTCACATCAGATGCTTTTATTTCCAAACCTTTTTCACC 226
QY 1462 TTTCTAGTGTGTGAGGGGGAAGGCTTACACAGACATCTTTAGATTTGAAAAATG 1521
DB 225 TTTCTAGTGTGTGAGGGGGAAGGCTTACACACATCTTTAGATTTGAAAAATG 167
QY 1522 AGACGAGGCAAGTGGCTTACACCTGTATATCCAGACATTTAGGAGACAGTCAAGAG 1581
DB 166 AGACGAGGCAAGTGGCTTACACCTGTATATCCAGACATTTAGGAGACAGTCAAGAG 107
QY 1582 ATTGATTAAGCTAGATTTAGAGACCAAGCCTGGGCAACGTATTGAGCCATGTCTATTA 1641
DB 106 ATTGATTAAGCTAGATTTAGAGACCAAGCCTGGGCAACGTATTGAGCCATGTCTATTA 47
QY 1642 AAAAATAAATGAAAAAGCAAGAAT 1666
DB 46 AAAAATAAATGAAAAAGCAAGAAT 22

RESULT 28
LOCUS CB959880 848 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT 13888198 NIH MGC 147 Homo sapiens cDNA clone
IMAGE:30342030 5', mRNA sequence.
ACCESSION CB959880
VERSION CB959880.1 GI:30215996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 848)
NIH-MGC <http://ngc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: NDAM374 row: h column: 07
High quality sequence strip: 591.
Location/Qualifiers

FEATURES

source

1. 848
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30342030"
/tissue_type="Human Placenta"
/lab_host="DH10B Tena"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescript; Site: 1; all-XhoI; Site 2: BamH; Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

Query Match 17.4%; Score 321; DB 14; Length 848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 GGAAGGTTTCTCTTGGGGAAGTAAAGGTGAAGCAAGACAGCATTAAGTCCCA 162
DB 320 GGAAGGTTTCTCTTGGGGAAGTAAAGGTGAAGCAAGACAGCATTAAGTCCCA 379
QY 163 AATGATGATGTTGAAGTGTTTATCAATTCAGATTCGAAATATATTCATGCTATCA 222
DB 380 AATGATGATGTTGAAGTGTTTATCAATTCAGATTCGAAATATATTCATGCTATCA 439
QY 223 GCTTTTACCTTTTATATTTCTTCAGGCGAAGTAAATGACAGCACTGAAGAAATATT 282
DB 440 GCTTTTACCTTTTATATTTCTTCAGGCGAAGTAAATGACAGCACTGAAGAAATATT 499
QY 283 ATGAATGTCAAAAAAGATGTGTAGTGTGTAACAATTCGTCATTCAGATCAAT 342
DB 500 ATGAATGTCAAAAAAGATGTGTAGTGTGTAACAATTCGTCATTCAGATCAAT 559
QY 343 CATGACGTTTAAAGAGGCTGCTTACAAAACCTTGACAGAGCATTTTCAACCAAGA 402
DB 560 CATGACGTTTAAAGAGGCTGCTTACAAAACCTTGACAGAGCATTTTCAACCAAGA 619
QY 403 CCTTGTCTTCTGCTATTAC 423
DB 620 CCTTGTCTTCTGCTATTAC 640

RESULT 29
LOCUS AA456838/c 370 bp mRNA linear EST 07-APR-1999
DEFINITION aa38904.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:81574 3',
similar to contains Alu repetitive element, mRNA sequence.
ACCESSION AA456838
VERSION AA456838.1 GI:2179558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 370)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1228 Std Error: 0.00
Seq primer: -41m3 fwd. RT from Amersham.
Location/Qualifiers

FEATURES
source

1.370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:6034969"
/db_xref="taxon:9606"
/clone="IMAGE:815574"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_id="NCR CGAP GC81"
/note="Vector: pT735-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marcu (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 17.3%; Score 319; DB 9; Length 370;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1322 TTGAGTACTTGCAGAAAGTTCATTTGTTTACTATGTCACCTGTTGAGTAATACA 1381
DB 370 TTGAGTACTTGCAGAAAGTTCATTTGTTTACTATGTCACCTGTTGAGTAATACA 311

QY 1382 CAGATACTCTTAGTGCACTTAATTCAACAAGTACTTTTCAACATCAGATGCTTTAT 1441
DB 310 CAGATACTCTTAGTGCACTTAATTCAACAAGTACTTTTCAACATCAGATGCTTTAT 251

QY 1442 TTCACAACCTTTTTCACCTTCACTAAGTTGTTGAGGGAAGGCTTACACAGACAT 1501
DB 250 TTCACAACCTTTTTCACCTTCACTAAGTTGTTGAGGGAAGGCTTACACAGACAT 191

QY 1502 TCTTTGAATTGGAAAAGTGAGCCAGGACAGTGGCTCACACCTGTAAATCCAGCACTT 1561
DB 190 TCTTTGAATTGGAAAAGTGAGCCAGGACAGTGGCTCACACCTGTAAATCCAGCACTT 131

QY 1562 AGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTACAGCCAGCCGGGCAAG 1621
DB 130 AGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTACAGCCAGCCGGGCAAG 71

QY 1622 TATTGAGACCATGCTATTAAATAAATGAAGAAAAGCAAGAAATAGCTTATTTTCAA 1681
DB 70 TATTGAGACCATGCTATTAAATAAATGAAGAAAAGCAAGAAATAGCTTATTTTCAA 11

QY 1682 AATTGGAAG 1691
DB 10 AATTGGAAG 1

RESULT 30
BI912725 778 bp mRNA linear EST 16-OCT-2001
LOCUS 603176385F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240564 5',
DEFINITION mRNA sequence.
ACCESSION BI912725
VERSION BI912725.1 GI:16176950
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 778)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLML1606 row: j column: 21
High quality sequence start: 3
High quality sequence stop: 625.
Location/Qualifiers

FEATURES

source

1.778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240564"
/lab_host="DH10B"
/clone_id="NIH_MGC_121"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 17.1%; Score 316; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1496 ACAATCTTTAGAAATGGAAAAGTGAGACAGGACAGTGGCTCAACCTGTAAATCCA 1555
DB 366 ACAATCTTTAGAAATGGAAAAGTGAGACAGGACAGTGGCTCAACCTGTAAATCCA 307

QY 1556 GCATTTAGGAAAGCAAGTACAGAGATTGATTGAAGCTAGAGTGAAGACAGAGCTGG 1615
DB 306 GCATTTAGGAAAGCAAGTACAGAGATTGATTGAAGCTAGAGTGAAGACAGAGCTGG 247

QY 1616 GCAACGATTGAGACCAATGCTATTAATAAATGAAGAAAAGCAAGAAATAGCTTAT 1675
DB 246 GCAACGATTGAGACCAATGCTATTAATAAATGAAGAAAAGCAAGAAATAGCTTAT 187

QY 1676 TTCAAAATATGAGAAAGAAATTTATGAATAATTTATCTGATTAATAATCTCTTAA 1735
DB 186 TTCAAAATATGAGAAAGAAATTTATGAATAATTTATCTGATTAATAATCTCTTAA 127

QY 1736 GTGATCTTTTGAAGTACATTATGCTAGAGTTGCCAGATTAATGCTGATATCAT 1795
DB 126 GTGATCTTTTGAAGTACATTATGCTAGAGTTGCCAGATTAATGCTGATATCAT 67

QY 1796 GCAATTAATTTGCAG 1811
DB 66 GCAATTAATTTGCAG 51

RESULT 31
AUI39555 668 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39555 PLACE1 Homo sapiens cDNA clone PLACE1010657 5', mRNA
DEFINITION sequence.

Mon Apr 19 12:46:07 2004

us-10-063-523-21.014g10.rst

Page 23

ACCESSION AU139555
VERSION AU139555.1 GI:11001076
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 668)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto.T., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Iwagaki.T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Iwagaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
source
1..668
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1010857"
/issue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: PME18SFL3"
ORIGIN
Query Match 17.0%; Score 314; DB 9; Length 668;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 297 AGAATGTGTAGTGTGTGTAACAATTCCTGTCATTCAGATCATGACGTTTAAAG 356
246 AGATGTGTAGTGTGTGTAACAATTCCTGTCATTCAGATCATGACGTTTAAAG 305
Qy 357 AGAGGTGTGTGTGTGTAACAATTCCTGTCATTCAGATCATGACGTTTAAAG 416
306 AGAGGTGTGTGTGTGTAACAATTCCTGTCATTCAGATCATGACGTTTAAAG 365
417 TATTAACACCAAGTATATATATACAGAAAGCTGCTCTACTCATGACATGAACTCTTAT 476
366 TATTAACACCAAGTATATATATACAGAAAGCTGCTCTACTCATGACATGAACTCTTAT 425
Qy 477 ATTAACCTCAAAAAGAGCTTTTTCACAGAGTACCTTATGTTGCAATCTGGCAGCT 536
426 ATTAACCTCAAAAAGAGCTTTTTCACAGAGTACCTTATGTTGCAATCTGGCAGCT 485
Qy 537 CTGAACAACCTGCTTAAACCTGATACAGTTCCTGATGTCACATGCTTTTAAAGCCGAG 596
486 CTGAACAACCTGCTTAAACCTGATACAGTTCCTGATGTCACATGCTTTTAAAGCCGAG 545
Db 597 CAGTCAACACACACAGCTCTAAATTTTGAAGAAATGATCTTAAAGAGGATACATA 656
546 CAGTCAACACACACAGCTCTAAATTTTGAAGAAATGATCTTAAAGAGGATACATA 605
Qy 657 AGATA 661
Db 606 AGATA 610
RESULT 32
B1909258 701 bp mRNA linear EST 16-OCT-2001
LOCUS 603067227F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216239 5',
DEFINITION mRNA sequence.

ACCESSION B1909258
VERSION B1909258.1 GI:16172451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 701)
NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: c9abds-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IMAGE1543 row: e column: 08
High quality sequence stop: 701.
FEATURES
source
1..701
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5216239"
/issue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: PCMV-SPORE6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 16.3%; Score 301; DB 12; Length 701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 406 TGTTCCTGCTATTAACACCAAGTATATATACAGAAAGCTGCTCTACTCATGACATGCA 465
Db 401 TGTTCCTGCTATTAACACCAAGTATATATACAGAAAGCTGCTCTACTCATGACATGCA 460
Qy 466 ACATTCCTTATATTAACCTCAAAAAGAGCTTTTTCACAGAGTACCTTATGTTGCAAA 525
461 ACATTCCTTATATTAACCTCAAAAAGAGCTTTTTCACAGAGTACCTTATGTTGCAAA 520
Db 526 TCTGGGCAATGCTGAACAACCTGGGTTATTAACCTGATACAGTTCCTGATGTCACATG 585
Qy 521 TCTGGGCAATGCTGAACAACCTGGGTTATTAACCTGATACAGTTCCTGATGTCACATG 580
Db 586 TTTTAAAGCGAGCACTAACAACAACCTGCTAAATTTTGAAGAAATGATGATCTTAA 645
Qy 581 TTTTAAAGCGAGCACTAACAACAACCTGCTAAATTTTGAAGAAATGATGATCTTAA 640
Db 646 GAGGATCATTAAGTATTAATGATATGTTCTCTTCAAGAGGATTAAGATATATG 705
Qy 641 GAGGATCATTAAGTATTAATGATATGTTCTCTTCAAGAGGATTAAGATATATG 700
Db 706 C 706
Qy 701 C 701
RESULT 33
B1909258 701 bp mRNA linear EST 16-OCT-2001
LOCUS 603067227F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216239 5',
DEFINITION mRNA sequence.

[illegible]

QY	1649	AAATGAAAAAGCAAGATACCCTTAATTTTC-AAAATGTGAAAAGAAATTTATATAGAAAT	170
Db	180	AAATGAAAAAGCAAGATACCCTTAATTTTCGAAAATATGAAAAGAAATTTATATAGAAAT	121
QY	1708	TTATCTGATGATTTAAATTTCTCTTAAAGTAAATCTTTTAAAGATACATTAAGGCTAG	1767
Db	120	TTATCTGATGATTTAAATTTCTCTTAAAGTAAATCTTTTAAAGATACATTAAGGCTAG	61
QY	1768	AGTGCAGATATAATGCTGATATCATGCAATTAATTTGCCAAACATCATCTTAAATTT	1827
Db	60	AGTGCAGATATAATGCTGATATCATGCAATTAATTTGCCAAACATCATCTTAAATTT	1
RESULT 34			
LOCUS	A1014808	316 bp	linear
DEFINITION	ORF303.621 Soares total fetus Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623029 3' Similar to contains Alu repetitive element;; mRNA sequence.		
ACCESSION	A1014808		
VERSION	A1014808.1	GI:3229144	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 316)		
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: scapbs-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 1686 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 303. Location/Qualifiers 1..316 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1623029" /dev_host="8-9 weeks" /lab_host="DH10B" /clone_id="Soares total fetus Nb2Hf8_9w" /note="Vector: pRT13D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAAGTGGAGGCGCGCTTAATTTTATTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT13D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Patricia Bonaldo."		
FEATURES			
Source			
ORIGIN			
Query Match	15.9%	Score 294	DB 9
Best Local Similarity	100.0%	Pred. No. 0	
Matches 294	Conservative	0	Mismatches 0
QY	1417	TTTTTCAAAACATGAGAGCTTTTATTTCCAAACCTTTTTCACCTTCACTTAAGTGT	1477
Db	23	TTTTTCAAAACATGAGAGCTTTTATTTCCAAACCTTTTTCACCTTCACTTAAGTGT	82
QY	1477	GAGGGGAAGGCTTACACAGACACATCTCTTTGAATGAAAAAGTGAACCGGACAGTG	1533
Db	83	GAGGGGAAGGCTTACACAGACACATCTCTTTGAATGAAAAAGTGAACCGGACAGTG	142
QY	1537	GCTGACACTGTAATCCGACCTTAAGGGAAGCAAGCAGAGATTGATTGAAGCTAG	1599

Db 143 GCTCACACCTGTATACCCAGCACTTAGGAGAGCAAGTCAGAGAGATGATTGAAGCTAG 202

QY 1597 GAGTTAGAGACCCAGCCTGGGCAACGCTATGAGACCTGTCTATTAATAATAATGGA 1656

Db 203 GAGTTAGAGACCCAGCCTGGGCAACGCTATGAGACCTGTCTATTAATAATAATGGA 262

QY 1657 AAGCAAGATAGCCTTATTTTCAAAATATGAAAGATTTATGAAATTTA 1710

Db 263 AAGCAAGATAGCCTTATTTTCAAAATATGAAAGATTTATGAAATTTA 316

RESULT 35
AA905493 652 bp mRNA linear EST 09-JUN-1998
LOCUS OK05612.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1506958 3' similar to TR:Q15018 Q15018 ORF ; mRNA sequence.
ACCESSION AA905493
VERSION AA905493.1 GI:3040616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS NCI-Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1047 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 321.

FEATURES
source
1..652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1506958"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pMT23D-Pac (Pharmacia) with
a modified polylinker; Site: 1; Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung Nhlh19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1 M.A.G.E. clones 297480-302087, 662632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 15.8%; Score 292; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 292; Conservative 0;

QY 406 TGTGTTTGTCTATTAACCAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 465

Db 611 TGTGTTTGTCTATTAACCAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 552

QY 466 AACTTCTATTAACCAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 525

Db 551 AACTTCTATTAACCAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 492

QY 526 TCTGGGCACTGTGGAACAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 585

Db 491 TCTGGGCACTGTGGAACAAGTATTAACAGAAAGCTGCTACTCATGCACTGGA 432

QY 586 TTTTAGCCGAGCAGTACCAACACAGCCTCTAAATTTTGAAGATGATCCTTAA 645

Db 431 TTTTAGCCGAGCAGTACCAACACAGCCTCTAAATTTTGAAGATGATCCTTAA 372

QY 646 GAGGTCATATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 697

Db 371 GAGGTCATATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 320

RESULT 36
AU144027 563 bp mRNA linear EST 05-AUG-2002
LOCUS AU144027 HEMBA1 Homo sapiens cDNA clone HEMBA1000684 3', mRNA
DEFINITION AU144027
ACCESSION AU144027
VERSION AU144027.1 GI:11005548
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Salto, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T.,
Sugano, S. and Isogai, T.).
HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
Salto, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M.,
Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source
1..563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1000684"
/issue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: PME18SFJ3"

ORIGIN
Query Match 15.4%; Score 284; DB 9; Length 563;
Best Local Similarity 99.7%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 334; Conservative 0;

QY 1496 ACAATTCCTTATGAAATGAAAGTGAGACGACGACAGTGGCTCAACCTGTATGCCA 1555

Db 81 ACAATTCCTTATGAAATGAAAGTGAGACGACGACAGTGGCTCAACCTGTATGCCA 140

QY 1556 GCACTTGGGAGACCAAGTACGAGAGATTTATTTGAAGCTGAGGTTTGAACCAAGCTGG 1615

Db 141 GCACTTGGGAGACCAAGTACGAGAGATTTATTTGAAGCTGAGGTTTGAACCAAGCTGG 200

QY 1616 GCAAGTATGAGCACTGTCTATTAATAATAATAATAATAATAATAATAATAATA 1675

Db 201 GCAAGTATGAGCACTGTCTATTAATAATAATAATAATAATAATAATAATAATA 260

QY 1676 TTCAAAATATGAGAAAGAAATTTATTAATAATAATAATAATAATAATAATAATA 1735

Db 261 TTCAAAATATGAGAAAGAAATTTATTAATAATAATAATAATAATAATAATAATA 320

QY 1736 GTGATACCTTTTATGAGAGTATGAGGCTAGAGTTCAGATTAATAATCTGTGATATCAT 1795

Db 321 GGAATCTTTTATAGAGATACATATAGCTAGAGTGCAGATAAATGCTGATATCAT 380
QY 1796 GCATTAATTTGCAAAACATCATCTTAATTTTAA 1830
Db 381 GCATTAATTTGCAAAACATCATCTTAATTTTAA 415

RESULT 37
AUI44581/c 645 bp mRNA linear EST 05-AUG-2002
LOCUS AUI44581 HEMBA1 Homo sapiens cDNA clone HEMBA1002381 3', mRNA
DEFINITION sequence.
ACCESSION AUI44581
VERSION AUI44581.1 GI:11006102
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Salto,K., Kawai,Y.,
Yamamoto,J., Makamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T.,
Sugano,S. and Isogai,T.).
HRI human cDNA project [Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S.,
Salto,K., Kawai,Y., Yamamoto,J., Makamatsu,A., Ozawa,M.,
Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)
CONTACT Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
TEL: 81-438-52-3975
FAX: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
LOCATION/Qualifiers
Source 1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1002381"
/issue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: PME18SFL3"

ORIGIN
Query Match 14.9%; Score 275; DB 9; Length 645;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1245 GATCTTTTAACTTACAGAGATTTTATTTGGCTGATGGTAAGCCAAACATTT 1304
Db 395 GATCTTTTAACTTACAGAGATTTTATTTGGCTGATGGTAAGCCAAACATTT 336
QY 1305 CTATGTTTTTACATGATGAGCTAGTGAAGTCACTTGTGTTTACTATGTTTAC 1364
Db 335 CTATGTTTTTACATGATGAGCTAGTGAAGTCACTTGTGTTTACTATGTTTAC 276
QY 1365 CTGTTTGCAGTAATACACAGATACTCTTAGTCATTACTTACAAAGTACTTTTCA 1424
Db 275 CTGTTTGCAGTAATACACAGATACTCTTAGTCATTACTTACAAAGTACTTTTCA 216
QY 1425 AACTCAATGCTTTATTTCCAAACCTTTTTCACCTTACCAATGTTGTTGAGGGAA 1484
Db 215 AACTCAATGCTTTATTTCCAAACCTTTTTCACCTTACCAATGTTGTTGAGGGAA 156
QY 1485 GGCTTACAGACATCTTTTGAATGAAAAAGTGAACCAAGCAAGTGGCTCAC 1544

Db 155 GGCTTACACA-AACATCTTTTGAATGAAAAAGTGAACCAAGCAAGTGGCTCAC 97
QY 1545 CTGTAATCCAGACTTAGAGAGACAGACAGATTTGATGAGTTAGATTTAGA 1604
Db 96 CTGTAATCCAGACTTAGAGAGACAGACAGATTTGATGAGTTAGATTTAGA 37
QY 1605 GACCAGCTTGGGCAAGTATTGACACATGTTATT 1640
Db 36 GACCAGCTTGGGCAAGTATTGACACATGTTATT 1

RESULT 38
AM977201/c 472 bp mRNA linear EST 02-JUN-2000
LOCUS AM977201
DEFINITION EST389310 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AM977201
VERSION AM977201.1 GI:8168444
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 472)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaepard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
CONTACT John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
TEL: 301 838 3528
FAX: 301 838 0208
Email: johnq@igr.org
Plate: 373
Seq primer: Forward.
LOCATION/Qualifiers
Source 1..472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptskm"

ORIGIN
Query Match 14.1%; Score 260; DB 10; Length 472;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 360; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1329 ACTTGACATTAATGTTGTTTATTTTACTATGTTTCACTGTTTGAAGTAATACAGATA 1388
Db 362 ACTTGACATTAATGTTGTTTATTTTACTATGTTTCACTGTTTGAAGTAATACAGATA 303
QY 1389 CTCTTAAGCATTTACTTCAAAAGTACTTTTCAAAATCAGATGCTTTATTTCCAAA 1448
Db 302 CTCTTAAGCATTTACTTCAAAAGTACTTTTCAAAATCAGATGCTTTATTTCCAAA 243
QY 1449 CTTTTTTTCACTTTTCACTAATGTTTGAAGGGAGGCTTACACACATTTCTTTAG 1508
Db 242 CTTTTTTTCACTTTTCACTAATGTTTGAAGGGAGGCTTACACACATTTCTTTAG 183
QY 1509 AATTGAAAAGTGAACCAAGCAAGTGGCTCACCTGTATCCAGCACTTAGGGAG 1568
Db 182 AATTGAAAAGTGAACCAAGCAAGTGGCTCACCTGTATCCAGCACTTAGGGAG 123
QY 1569 ACAAAGTCAGAGATTGATTGAAGTGAAGTGAAGCAAGCTGGGCAACGTAATGAG 1628
Db 122 ACAAAGTCAGAGATTGATTGAAGTGAAGTGAAGCAAGCTGGGCAACGTAATGAG 63
QY 1629 ACAAAGTCATTAATAAATAAATGAAAAAGCAAGTATGCTATTTTCAAAATATGA 1688
Db 62 ACAAAGTCATTAATAAATAAATGAAAAAGCAAGTATGCTATTTTCAAAATATGA 3

QY 1689 AA 1690
Db 2 AA 1

RESULT 39
LOCUS C01486/c
DEFINITION HUMS0008480 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
ACCESSION C01486
VERSION C01486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 264)
BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

REFERENCE
AUTHORS Okubo, K.
TITLE BodyMap: human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES

source
1. .264
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN

Query Match 11.5%; Score 213; DB 13; Length 264;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 832 AGACCTCAGAGAACATTTCTTTGTCAGGCAATTAAGACCTTTTCCAAATTCGA 891
Db 264 AGACCTCAGAGAACATTTCTTTGTCAGGCAATTAAGACCTTTTCCAAATTCGA 205
QY 892 ATTCTTCATGATGTTATGCTTTAAATAATGACATGTTCTTAAAGAGCTGTA 951
Db 204 ATTCTTCATGATGTTATGCTTTAAATAATGACATGTTCTTAAAGAGCTGTA 145
QY 952 CTACACCAACCATCTTCGATGATGATGACATCTGACCTTAATGATGACACACTGACAT 1011
Db 144 CTACACCAACCATCTTCGATGATGATGACATCTGACCTTAATGATGACACACTGACAT 85
QY 1012 TCCCTGAAGTACGCTGACGCTTACGACCAATCAATTAAGCTTAAGACTTGA 1071
Db 84 TCCCTGAAGTACGCTGACGCTTACGACCAATCAATTAAGCTTAAGACTTGA 25

QY 1072 TGACAGATGCAATTCAGAGATC 1095
Db 24 TGACAGATGCAATTCAGAGATC 1

RESULT 40
LOCUS AA280141
DEFINITION zt09g10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712674.5;
209 bp mRNA linear EST 15-AUG-1997

ACCESSION AA280141
VERSION AA280141.1 GI:1922002
EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 209)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 2695 Std Error: 0.00
Seq primer: -26m13 rev2 RT from Amersham
High quality sequence stop: 145.

FEATURES
source
1. .209
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGATGAGGCGCGCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 11.3%; Score 209; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 CTAAATTTTGAAGAGATGATCCTTAAGAGGATCAATTAATGAATGATG 674
Db 1 CTAAATTTTGAAGAGATGATCCTTAAGAGGATCAATTAATGAATGATG 60
QY 675 CTTCATTACAGAGGATTTAAGATGATGCAAAAAGTGAAGACAGTGAACAAGCAG 724
Db 61 CTTCATTACAGAGGATTTAAGATGATGCAAAAAGTGAAGACAGTGAACAAGCAG 120
QY 735 TAGATAACTAGTAAAGATGTAACAGATTAACAGAGAAATGAGAAAGAGAGAG 794
Db 121 TAGATAACTAGTAAAGATGTAACAGATTAACAGAGAAATGAGAAAGAGAGAG 180
QY 795 CACAGATTCAGGACAGAGAGAGAGAC 823
Db 181 CACAGATTCAGGACAGAGAGAGAGAC 209

RESULT 41
LOCUS BF826597
DEFINITION CM4-HN0023-221100-447-e06 HN0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF826597
VERSION BF826597.1 GI:12169942
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 350)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, N. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bais, G.S., Simpson, D.H.,
Brustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, U.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SF,
Brazil
Tel: +55-11-27049922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CW4&t2=CW4-HN0023-
22100-447-e06&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 350.
Location/Qualifiers

FEATURES
source
1..350
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="HN0023"
/note="Organ: head, normal. Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 9.4%; Score 174; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1657 AAGCAAAATAGCCTTATTTCAAAATAGGAAGAATTTATATGAATTTATCTGAG 1716
1717 TCATTAATATCTCTTAACTAGTACTTTTGAAGTACATTATGGCTGAGTCCGAG 1776
135 TCATTAATATCTCTTAACTAGTACTTTTGAAGTACATTATGGCTGAGTCCGAG 194

Qy 1777 ATTAATAGCTGATATCATGCAATTAATTTGCAAAACATCATCTAAATTTAA 1830
195 ATTAATAGCTGATATCATGCAATTAATTTGCAAAACATCATCTAAATTTAA 248

Db

RESULT 42
LOCUS BQ431082 977 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7769131 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6069503
5', mRNA sequence.
ACCESSION BQ431082
VERSION BQ431082.1 GI:21170158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 977)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LHM13352 row: e column: 24
High quality sequence stop: 375.
Location/Qualifiers

FEATURES
source
1..977
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6069503"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; 0150-07 primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN
Query Match 8.9%; Score 165; DB 13; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 GGAAGTTTCTTTGGGGAAGTAAAGGAGCAAGCAAGCACTACTGATTCCTCA 162
272 GGAAGTTTCTTTGGGGAAGTAAAGGAGCAAGCAAGCACTACTGATTCCTCA 331

Qy 163 AATGATGATGTTGAAGTTGTTTATACATTGACATTCAGAAATATTTCCATGCTCA 222
332 AATGATGATGTTGAAGTTGTTTATACATTGACATTCAGAAATATTTCCATGCTCA 391

Db 223 GCTTTAGCTTTTATATCTTTCAGGCGAAGTAAATGAGCAAGC 267
392 GCTTTAGCTTTTATATCTTTCAGGCGAAGTAAATGAGCAAGC 436

Qy

Db

RESULT 43
LOCUS BF218805 857 bp mRNA linear EST 06-NOV-2000
DEFINITION 6018821671 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4094834 5',
mRNA sequence.
ACCESSION BF218805
VERSION BF218805.1 GI:11112495
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 857)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM955 row: p column: 03
 High quality sequence stop: 620.
 Location/Qualifiers

FEATURES

source

1..857
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4094834"
 /issue_type="G10B (T1 phage-resistant)"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_57"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dT(30)-BN-3' (where B = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 8.4%; Score 156; DB 10; Length 857;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 GCGACGATTGAGCCATGCTATTAAATAATGAAAGCAAGATAGCCTTAT 1674
 DB 171 GCGACGATTGAGCCATGCTATTAAATAATGAAAGCAAGATAGCCTTAT 230
 QY 1675 TTTCAAAATATGAAAGAAATTTATATGAAAAATTTATCTGAGTCATTAAATTCCTTA 1734
 DB 231 TTTCAAAATATGAAAGAAATTTATATGAAAAATTTATCTGAGTCATTAAATTCCTTA 290
 QY 1735 AGTGATCTTTTGAAGTACATATAGGCTAGAGT 1770
 DB 291 AGTGATCTTTTGAAGTACATATAGGCTAGAGT 326

RESULT 44
 BF240591 869 bp mRNA linear EST 14-NOV-2000
 LOCUS 60187571181 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4095563 5',
 DEFINITION mRNA sequence.
 ACCESSION BF240591
 VERSION BF240591.1 GI:11154515
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 869)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM955 row: e column: 04
 High quality sequence stop: 512.
 Location/Qualifiers

FEATURES

source

1..869
 /organism="Homo sapiens"

ORIGIN

Query Match 7.6%; Score 140; DB 10; Length 869;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 TTGAGACATGCTATTAAATAATGAAAGCAAGATAGCCTTATTTCAAAAT 1683
 DB 340 TTGAGACATGCTATTAAATAATGAAAGCAAGATAGCCTTATTTCAAAAT 399
 QY 1684 ATGAAAGAAATTTATATGAAATTTATCTGAGTCATTAAATTCCTTAAGTACT 1743
 DB 400 ATGAAAGAAATTTATATGAAATTTATCTGAGTCATTAAATTCCTTAAGTACT 459
 QY 1744 TTTTGAAGTACATTATGG 1763
 DB 460 TTTTGAAGTACATTATGG 479

RESULT 45
 BE894160 948 bp mRNA linear EST 20-OCT-2000
 LOCUS 60143829181 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923326 5',
 DEFINITION mRNA sequence.
 ACCESSION BE894160
 VERSION BE894160.1 GI:10356248
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 948)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCPD/PTP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1M9755 row: e column: 23
 High quality sequence stop: 605.
 Location/Qualifiers

FEATURES

source

1..948

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3923326"
 /issue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"

Db	101	AGTAAAGGTAAAGCCAGAAACAGATTA	CTGATTCCCAATTCGATGATGTTGAAGTTGT	160
Oy	184	TTATACAAATGA	195	
Db	161	TTATACAAATGA	172	
RESULT 48				
LOCUS	F08936			
DEFINITION	H852UG082, normalized infant brain cDNA Homo sapiens CDNA clone			
ACCESSION	F08936			
VERSION	F08936.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 346)			
AUTHORS	Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houligatte,R., Jumeau,M.N., Lamy,B., Sebastiani,Kakachis,C., and Tessier,A.			
TITLE	IMAGE: molecular integration of the analysis of the human genome and its expression			
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)			
MEDLINE	95277534			
PUBMED	7757816			
COMMENT	Contact: Genethon Genexpress-Genethon Genethon Centre de recherche sur le Genome Humain 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE Tel: 33169472800 Fax: 33160778698 Email: genexpress@genethon.fr Single read, removed at sequence 5' end Genexpress_library_idc: C; Genexpress_sequence_idc: alc-2ug08 Seq primer: (-21)M13_universal. Location/Qualifiers			
FEATURES				
source	1..346			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="c-2ug08"			
	/sex="Female"			
	/tissue_type="total brain"			
	/dev_stage="3 months old"			
	/clone_lib="normalized infant brain cDNA"			
	/note="Organ: brain; Vector: lafmd BA; Site: 1: HindIII; Site:2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmd BA vector. Clone library from B.Saeres, Psychiatry Dept. Columbia University, USA			
ORIGIN	Bento Soares, P.N.A.S in press			
Query Match	6.5%;	Score 121;	DB 14;	Length 346;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 171;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Oy	1474	GTTAGGGGGAAGGCTTACACACACATCTTTAGATTGGAAAAGTGAAGCCAGGACCA	1533	
Db	53	GTTGAGGGGAAGGCTTACACACACATCTTTAGAAATGGAAAAGTGAAGCCAGGACCA	112	
Oy	1534	GTTGCTCACACCTGTAAATCCCGACGACTTAGGGAAGACAAAGTCAGAGGATTTGAAGAAGC	1593	
Db	113	GTTGCTCACACCTGTAAATCCCGACGACTAGGGAAGACAAAGTCAGAGGATTTGAAGC	172	
Oy	1594	TAGAGTTTGAAGACCAAGCTGGGCAACGATTGAAGCAATGTCTTTAAAA	1645	

```

Db          173 TAGAGGTTAGAGCACCGACCTGGGAGCAAGTATTGAGACCATCTCATTTAAAAA 224

RESULT 49
BG494352
LOCUS      602539307F1 NIH_MGC_59 Homo sapiens CDNA clone IMAGE:4660416 5',
DEFINITION mRNA sequence.
ACCESSION  BG494352
VERSION     BG494352.1  GI:13455866
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 534)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: LIML457 row: n column: 01
High quality sequence stop: 534.
Location/Qualifiers
1. 534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4660416"
/issue_type="mucoepidermoid carcinoma"
/lcd_host="DH10B (TI phage-resistant)"
/clone_id="NIH_MGC_59"
/clone_organ="lung; Vector: pDNR-LIB (Clontech); Site_1:
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAAGCGCAGGCGCCAGCAGT-dt(30)BN-3'
sequence: 5'-ATTCTAGAAGCGCAGGCGCCAGCAGT-dt(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 6.3%; Score 117; DB 12; Length 534;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1714 GAGCATTAAATTCCTCTTAAGAGARACTTTTAAAGTACATTAAGCTAGAGTGC 1773
Db 1 GAGCATTAAATTCCTCTTAAGAGARACTTTTAAAGTACATTAAGCTAGAGTGC 60

Cy 1774 CAGATTAAGTCTGATCATCATGATTAATTTGCAAAACATCATTAATTTTAA 1830
Db 61 CAGATTAAGTCTGATCATCATGATTAATTTGCAAAACATCATTAATTTTAA 117

RESULT 50
AL599192 472 bp mRNA linear EST 04-SEP-2003
LOCUS AL599192
DEFINITION DKFZP3130324.t1.313 (synonym: hicc2) Homo sapiens CDNA clone
DKFZP3130324.5, mRNA sequence.
ACCESSION AL599192
VERSION AL599192.1 GI:15162480

```

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 472)
TITLE Koehrer K., Beyer A., Mewes W., Weill B. and Wiemann S.
JOURNAL EST (Koehrer K., Beyer A., Mewes W., Weill B. and Wiemann S.)
COMMENT Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the CDNA sequencing consortium of the German
Genome Project.
No s1 sequence available.
This clone (DKFZp313p0324) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg; GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313p0324"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="313 (synonym: hlc2)"
/note="Vector: pT713; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"

ORIGIN
Query Match 5.6%; Score 104; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGCGGTAGCATGAGGAGGAGTACGCGCGGTCTCTCGGGCTTTGTCT 60
DB 72 CTGAGCGCGCGGTAGCATGAGGAGGAGTACGCGCGGTCTCTCGGGCTTTGTCT 131
QY 61 CGGCGCATCGCTTCCAGCACTCAACCGGAGCGTGGACAGCG 104
DB 132 CGGCGCATCGCTTCCAGCACTCAACCGGAGCGTGGACAGCG 175

RESULT 51
AI024776 480 bp mRNA linear EST 27-AUG-1998
LOCUS cu52f08.x1 NCI_CGAP Br2 Homo sapiens cDNA clone IMAGE:1631463.3
DEFINITION Similar to contains A1u repetitive element; contains element MER22
repetitive element; mRNA sequence.
ACCESSION AI024776
VERSION AI024776.1 GI:3240389
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 480)
TITLE NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lemon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINK at:
www.bio.linn.gov/bdip/image/image.html
Insert Length: 1044 Std Error: 0.00
Seq primer: -40m13 fwd, Ex from Amersham
High quality sequence stop: 470.
Location/Qualifiers
1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1631463"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_1lb="NCI CGAP Br2"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT713
vector. This library is the normalized version of
NCI CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."

ORIGIN
Query Match 4.8%; Score 88; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 610 CAGCTTAAATTTTGAAGAAGTGAATCTTAAAGAGTCAATTAATGAAT 669
DB 480 CAGCTTAAATTTTGAAGAAGTGAATCTTAAAGAGTCAATTAATGAAT 421
QY 670 GTATGCTTCAATTAAGAAGATTAAG 697
DB 420 GTATGCTTCAATTAAGAAGATTAAG 393

RESULT 52
AA089592 225 bp mRNA linear EST 24-OCT-1996
LOCUS cgp2708.seq.F Human fetal heart, lambda ZAP Express Homo sapiens
DEFINITION CDNA 5', mRNA sequence.
ACCESSION AA089592
VERSION AA089592.1 GI:1636084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 225)
TITLE Liew, C.C.
JOURNAL cDNAs from fetal heart (1996)
COMMENT Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177228915
Fax: 6179750595
Email: clliew@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAAGCTCGAATTAACCTCACTAAAGG 3'
BACKWARD: 5' CCAAGTATGATTAACGACTCACTATGAGGCG 3'
Seq primer: 5' GAATTAACCTCACTAAAGG 3'.
Location/Qualifiers
1..225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="E. coli XL1-Blue"

and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalisation to a Cot = 20. Library constructed by Bento Soares and M.Fátima Bonaldo."

Query Match	4.3%	Score 79;	DB 14;	Length 347;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	324	GTCGTCATTCAGATCGATCATACGTTAGAGAGAGGCTGCTTCAAAAACTTGAGG	383
Dd	304	GTCGTCATTCAGATCGATCATGCGTTAGAGAGAGGCTGCTTCAAAAACTTGAGG	245
QY	384	AGCATTTTCAACCAAGA	402
Dd	244	AGCATTTTCAACCAAGA	226

RESULT 54	LOCUS	DEFINITION
AI820815/c	508 bp	508 bp
	AT820815	AT820815
	VP16d11.y5	VP16d11.y5
	IMAGE:187605	IMAGE:187605
	5'	5'
	similar to	similar to
	TR:Q15018	TR:Q15018
	Q15018 ORF ;	Q15018 ORF ;
	mrna	mrna
	linear	linear
	EST 24-OCT-2000	EST 24-OCT-2000
	clone	clone
	3nBstHsc Homo sapiens	3nBstHsc Homo sapiens
	cdna	cdna
	sequence.	sequence.

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE	1 (bases 1 to 508)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Other ESTs: yf16d11.x5

JOURNAL
COMMENT
Unpublished (1997)
Other_ESTs: yp16d11.x5
Contact: Robert Strausberg, Ph.D
Fred J. Beckwith, Ph.D

```

information
This read has been verified (found to hit its original self in the
correct orientation)
Putative full length read
The vector to vector length is 714
Possible reversed clone: similarity on wrong strand
Insert Length: 796 Std Error: 0.00
Seq primer: -40Rp from Glbco
High quality sequence stop: 455.

```

FEATURES	Location/Qualifiers
source	1. . 508

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3MDHBst"
/notes="Organ: breast; Vector: pT73TD (Pharmacia) with a modified polylinker; Site 1: Not I; site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAAGTGGAGCGCGCCCTTTTCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

```

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTGCTTCAAAAACCTTGACG 383
DB 313 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTGCTTCAAAAACCTTGACG 254

QY 384 AGCATTTTCAACCAAGA 402
DB 253 AGCATTTTCAACCAAGA 235

RESULT 56
A1820814 523 bp mRNA linear EST 24-OCT-2000
LOCUS YP16a12.x5 Soares breast 3MBHst Homo sapiens cDNA clone
DEFINITION IMAGE:187582 5', similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.
ACCESSION A1820814 GI:5439893
VERSION A1820814.1 GI:5439893
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: YP16a12.x5
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
Information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Putative full length read
The vector to vector length is 706
Possible reversed clone: similarity on wrong strand
Insert length: 780 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 441.
Location/Qualifiers

FEATURES
source

1..523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Soares breast 3MBHst"
/clone_lib="Soares breast 3MBHst"
/note="Organ: breast; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGAAGCGCGCCCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pRT3D vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTTCAAAAACCTTGACG 383
DB 405 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTTCAAAAACCTTGACG 464

QY 384 AGCATTTTCAACCAAGA 402

Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTGCTTCAAAAACCTTGACG 383
DB 313 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTGCTTCAAAAACCTTGACG 254

QY 384 AGCATTTTCAACCAAGA 402
DB 253 AGCATTTTCAACCAAGA 235

RESULT 56
A1821443 526 bp mRNA linear EST 24-OCT-2000
LOCUS YP16a12.x5 Soares breast 3MBHst Homo sapiens cDNA clone
DEFINITION IMAGE:187582 3', similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.
ACCESSION A1821443 GI:5440522
VERSION A1821443
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
Information
This read has been verified (found to hit its original self in the
correct orientation)
Possible reversed clone: similarity on wrong strand
Insert length: 780 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 466.
Location/Qualifiers

FEATURES
source

1..526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Soares breast 3MBHst"
/clone_lib="Soares breast 3MBHst"
/note="Organ: breast; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGAAGCGCGCCCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pRT3D vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTTCAAAAACCTTGACG 383
DB 405 GTGCTCATTCAGATCATGATCGTTTAGAGAGAGCGCTTCAAAAACCTTGACG 464

QY 384 AGCATTTTCAACCAAGA 402

Db 465 AGCATTTCACACCAAGA 463

RESULT 57
R83653
LOCUS
DEFINITION YP16a12.s1 Soares breast 3NBHstc Homo sapiens cDNA clone
IMAGE:187582 3', mRNA sequence.
ACCESSION R83653
VERSION R83653.1 GI:928530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 469)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Mashu-Merck EST Project
Unpublished (1995)
JOURNAL
COMMENT Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 780
High quality sequence stops: 348
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 780 Std Error: 0.00
Seq primer: T3
High quality sequence stop: 348.
Location/Qualifiers
1..469
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_11b="Soares breast 3NBHstc"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 3.9%; Score 73; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 146 AGCATTTCACACCAAGTGAAGTGTTCATCAATTGACATTCAGAAA 205
DB 196 AGCATTTCATGATTCACCAATGGATGATGTGAAGTGTTCATCAATTGACATTCAGAAA 255
QY 206 TATATTCATGCT 218
DB 256 TATATTCATGCT 268

RESULT 58
A1821445
LOCUS
DEFINITION YP16d11.x5 Soares breast 3NBHstc Homo sapiens cDNA clone
IMAGE:187605 3' similar to TR:Q15018 Q15018 ORF; mRNA sequence.
ACCESSION A1821445
VERSION A1821445.1 GI:5440524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 505)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This read has been verified (found to hit its original self in the
correct orientation)
Possible reversed clone: similarity on wrong strand
Insert length: 796 Std Error: 0.00
Seq primer: -40up from G1bco
High quality sequence stop: 458.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_11b="Soares breast 3NBHstc"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 3.9%; Score 73; DB 9; Length 505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 146 AGCATTTCATGATTCACCAATGGATGATGTGAAGTGTTCATCAATTGACATTCAGAAA 205
DB 232 AGCATTTCATGATTCACCAATGGATGATGTGAAGTGTTCATCAATTGACATTCAGAAA 291
QY 206 TATATTCATGCT 218
DB 292 TATATTCATGCT 304
RESULT 59
R83668
LOCUS
DEFINITION YP16d11.s1 Soares breast 3NBHstc Homo sapiens cDNA clone
IMAGE:187605 3', mRNA sequence.
ACCESSION R83668

VERSION R83668.1 GI:928545
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 521)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kuchaba, T., Le, N., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 796
 High quality sequence stops: 328
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 796 Std Error: 0.00
 Seq primer: T3
 High quality sequence stop: 328.
 Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3818501"
 /db_xref="taxon:9606"
 /clone="IMAGE:187605"
 /sex="Female"
 /dev_stage="Adult"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_lib="Soares Breast 3rdHBst"
 /note="Organ: Breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCACTGAGTGGAGCGCCGCTTTTCTTTTCTTTT 3'], (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bernaldo."

ORIGIN
 Query Match 3.9%; Score 73; DB 14; Length 521;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCATTACTGATTCACCAATGATGATGTTGAAGTTGTTATACATTGACATTGAGAA 205
 DB 222 AGCATTACTGATTCACCAATGATGATGTTGAAGTTGTTATACATTGACATTGAGAA 281

QY 206 TATATTCATGCT 218
 DB 282 TATATTCATGCT 294

RESULT 60
 BF742611 379 bp mRNA linear EST 10-JAN-2001
 LOCUS BF742611
 DEFINITION RC2-BT0841-021000-011-g08 BT0841 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF742611
 VERSION BF742611.1 GI:12069287
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 379)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jungeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC2&cl2=RC2-BT0841-021000-011-g08&cl3=2000-10-02&cl4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 377.
 Location/Qualifiers
 1..379
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BT0841"
 /note="Organ: Breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 3.7%; Score 69; DB 10; Length 379;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1348 GTTTTACTGATGTTACCTGCTTGGAGTATACAGATTAACCTTATAGTGCACTTCTC 1407
 DB 311 GTTTTACTGATGTTACCTGCTTGGAGTATACAGATTAACCTTATAGTGCACTTCTC 370

QY 1408 ACAAGTAC 1416
 DB 371 ACAAGTAC 379

RESULT 61
 BE465988/c 316 bp mRNA linear EST 27-JUL-2000
 LOCUS BE465988
 DEFINITION hy08g04.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3196758 3'
 Similar to contains 11u repetitive element; mRNA sequence.
 ACCESSION BE465988
 VERSION BE465988.1 GI:9511763
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 316)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNU, send email to: infoimage.llnl.gov
Seq primer: -40UP from Gibco.

FEATURES

source

1. .316
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="316758"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: DT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonides 1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.7%; Score 68; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GGGGGTCTCTGGGCTTTGTGCTCGGCGACCTGCTTTCAGACACTCAACAGGACATC 96
Db 316 GGGGGTCTCTCGGCTTTGTGCTCGGCGACCTGCTTTCAGACACTCAACAGGACATC 257
Qy 97 GGAACACG 104
Db 256 GGAACACG 249

RESULT 62
LOCUS BF171490 124 bp mRNA linear EST 23-MAR-2001
DEFINITION PCL2672 Myeloma (PCL) cDNA library Homo sapiens cDNA, mRNA
ACCESSION BF171490
VERSION BF171490.1 GI:13437641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 124)
AUTHORS Claudio J.O., Mash-Khan, E., Tang, H., Goncalves, J., Voralia, M., Li, Z.H., Nadeem, V., Cukerman, E., Francisco-Pabalan, O., Liew, C.C., Woodgett, J.R. and Stewart, A.K.
TITLE A molecular compendium of genes expressed in multiple myeloma
JOURNAL Blood 100 (6), 2175-2186 (2002)
MEDLINE 22188429
PUBMED 12200383
COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546

Email: k.stewart@utoronto.ca
PCR primers
FORWARD: 5'-GCCAAGCTCGAATTAACCTCACTAAGG-3'
BACKWARD: 5'-CCAGTGAATTGATAGATCACTATAGGGC-3'
Seq primer: 5'-GAAATTAACCTCACTAAGG-3'.
Location/Qualifiers

FEATURES

source

1. .124
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="plasma cell leukemia"
/clone_image="myeloma (PCL) cDNA library"
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from plasma cell leukemia patient's peripheral blood containing >95% myeloma. An oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and [alpha-32P]dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using GigaPack II packaging extract. The library had primary titre of approx. 1x10⁶ clones from the primary library were randomly selected for single pass sequencing."

ORIGIN

Query Match 2.9%; Score 53; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1513 GAAAAGTGAGACGACGACAGTGCTGCTGATATCCAGCACTTAGG 1555
Db 1 GAAAAGTGAGACGACGACAGTGCTGCTGATATCCAGCACTTAGG 53

RESULT 63
LOCUS A1627970 300 bp mRNA linear EST 23-APR-1999
DEFINITION cy83d05.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2285673 3'
ACCESSION A1627970
VERSION A1627970.1 GI:4664770
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 300)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNU at: www-bio.llnl.gov/bdip/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source

Location/Qualifiers
1. 300
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2285673"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonides 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 2.9%; Score 53; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 CTTTGGCTGGGGCACTCGCTTCCAGACCTCAACAGGACTCGGACACG 104
DB 300 CTTTGGCTGGGGCACTCGCTTCCAGACCTCAACAGGACTCGGACACG 248

RESULT 64
R83736 377 bp mRNA linear EST 04-AUG-1995
LOCUS R83736
DEFINITION YP15H1.r1 Soares breast 3NBH8c Homo sapiens cDNA clone
IMAGE:187557 5', mRNA sequence.
R83736.1 GI:928613

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 377)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Treveski, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
JOURNAL
COMMENT
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 322
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 322.
Location/Qualifiers

1. 377
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="GDB:3818453"
/db_xref="taxon:9606"
/clone="IMAGE:187557"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"

ORIGIN

Query Match 2.7%; Score 50; DB 14; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTATTGAGATCATGACGTTTAGAGAGAGGCTGCTTCAACAA 373
DB 314 GTGCTATTGAGATCATGACGTTTAGAGAGAGGCTGCTTCAACAA 265

/clone_lib="Soares breast 3NBH8c"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - 0190 (dt) primer [5' TGTTACCAATCTGAAGTGGAGAGGGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo."

RESULT 65
LOCUS BM089787
DEFINITION 503634 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM089787
VERSION BM089787.1 GI:17000415
KEYWORDS
SOURCE
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
1 (bases 1 to 466)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chicko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPJ
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -minmatch 12 options.

PCR primers
FORWARD: ACGAAGACATGACCAT
BACKWARD: GTTTTCCAGTACGACG
Plate: 5 row: B column: 17
Seq primer: ATTATGGACATGATAG.

FEATURES
source

1. 466
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semilendous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN

Query Match 2.7%; Score 49; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 465
|||||
DB 397 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 445
|||||

RESULT 66
BM254410 472 bp mRNA linear EST 17-DEC-2001
LOCUS BM254410
DEFINITION 515632 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM254410
VERSION BM254410.1 GI:17890009
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 472)
Smith, R.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Cassas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pette, G., Holt, I., Karanycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED 11802913
1182978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACGCTATGACCAT
BACKWARD: GTTTCCTGCTGACGACG
Plate: 112 row: B column: 9
Seq primer: ATTGAGTGACACTATAG.
Location/Qualifiers
1. 472
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN
Query Match 2.7%; Score 49; DB 12; Length 472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 465
|||||
DB 403 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 451
|||||

RESULT 67
AA847569 467 bp mRNA linear EST 07-APR-1998
LOCUS AA847569/c
DEFINITION oea9a04.s1 NCI_CGAP_lus Homo sapiens cDNA clone IMAGE:1414926

similar to contains Alu repetitive element/contains element MER8
repetitive element/, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Bennett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL ac:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 1183 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 456.
Location/Qualifiers
1. 467
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1414926"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP lus"
/note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTZ19 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 2.3%; Score 43; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1002 ACACTGACATTCCTGAGCTAGTCCAGCTAGTACACCAAT 1044
|||||
DB 460 ACACTGACATTCCTGAGCTAGTCCAGCTAGTACACCAAT 418
|||||

RESULT 68
AA744439 79 bp mRNA linear EST 23-JAN-1998
LOCUS AA744439/c
DEFINITION ny59e10.s1 NCI CGAP P18 Homo sapiens cDNA clone IMAGE:1276074
similar to contains Alu repetitive element/contains element MER22
repetitive element/, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Bennett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL ac:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 1183 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 456.
Location/Qualifiers
1. 467
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1414926"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP lus"
/note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTZ19 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cga9bbs-remail.nih.gov
Tissue Procurement: Paul H. Durray, M.D., Rodrigo F. Chuagui, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/URL at:
www.bio.lnlnl.gov/bbrp/image/image.html
Insert length: 361 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 62.
Location/Qualifiers

FEATURES

source

1. 79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="1276074"
/sex="male"
/tissue_type="stroma"
/lab_host="DH10B"
/clone_lib="NCI-CCAP_Pri18"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
prostate BPH, stroma, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN

Query Match 2.3%; Score 42; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566

DB 75 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 34

RESULT 69

BX482424/C

LOCUS BX482424 449 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP686L16230.1 666 (synonym: hicc3) Homo sapiens CDNA clone
ACCESSION DKFZP686L16230.5, mRNA sequence.
VERSION BX482424
KEYWORDS BX482424.1 GI:31942305
SOURCE EST.
ORGANISM Homo sapiens (human)

Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 449)

Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amlid, C., Osanger, A.,
Fob, G., Han, M., and Wiemann, S.

EST (Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amlid, C., et al.)

Unpublished (2003)

Contact: MIPS

Location/Qualifiers

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

Heine-University, Dueseldorf/Germany) within the CDNA sequencing

consortium of the German Genome Project. No sl sequence available.

This clone (DKFZ686L16230) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.

Location/Qualifiers

1. 449

COMMENT

/clone="DKFZP686L16230"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B;
CDNA-collection"

ORIGIN

Query Match 2.3%; Score 42; DB 13; Length 449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566

DB 366 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 325

RESULT 70

AV755170

LOCUS AV755170 TP Homo sapiens CDNA clone TPGACCO8 5', mRNA sequence.

DEFINITION AV755170

ACCESSION AV755170.1 GI:10913018

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 280)

Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,

Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, J., Xu, S.,

Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Ye, M.,

Zhang, Q., Han, Z., Chen, Z., and Chen, J.

Homo sapiens TP library CDNA clones

Unpublished (2000)

Contact: Qinghua Zhang

Shanghai Institute of Endocrinology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Tel: 86-21-64370045 (ex.663332)

Fax: 86-21-64743206

Email: mshl@ms.sh.cn

This clone is available at Shanghai Hematology Institute in

Shanghai.

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

Location/Qualifiers

1. 280

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TPGACCO8"

/tissue_type="pituitary tumor"

/dev_stage="Adult"

/lab_host="BM25.8"

/clone_lib="TP"

/note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN

Query Match 2.3%; Score 40; DB 9; Length 280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCGACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 81 AGACCGACAGTGGCTCACACCTGTATCCAGCACTT 120

RESULT 71

BG388112/C

LOCUS BG388112 295 bp mRNA linear EST 12-MAR-2001

DEFINITION 602413075F1 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:4521594 5',

mRNA sequence.

ACCESSION BG388112

VERSION BG388112.1 GI:13281558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
1 (bases 1 to 285)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L14M10421 row: e column: 19
High quality sequence scdp: 293.
Location/Qualifiers
1..295
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4521594"
/issue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

ORIGIN
Query Match 2.2%; Score 40; DB 12; Length 295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
83 AGACGAGCAGAGTGGCTCACACCTGTATCCAGCACTT 44

RESULT 72 441 bp mRNA linear EST 15-DEC-1999
LOCUS AI623152
DEFINITION t189d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258209 3'
similar to SW-BS19_HUMAN P39019 40S RIBOSOMAL PROTEIN S19.
; contains element MER22 repetitive element; mRNA sequence.
ACCESSION AI623152 GI:4648077
VERSION AI623152
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (bases 1 to 441)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

FEATURES
source
www-bio.llnl.gov/bdrc/image/image.html
Insert Length: 1710 Std Error: 0.00
Seq primer: -40UP from Gibco
POLYA=No.
Location/Qualifiers
1..441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2258209"
/issue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 Kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 2.2%; Score 40; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
289 AGACGAGCAGAGTGGCTCACACCTGTATCCAGCACTT 250

RESULT 73 591 bp DNA linear GSS 04-MAY-1999
LOCUS AQ285508
DEFINITION RGC111-77N18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-77N18,
genomic survey sequence.
ACCESSION AQ285508
VERSION AQ285508.1 GI:3911748
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Sub, E., Wible, C., de Jong, P. and Venter, J.C.
1 (bases 1 to 591)
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Other GSSs: RPCI11-77N18.TJ
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..591
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7529513"
/db_xref="taxon:9606"
/clone="RPCI-11-77N18"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1ib="RPCI-11"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

RC111 Human Male BAC Library"

Query Match 2.1%; Score 40; DB 26; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 352 AGACGAGCAGTGGCTCACACCTGTATCCAGCACTT 391

RESULT 74
BF846262 339 bp mRNA linear EST 16-JAN-2001

LOCUS BF846262
DEFINITION PM1-EN0060-201000-003-c01 EN0060 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF846262
VERSION BF846262.1 GI:12233412
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 339)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-EN0060-
201000-003-c01&t3=2000-10-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 339.
Location/Qualifiers
1..339

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_idb="EN0060"
/note="Organ: lung normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESMS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 1563
DB 185 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 223

RESULT 75
BG984390 423 bp mRNA linear EST 12-JUN-2001
LOCUS CM0-CN0159-260301-803-h07 CN0159 Homo sapiens cDNA, mRNA sequence.
DEFINITION BG984390
VERSION BG984390.1 GI:14387125
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 423)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-CN0159-
260301-803-h07&t3=2001-03-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 422.
Location/Qualifiers
1..423

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_idb="CN0159"
/note="Organ: colon normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESMS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 2.1%; Score 39; DB 12; Length 423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGCAGTGGCTCACACCTGTATCCAGCACT 1560
DB 340 AGACGAGCAGTGGCTCACACCTGTATCCAGCACT 378

RESULT 76
BE298406 485 bp mRNA linear EST 20-JUL-2000
LOCUS BE298406
DEFINITION 601117988F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028076 5',
mRNA sequence.
ACCESSION BE298406
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 485)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at: image.llnl.gov
Plate: L10W85 row: 0 column: 21
High quality sequence stop: 480.

FEATURES
source
Location/Qualifiers
1..485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3028076"
/issue_type="rhadowysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_1"
/note="Organ: muscle; Vector: pOTB7; Site: 1: EcoRI;
Site 2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 2.1%; Score 39; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCACCACTTAGGA 1566
DB 399 GGCACAGTGGCTCACACCTGTATCCACCACTTAGGA 437

RESULT 77
LOCUS AQ181916 493 bp DNA linear GSS 28-OCT-1998
DEFINITION HS_3230_A1_B02_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3230 Col=3 Row=C, genomic survey
sequence.
ACCESSION AQ181916
VERSION AQ181916.1 GI:3579283
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 493)
TITLE Mahitras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holman, T.,
Keller, A., Shaker, R., Fulton, S., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE 10449764
COMMENT Contact: Mahitras G.G., Wallace J.C., Hood L.
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618

FEATURES
source
Location/Qualifiers
1..493
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3230 Col=3 Row=C"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: colon; Vector: pBE10Acl1; BAC clones in
E-Coli DH10B"

ORIGIN
Query Match 2.1%; Score 39; DB 28; Length 493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GACACGACAGTGGCTCACACCTGTATCCACCACTT 1561
DB 340 GACACGACAGTGGCTCACACCTGTATCCACCACTT 302

RESULT 78
LOCUS BF754368 495 bp mRNA linear EST 10-JAN-2001
DEFINITION IIS-CT0519-091000-171-a06 CT0519 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF754368
VERSION BF754368.1 GI:12080953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 495)
TITLE Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202863
MEDLINE 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IIS&t2=IIS-CT0519-
091000-171-a06&t3=2000-10-09&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 387.

FEATURES
source
Location/Qualifiers
1..495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="CT0519"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived

from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 248 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 286

RESULT 79
LOCUS BF676525 607 bp mRNA linear EST 21-DEC-2000
DEFINITION 602084432F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248823 5',
RNA sequence.
ACCESSION BF676525
VERSION BF676525.1 GI:11950420
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 607)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1067 row: P column: 08
High quality sequence stop: 600.
Location/Qualifiers

1. 607
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248823"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDMR-LTB (Clontech); Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggcgctatcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATCTTAGAGCGCCGCGCCGACAGG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

FEATURES
Source

1. 607
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248823"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDMR-LTB (Clontech); Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggcgctatcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATCTTAGAGCGCCGCGCCGACAGG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 328 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 366

RESULT 80
LOCUS BG249266/c 635 bp mRNA linear EST 13-FEB-2001
DEFINITION 602361519F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4469764 5',
RNA sequence.
ACCESSION BG249266
VERSION BG249266.1 GI:12759082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 635)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10286 row: F column: 05
High quality sequence stop: 623.
Location/Qualifiers

FEATURES
Source

1. 635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4469764"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 2.1%; Score 39; DB 12; Length 635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 257 GACCAGGACAGTGGCTCACACCTGTATCCGACACTT 219

RESULT 81
LOCUS AL045232 489 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp434H0750.r1 434 (synonym: htes3) Homo sapiens cDNA clone
IMAGE:4469764 5', RNA sequence.
ACCESSION AL045232
VERSION AL045232.1 GI:5433394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 489)
AUTHORS Poustka, A., Klein, M., Mewes, H. W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Poustka, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No 51 sequence available.
This clone (DKFZ434H0750) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ434H0750"
/issue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="434 (synonym: hres3)"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 2.1%; Score 38; DB 9; Length 489;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1524 ACCAGGACAGTGGCTCACACCTGTATATCCACGACTT 1561
|||||
DB 270 ACCAGGACAGTGGCTCACACCTGTATATCCACGACTT 307
|||||

RESULT 82
LOCUS AM130036 511 bp mRNA linear EST 27-OCT-1999
DEFINITION x127b09.x1 NCI_CGAP Utl Homo sapiens cDNA clone IMAGE:2619257 3'
similar to contains Alu repetitive element, mRNA sequence.
ACCESSION AM130036
VERSION AM130036.1 GI:6131641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 511)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at:
www.bio.lnlnl.gov/bbir/image/image.html
Seq primer: -40up from Gibco
High quality sequence stop: 419.
Location/Qualifiers
1..511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2619257"
/issue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_11b="NCI_CGAP_Utl1"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

FEATURES

source
1..511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2619257"
/issue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_11b="NCI_CGAP_Utl1"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN
Query Match 2.1%; Score 38; DB 10; Length 511;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1524 ACCAGGACAGTGGCTCACACCTGTATATCCACGACTT 1561
|||||
DB 473 ACCAGGACAGTGGCTCACACCTGTATATCCACGACTT 436
|||||

RESULT 83
LOCUS AQ471606 624 bp DNA linear GSS 23-APR-1999
DEFINITION CITBI-E1-2590G17.TF CITBI-E1 Homo sapiens genomic clone 2590G17, genomic survey sequence.
ACCESSION AQ471606
VERSION AQ471606.1 GI:4655260
KEYWORDS GSS.

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 624)
Zhao,S., Adams,M.D., Nieman,W., Malek,J., Shizuya,H., Simon,W. and Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
Unpublished (1997)
Other GSSes: CITBI-E1-2590G17.TR
Contact: Shaying Zhao, William Nieman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@igf.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

source
1..624
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2590G17"
/sex="male"
/cell_type="sperm"
/clone_11b="CITBI-E1"
/note="Vector: pBelOAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"

ORIGIN

Query Match 2.1%; Score 38; DB 28; Length 624;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGGACAGTGGCTCACACCTGTATATCCACGACA 1558
|||||
DB 582 GAGACCGGACAGTGGCTCACACCTGTATATCCACGACA 619
|||||

RESULT 84
LOCUS AQ532906 138 bp DNA linear GSS 18-MAY-1999
DEFINITION RPCI-11-354U6.TU RPCI-11 Homo sapiens genomic clone RPCI-11-354U6, genomic survey sequence.
ACCESSION AQ532906
VERSION AQ532906.1 GI:4844596
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 138)
 AUTHORS Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and
 Venter, J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@igf.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet. cs (http://resgen.com). BAC end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..138
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7635773"
 /db_xref="taxon:9606"
 /clone="RPCI-11-354J6"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_1ib="RPCI-11"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"

ORIGIN
 Query Match 2.0%; Score 37; DB 28; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACACTT 1561
 |||||
 10 CCAGGACAGTGGCTCACACCTGTATCCAGACACTT 46

Db

RESULT 85
 CA947091/c 154 bp mRNA linear EST 31-DEC-2002
 Is11b04.Y1 HR85 islet Homo sapiens cDNA IMAGE:6364374 5',
 mRNA sequence.
 CA947091
 CA947091.1 GI:27439968
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 154)
 Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Maizumi, B., Rutter, E., Ronko, I., Bennett, J.,
 Schmitt, A., Theising, B., Rutter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsegateishvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: Is11b04.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@lhp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoe@im.wustl.edu)
 Seq primer: -40UP from Gibco.

FEATURES
 source
 1..154
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6364374"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_1ib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permut Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoe@im.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN
 Query Match 2.0%; Score 37; DB 14; Length 154;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACACTT 1561
 |||||
 63 CCAGGACAGTGGCTCACACCTGTATCCAGACACTT 27

Db

RESULT 86
 BF858536 173 bp mRNA linear EST 16-JAN-2001
 RCI-FT0190-221100-021-h08 FT0190 Homo sapiens cDNA, mRNA sequence.
 BF858536
 BF858536.1 GI:12246280
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 173)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunschein, A., Oliveira, P.S., Bucher, P., Jorgensen, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202863
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: aelms@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?PL=RC1&t2=RC1-FT0190-
 221100-021-h08&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 173.
Location/Qualifiers

FEATURES

source

```
1..173
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/def_stage="Adult"
/clone_lib="FT0190"
/clone="Organ: prostate tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
```

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 1561
|||||
DB 68 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 104

RESULT 97
BE061853 198 bp mRNA linear EST 09-JUN-2000
LOCUS RCI-BT0254-290100-015-cl2 BT0254 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE061853
ACCESSION BE061853
VERSION BE061853.1 GI:8406503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 198)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zagor, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.U. and
Simpson, A.U.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
CONTACT: Simpson A.U.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704932
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-RCI-BT0254-290
100-015-cl2&ct=2000-01-29&f4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 198.
Location/Qualifiers

FEATURES

source

```
1..198
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/def_stage="Adult"
/clone_lib="BT0254"
```

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 1561
|||||
DB 93 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 129

RESULT 88
BX476932 200 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686B17190.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686B17190.5, mRNA sequence.
ACCESSION BX476932
VERSION BX476932.1 GI:31674181
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 200)
Bahar, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Bahar, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 3' sequence available.
This clone (DKFZp686B17190) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source

```
1..200
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686B17190"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTritp18x2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"
```

ORIGIN

Query Match 2.0%; Score 37; DB 13; Length 200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 1561
|||||
DB 183 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 147

RESULT 89
T02927 204 bp mRNA linear EST 14-FEB-1997
LOCUS FB1688 Fetal brain, Striatagene Homo sapiens cDNA clone FB1688
DEFINITION

3'end, mRNA sequence.
 ACCESSION T02927
 VERSION T02927.1 GI:314168
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 204)
 AUTHORS Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikelis, J.M.
 TITLE Single pass sequencing and physical and genetic mapping of human CDNBs
 JOURNAL Nat. Genet. 2, 180-185 (1992)
 MEDLINE 94258200
 PUBMED 1345165
 COMMENT On Sep 21, 1992 this sequence version replaced gi:279067.
 Contact: Sikelis JM
 Department of Pharmacology
 University of Colorado Health Sciences Center
 Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
 Tel: 3032708637
 Fax: 3032707097
 Email: nikki@ccah.ucshc.edu
 Seq primer: -21m3 Universal.
 Location/Qualifiers
 1..204
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ARCC (inhost):86573"
 /db_xref="GDB:D0S2697E"
 /db_xref="taxon:9606"
 /clone="FB16B8"
 /clone_lib="Fetal brain, Stragene"
 /note="Vector: Lambda ZAP II; The FB library (catalog #937201, Stragene) was constructed by directional cloning and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
 ORIGIN
 Query Match 2.0%; Score 37; DB 14; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1525 CCAGGCACAGTGGCTCACCCTGTATCCAGACCTT 1561
 DB 92 CCAGGCACAGTGGCTCACCCTGTATCCAGACCTT 128
 RESULT 90
 AM891716 215 bp mRNA linear EST 24-MAY-2000
 LOCUS CM3-NT0090-040500-171-g08 NT0090 Homo sapiens CDNA, mRNA sequence.
 DEFINITION AM891716
 ACCESSION AM891716
 VERSION AM891716.1 GI:8056025
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 215)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ct2=CM3-NT0090-040500-171-g08&ts=2000-05-04&ta=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 172.
 Location/Qualifiers
 1..215
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0090"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from GRESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
 Query Match 2.0%; Score 37; DB 10; Length 215;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1525 CCAGGCACAGTGGCTCACCCTGTATCCAGACCTT 1561
 DB 79 CCAGGCACAGTGGCTCACCCTGTATCCAGACCTT 115
 RESULT 91
 BF798259 220 bp mRNA linear EST 12-JAN-2001
 LOCUS RC3-C10043-021000-012-a05 C10043 Homo sapiens CDNA, mRNA sequence.
 DEFINITION BF798259
 ACCESSION BF798259
 VERSION BF798259.1 GI:12127248
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 220)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&ts=RC3-C10043-021000-012-a05&ta=2000-10-02&ta=1)

Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 220.
Location/Qualifiers
1..220

FEATURES
source
1..220
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="CI0043"
/dev_stage="Adult"

ORIGIN
Query Match 2.0%; Score 37; DB 10; Length 220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1535 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 1561
145 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 181
/note="Organ: colon ins; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

RESULT 92
BE011851/c 226 bp mRNA linear EST 05-JUN-2000
LOCUS BE011851
DEFINITION RCO-BN0230-100500-031-a05 BN0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE011851
VERSION BE011851.1 GI:8272084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-RCO-BN0230-100
500-031-a05&t3=2000-05-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 226.
Location/Qualifiers
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0230"

FEATURES
source

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 2.0%; Score 37; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 1561
110 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTT 74

RESULT 93
AA382050 233 bp mRNA linear EST 21-APR-1997
LOCUS AA382050
DEFINITION EST95255 Activated T-cells I Homo sapiens cDNA 5' end similar to
EST containing Alu repeat.
ACCESSION AA382050
VERSION AA382050.1 GI:2034421
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 233)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Sutton, G., Blake, J.A., Brannon, R.C., Man, W.-C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fritch, W.M., Fritchman, J.L., Geoghegan, N.S.,
Glock, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., Jr.,
Kelleys, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonnell, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utebbeck, T.R., Weidman, J.F., Li, Y.,
Rednair, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dincke, D., Feng, D.F., Ferris, A., Fischer, C., Hastings, G.A.,
He, M.W., Hu, J.S., Greene, J.W., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
96026280
7566098

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/db/hgi/hgi.html)
Seq primer: M13 Reverse
Location/Qualifiers
1..233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):186485"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/clone_lib="Activated T-cells I"

FEATURES
source

ORIGIN

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

Query Match 2.0%; Score 37; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 95 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 131

RESULT 94
BF747366 258 bp mRNA linear EST 10-JAN-2001
LOCUS RC3-BT0333-281100-122-c08 BT0333 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF747366
ACCESSION BF747366 GI:12074042
VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shogun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE PUBLISHED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0333-281100-122-c08&t3=2000-11-28&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 258.

Location/Qualifiers

1. 258

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BT0333"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 40 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 76

RESULT 95
BF746653 260 bp mRNA linear EST 10-JAN-2001
LOCUS RC3-BT0333-111100-121-b10 BT0333 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF746653
ACCESSION BF746653 GI:12073329

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shogun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE PUBLISHED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0333-111100-121-b10&t3=2000-11-11&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 260.

Location/Qualifiers

1. 260

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BT0333"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 42 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 78

RESULT 96

R00543 266 bp mRNA linear EST 31-MAR-1995
LOCUS yf78a07.s1 Soares fetal liver spleen INPIS Homo sapiens cDNA clone IMAGE:123828 3' similar to contains Alu repetitive element; contains MER20 repetitive element; mRNA sequence.

ACCESSION R00543
VERSION R00543.1 GI:750279

KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J., Ralfkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 1314
 High quality sequence stops: 249 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: polyT not found
 Insert Length: 1314 Std Error: 0.00
 Seq primer: -21ml3
 High quality sequence stop: 249.
 Location/Qualifiers
 1..266
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:476373"
 /db_xref="taxon:9606"
 /clone="IMAGE:123828"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFUS"
 /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGCAAGATTAAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 2.0%; Score 37; DB 14; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 39 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 3

RESULT 97
 LOCUS AW798708 267 bp mRNA linear EST 16-MAY-2000
 DEFINITION RC2-UM0050-170300-016-d03 UM0050 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW798708
 VERSION AW798708.1 GI:7850578
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 267)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

TITLE O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=6&2=RC2-UM0050-170300-016-d09&3=2000-03-17&4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 267.
 Location/Qualifiers
 1..267
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="UM0050"
 /note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 2.0%; Score 37; DB 10; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 191 CCAGGCAAGTGGCTCACACCTGTATCCAGCACTT 155

RESULT 98
 LOCUS AW803362 267 bp mRNA linear EST 16-MAY-2000
 DEFINITION IL2-UM0079-090300-050-C10 UM0079 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW803362
 VERSION AW803362.1 GI:7855232
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 267)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-1l2-UM0079-0930>)
 300-050-Cl06r3=2000-03-09&f4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 11
 High quality sequence stop: 212.
 Location/Qualifiers
 1..267
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="UM0079"
 /note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716- Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 267;
 Best Local Similarity 100.0%; Pred.No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 1561
 |||||
 Db 174 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 210

RESULT 99 269 bp mRNA linear EST 16-AUG-1995
 H30560/c
 LOCUS
 DEFINITION YP45603.s1 Soares retina N2D4HR Homo sapiens cDNA clone IMAGE:190373 3' similar to contains Alu repetitive element; mRNA sequence.
 ACCESSION H30560 GI:901470
 VERSION H30560.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 269)
 Hillier,L., Clark,N., Dubuque,T., Ellston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
 The Washu-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 2355
 High quality sequence stops: 212
 Source: IMAGE Consortium, LML
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2355 Std Error: 0.00
 Seq primer: Promega -21m13
 High quality sequence stop: 212.
 Location/Qualifiers

TITLE
 JOURNAL
 COMMENT

FEATURES

Location/Qualifiers

source

1..269
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="GDB:3846782"
 /db_xref="taxon:9606"
 /clone="IMAGE:190373"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 Year old"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares retina N2D4HR"
 /note="Organ: eye; Vector: p777D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 2.0%; Score 37; DB 14; Length 269;
 Best Local Similarity 100.0%; Pred.No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 1561
 |||||
 Db 84 CCAGGACAGTGGCTCACACCTGTATCCAGACTT 48

RESULT 100 279 bp mRNA linear EST 14-JUN-1999
 A1735064/c
 LOCUS
 DEFINITION A68802.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335778 3' similar to contains Alu repetitive element; contains element PTR7 repetitive element; mRNA sequence.
 ACCESSION A1735064 GI:5056663
 VERSION A1735064.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 279)
 Hillier,L., Allan,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Matra,M., Martin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
 Washu-NCI human EST Project
 Unpublished (1997)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from GIDCO.
 Location/Qualifiers

FEATURES

1..279
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2335778"
 /sex="male"
 /dev_stage="adult, age 25"
 /lab_host="DH10B (page resistant)"

/clone.lib="Barslead colon HPLB37"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACGAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 [5' ATTCACTAGTAAT 3' and 5' ATTCTAGTC 3'], digested
 with Not I and cloned into the Not I and Eco RI sites of
 the modified pT73 vector. Library constructed by Bob
 Barslead."

ORIGIN

Query Match 2.0%; Score 37; DB 9; Length 279;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTTCACACTGTATCCAGCACTT 1561
 Db 118 CCAGGCACAGTGGCTTCACACTGTATCCAGCACTT 82

Search completed: April 18, 2004, 00:54:17
 Job time : 5072 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 / Search time 46 Seconds
(without alignments)

2805.368 Million cell updates/sec

Title: US-10-063-523-22

Sequence: 1 MEGESTSAVLGSGFLGALAF.....TDEIEKKMGFGEGYSRPTF 409

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteria.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545	73.3	300	4 Q9H811	Q9H811 homo sapien
2	1541	73.1	300	4 Q9H8N4	Q9H8N4 homo sapien
3	1509	71.6	407	11 Q8BPR28	Q8BPR28 mus musculu
4	1007	47.7	298	11 Q8K2T7	Q8K2T7 mus musculu
5	999	47.4	261	11 Q8BFW6	Q8BFW6 mus musculu
6	832	39.4	212	11 Q8BT69	Q8BT69 mus musculu
7	535	25.4	419	4 Q15018	Q15018 homo sapien
8	287	13.6	311	4 Q96H11	Q96H11 homo sapien
9	282.5	13.4	311	11 Q8K0R4	Q8K0R4 mus musculu
10	160.5	7.6	313	10 Q8RY09	Q8RY09 arabidopsis
11	153.5	7.3	378	10 Q8CY92	Q8CY92 arabidopsis
12	134	6.4	537	13 Q7ZVLO	Q7ZVLO brachydanio
13	134	6.4	1338	13 Q7SZLS	Q7SZLS xenopus lae
14	132	6.3	1738	5 Q76329	Q76329 dictyostell
15	132	6.3	4405	5 Q81LZ2	Q81LZ2 plasmodium
16	131	6.2	1931	5 Q9NCF9	Q9NCF9 drosophila

17	130	6.2	1931	5 Q9VKH9	Q9VKH9 drosophila
18	129	6.1	440	11 Q80Z99	Q80Z99 rattus norv
19	128.5	6.1	455	11 Q8C4F6	Q8C4F6 mus musculu
20	128.5	6.1	631	11 Q8K2Q9	Q8K2Q9 mus musculu
21	127.5	6.0	720	4 Q81UD4	Q81UD4 homo sapien
22	127.5	6.0	992	4 Q81UD5	Q81UD5 homo sapien
23	127.5	6.0	1003	4 Q9UP51	Q9UP51 homo sapien
24	127.5	6.0	1088	4 Q81UD3	Q81UD3 homo sapien
25	127.5	6.0	1116	4 Q81UD2	Q81UD2 homo sapien
26	126.5	6.0	600	5 Q01530	Q01530 trypanosoma
27	126	6.0	742	5 Q813B2	Q813B2 plasmodium
28	126	6.0	747	10 Q94GH4	Q94GH4 oryza sativ
29	125.5	6.0	877	16 Q8ESR2	Q8ESR2 streptococ
30	125.5	6.0	948	11 Q8CIY9	Q8CIY9 rattus norv
31	125.5	6.0	948	11 Q81IU3	Q81IU3 rattus norv
32	125.5	6.0	976	11 Q99MI2	Q99MI2 mus musculu
33	125.5	6.0	1120	11 Q99MI1	Q99MI1 mus musculu
34	125.5	6.0	1288	5 Q8IKY1	Q8IKY1 plasmodium
35	125	5.9	436	4 Q8WTF9	Q8WTF9 homo sapien
36	125	5.9	1245	4 Q9UID2	Q9UID2 homo sapien
37	124.5	5.9	948	4 Q9UIK7	Q9UIK7 homo sapien
38	124.5	5.9	1030	13 Q80ZR8	Q80ZR8 fugu rubrip
39	123.5	5.9	825	3 Q03088	Q03088 saccharomyc
40	123.5	5.9	1185	16 Q8XJP0	Q8XJP0 clostridium
41	123	5.8	446	4 Q9HCH4	Q9HCH4 homo sapien
42	123	5.8	505	4 Q8N3S2	Q8N3S2 homo sapien
43	123	5.8	718	4 Q86T52	Q86T52 homo sapien
44	123	5.8	4524	5 Q813J9	Q813J9 plasmodium
45	122.5	5.8	957	11 Q8K3M6	Q8K3M6 rattus norv

ALIGNMENTS

RESULT 1					
Q9H811	PRELIMINARY;	PRT;	300 AA.		
AC Q9H811;					
DT 01-MAR-2001 (TRENBERL 16, Created)					
DT 01-MAR-2001 (TRENBERL 16, Last sequence update)					
DT 01-MAR-2003 (TRENBERL 23, Last annotation update)					
DE Hypothetical protein FLJ13614.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
NCBI_TaxId=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Placenta;					
RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,					
RA Nishikawa T., Nagai K., Sato H., Sugano S., Ishihashi T., Fujimori K.,					
RA Tanei H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,					
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,					
RA Masuno Y., Kanehori K.;					
RT "NEBO human cDNA sequencing project.";					
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Testis;					
RA Straube R.;					
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AK03676; BAB14635.1; -					
DR EMBL; BC039573; BAB14635.1; -					
KV Hypothetical protein.					
SQ SEQUENCE 300 AA; 34447 MW; A22EF29B4B0FCFAF CRC64;					
Query Match	73.3%	Score 1545;	DB 4;	Length 300;	
Best local similarity	99.7%	Pred. No. 7.5e-53;			
Matches 299;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 110 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSSGTHRLHSLVYPQKGLFRRVPLVVA 169					
DB 1 MTFERLLHKNLQEHFNSQDLVFLLLTPSIITSSGTHRLHSLVYPQKGLFRRVPLVVA 60					

QY 170 NLGMSBQLGKTVSGSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI 229
 DB 61 NLGMSBQLGKTVSGSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI 120
 QY 230 CKKVEDEQAQVLDVAVNRLKREIEKRRGAQIOAREKNIQKDPENIFLCOALRTFFP 289
 DB 121 CKKVEDEQAQVLDVAVNRLKREIEKRRGAQIOAREKNIQKDPENIFLCOALRTFFP 180
 QY 290 NSEFLHSCVMSLKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL 349
 DB 181 NSEFLHSCVMSLKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL 240
 QY 350 DLDNRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSPEDEIEKXKGFGEYSRSPTF 409
 DB 241 DLDNRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSPEDEIEKXKGFGEYSRSPTF 300

RESULT 2

Q9H9N4 PRELIMINARY; PRT; 300 AA.
 AC Q9H9N4;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ12642.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Magatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Makamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
 RA Ninomiya K., Iwayanagi T.,
 RT "NEDO human cDNA sequencing project."
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AK022704; BAB14189.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 300 AA; 34477 MW; BE42829B4B1ADFF CRC64;

Query Match 73.1%; Score 1541; DB 4; Length 300;
 Best Local Similarity 99.3%; Pred. No. 1.4e-92;
 Matches 298; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 110 MFERRLHKNLQEHFNSODLVFLLLPSITTESCSTRLEHSLYKPKQGLFHRVPLVVA 169
 DB 1 MFERRLHKNLQEHFNSODLVFLLLPSITTESCSTRLEHSLYKPKQGLFHRVPLVVA 60
 QY 170 NLGMSBQLGKTVSGSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI 229
 DB 61 NLGMSBQLGKTVSGSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI 120
 QY 230 CKKVEDEQAQVLDVAVNRLKREIEKRRGAQIOAREKNIQKDPENIFLCOALRTFFP 289
 DB 121 CKKVEDEQAQVLDVAVNRLKREIEKRRGAQIOAREKNIQKDPENIFLCOALRTFFP 180
 QY 290 NSEFLHSCVMSLKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL 349
 DB 181 NSEFLHSCVMSLKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL 240
 QY 350 DLDNRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSPEDEIEKXKGFGEYSRSPTF 409
 DB 241 DLDNRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSPEDEIEKXKGFGEYSRSPTF 300

RESULT 3
 Q8BP28 PRELIMINARY; PRT; 407 AA.

AC Q8BP28;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN 3830405G04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Eye;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK051816; BAC34780.1; -
 DR MGI; MGI:191931; 3830405G04RIK.
 KW Hypothetical protein.
 SQ SEQUENCE 407 AA; 46039 MW; FB8B05A197A2BC64 CRC64;

Query Match 71.6%; Score 1509; DB 11; Length 407;
 Best Local Similarity 71.2%; Pred. No. 2.4e-90;
 Matches 297; Conservative 42; Mismatches 60; Indels 18; Gaps 3;

QY 1 MEGSSTAVISGTYLALAFQHLNTSDTREGFLGVEYKGAHKSITDSQMDVYVYTTID 60
 DB 1 MEGSSTAVISGTYLALAFQHLNTSDTREGFLGVEYKGAHKSITDSQMDVYVYTTID 60
 QY 10KTIPTCYOLFSPFNSGVEYNEOALKKILSNVKNVGVWYKFRHSDDQMTFERRLHKN 120
 DB 61 10KTIPTCYOLFSPFNSGVEYNEOALKKILSNVKNVGVWYKFRHSDDQMTFERRLHKN 120
 QY 121 LOEHFNSODLVFLLLPSITTESCSTRLEHSLYKPKQGLFHRVPLVVA NLGMSBQLGK 180
 DB 121 LOEHFNSODLVFLLLPSITTESCSTRLEHSLYKPKQGLFHRVPLVVA NLGMSBQLGK 180
 QY 181 TVSSSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI CKKVEDEQAQ 240
 DB 181 TVSSSCMSTGFSRAVQTHSSKFFEDDSLKVEHKINEMVYASLOEBLSKI CKKVEDEQAQ 240
 QY 241 DKLVDVNRRLKREIEKRRGAQIOAREKNIQKDPENIFLCOALRTFFP NSEFLHSCVMS 300
 DB 241 EKLMDVNRK-EVRRFQOARATGAGKQVGRNPOENIILCOALRTFFP NSEFLHSCVMS 299
 QY 301 LKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL DLDNRWQFKRS 360
 DB 301 LKNRHVSCKSCNHNHLDVNDLTLMEHTDIPASPASTPQIIKHKL DLDNRWQFKRS 360
 QY 361 RLDTODKRSKANTGSSNQDKAS-----KNSSPEDEIEKXKGFGEYSRSPTF 409
 DB 360 RLDTODKRSKANTGSSNQDKAS-----KNSSPEDEIEKXKGFGEYSRSPTF 407

RESULT 4

Q8K2T7 PRELIMINARY; PRT; 298 AA.
 AC Q8K2T7;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein FLJ13614.
 GN 3830405G04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;

RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Tortum M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RL "Arabidopsis cDNA clones."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carriotti P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamaya A., Karlh-Neumann G., Kawai U., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Tortum M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RL "Arabidopsis ORF clones."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY078028; AA049821; -
 DR EMBL: AY078028; AA049821; -
 SQ SEQUENCE 313 AA; 34485 MW; EAACCOBAF692C4A1 CRC64;
 Query Match 7.6%; Score 160.5; DB 10; Length 313;
 Best Local Similarity 20.5%; Pred. No. 0.0096;
 Matches 62; Conservative 60; Mismatches 123; Indels 57; Gaps 8;
 QY 10 LSGFVLGALAFQHLNTDPTGFLGEGVGEAKNSITDSQMDV-----EYVYTI 61
 DB 11 ISGFLTLASLIGRASSPSVDGLIFGQIHRIVSSNLSDDSPADIASSSSSDQIVAT--V 68
 QY 62 QKVIYCYOLFSPYNSGGEVNEQALKILSNVKNVGVKFRHSDQIMTERRLHKNL 121
 DB 69 TSFLSCGKTVSFYDPLGRVDSRRIDSLRVSDPDHLIGMSARKKTNAPSRMELAVTSSL 128
 QY 122 -QEHFSNODL-----VFLTLPSITTESCSTHRLHSILYKPKQGFHRVPLV 168
 DB 129 SSQFHLPIEDLQNPSSMMNASVFFLLTMDQCITHREYRAYQFRSSKORLEPRVGI 188
 QY 169 ANLG-----MSEQLGK-----TVSSGCMSTG---FSRAVQTHSKFEEDGSLKEV 212
 DB 189 VNIGAFRGHYGSFSPKSGFPLPILCELSSNAMSVDCESSLSAKQSKDQKEIDALAE 248
 QY 213 HK-----INEMVASLQBELKSIKCKVEDESEQAVDXLVNDVNRKKEI 254
 DB 249 FQVGELKRLVGAEANVTGIEEMERMLAKIESLASDVEKSSANVPQGEKHNRKLNRV 308
 QY 255 EK 256
 DB 309 AR 310
 RESULT 11
 Q9C9Y2 PRELIMINARY; PRT; 378 AA.
 AC Q9C9Y2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F17014.25.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=1130713;
 RA Salanoudat M., Lemcke K., Rieger W., Anseorge W., Unselid M.,
 RA Fartmann B., Valle G., Bloescher H., Perez-Alonso M., Obermaier B.,
 RA Deleeny M., Boutry M., Grivell L.A., Mache R., Pulgdenesch P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Broctier P.,
 RA Wincker P., Cattoico L., Weisenbach J., Saurin W., Queirer F.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonk H., Erle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Topo S., Sindona B.,
 RA Conrad A., Hornischer K., Kauer G., Loehert T.-H., Nordstiek G.,
 RA Reichelt J., Scharte M., Schoen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenmaier B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Llauró C., Punelle B., Maury D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cortes A., Casacuberta E.,
 RA Monfort A., Argiridou A., Flores M., Liguori R., Vitale D.,
 RA Mammuto G., Haase D., Schoof H., Ruid S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Wals A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pail G., Miltsecher J., Sellers P., Gill J.E., Feildlynn T.V.,
 RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shimo S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana."
 RL Nature 408:820-822(2000).
 RL EMBL: AC012562; AAC51366.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 378 AA; 41859 MW; 6831DD49E44B3B22 CRC64;
 Query Match 7.3%; Score 153.5; DB 10; Length 378;
 Best Local Similarity 21.0%; Pred. No. 0.034;
 Matches 60; Conservative 55; Mismatches 114; Indels 57; Gaps 8;
 QY 10 LSGFVLGALAFQHLNTDPTGFLGEGVGEAKNSITDSQMDV-----EYVYTI 61
 DB 11 ISGFLTLASLIGRASSPSVDGLIFGQIHRIVSSNLSDDSPADIASSSSSDQIVAT--V 68
 QY 62 QKVIYCYOLFSPYNSGGEVNEQALKILSNVKNVGVKFRHSDQIMTERRLHKNL 121
 DB 69 TSFLSCGKTVSFYDPLGRVDSRRIDSLRVSDPDHLIGMSARKKTNAPSRMELAVTSSL 128
 QY 122 -QEHFSNODL-----VFLTLPSITTESCSTHRLHSILYKPKQGFHRVPLV 168
 DB 129 SSQFHLPIEDLQNPSSMMNASVFFLLTMDQCITHREYRAYQFRSSKORLEPRVGI 188
 QY 169 ANLG-----MSEQLGK-----TVSSGCMSTG---FSRAVQTHSKFEEDGSLKEV 212
 DB 189 VNIGAFRGHYGSFSPKSGFPLPILCELSSNAMSVDCESSLSAKQSKDQKEIDALAE 248
 QY 213 HK-----INEMVASLQBELKSIKCKVEDESEQAVDXLVNDVNRKKEI 254
 DB 249 FQVGELKRLVGAEANVTGIEEMERMLAKIESLASDVEKSSANVPQGEKHNRKLNRV 294
 QY 255 EK 256
 DB 294 AR 295
 RESULT 12
 Q7ZVLO PRELIMINARY; PRT; 537 AA.
 AC Q7ZVLO;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to synaptonemal complex protein 1 (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC045503; AA445503.1; -
 FT NON_TER 537

SQL SEQUENCE 537 AA, 62570 MW, 54EB1EB370CED9D CRC64;
Query Match 6.4%; Score 134; DB 13; Length 537;
Best Local Similarity 18.3%; Pred. No. 0.96;
Matches 70; Conservative 76; Mismatches 151; Indels 86; Gaps 14;
QY 72 SFYNSGSEVNEQALKILSNVKNVGMVKKFRHS----- 106
DB 185 NFEFAERETHTDLFMQISENVQRMVAAPFESLKKQAEADQDMKRECLAQFEDIKVQLE 244
QY 107 -----DQIMTFRERLHK-----NLOEHSNODVFLITPSITTESGSTR-L 149
DB 245 SSCQFKEBQVAIFQELQCKENDPKDVSLKQE-----TQHC-----SVLEESSKHQEL 295
QY 150 EHSLYEPQKGLFHRVPLVAVANIGMSEQLGYTVSGS-CMSTGFSRAVQTHSSKFFEEBGS 208
DB 296 LHSATQDRALBEK-----LNVIQQLKWELEENQALTYKLREQMENHEKTLQCKOTE 348
QY 209 LKEVHKINEMVA-----SLOEBLSICKYVESEQAVDKLVAVNLKREIEKR 257
DB 349 IEDLNNTKQORNTQADMLQJLVNSLQSSITSEIQADILEFTLSVNMDSLKAEIIVT 408
QY 258 RGAQIQAAEKKNI-QKD-POENIFLCQALRTFFPNSFLHSCVMSLKRRHVSCKSCNYNH 315
DB 409 KSQNVDHCEQLQILFRKDLDEKSNLSLSIKELKASBTQILKLITSLK-----ETQSEANH 463
QY 316 HLDVYNLTLMWEHTDIPASPASTPQIIRKHALDIDQWQFRRLLDTODKRSKANTG 375
DB 464 LKDTYENIT--TENKSVQ-----TITKRCENENLQSVSLKKAELKAMEHELSGALS 516
QY 376 SSNODKASKSSPPTDEIEIKK 398
DB 517 RCKSKK--KVEKLERDIKQKKK 537
RESULT 13
Q7SZLS PRELIMINARY; PRT; 1338 AA.
AC Q7SZLS;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE TGIS.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohl R., Coughlin W.L., Lane W.S., Mitchison T.J.;
RT "An inner centromere protein that stimulates the activity of a kint
RT kinesin.";
RL Dev. Cell 0:0-0(2003).
DR EMBL; AY352638; AAC22723.1;
SQ SEQUENCE 1338 AA, 147066 MW, 628843528301A2EF CRC64;
Query Match 6.4%; Score 134; DB 13; Length 1338;
Best Local Similarity 22.8%; Pred. No. 2.8; Mismatches 131; Indels 60; Gaps 14;
Matches 74; Conservative 59; Mismatches 131; Indels 60; Gaps 14;
QY 108 QIMTFRERLHKVLOEHSNODVFLITPSITTESGSTRLE-----HSLYEPQKGLFHRV 164
DB 1004 QILNQEETLTKR--RKALSGEL--LNLKGDVLVCASTGERLKEKNELTKVYBGLQKV 1058
QY 165 PLV-VANLGNSEQLGYTVSGS-C-MSTGFSRAVQTHSSKFFP-----E 205
DB 1059 KEHHNLESLBEKTLQFYTGCECKLQSFIEBAEKYKNLEQKVDLNTTHEAVYLOAE 1118
QY 206 DGLKAEHKINEMVAYSLQELKSIKK--VEDS-----EQAVDKLV--KQVNRLLKREI 254
DB 1119 TSGIETITHTKEDYKSLTTLKDAKQENKILDSFKKQAAVEKICILKQVNSBKSK 1178

QY 255 ERKGAQIQAAEKKNIQKDPOENIFLCQALRTFFPNSFLHSCVMSLKRRHVSCKSCNYN 314
DB 1179 LKYEERQKLTREKSVQKNPV-MYDEQLESL-----KAVLEIKNEKHLQDDKLM 1229
QY 315 HLDVYNLTLMWEHTD-IPASPASTPQIIRKHALDIDRWQFRRLLDTQDKRSKAN 373
DB 1230 QVEKLVETMTTLVERLNKQOEDEDKARVNVVAL-----SRQLSTEQEVLRGS 1279
QY 374 TSSNODKASKSSPPTDEIEIKK 397
DB 1280 L--EKESKANKRLSMENBELMKT 1301
RESULT 14
Q76329 PRELIMINARY; PRT; 1738 AA.
AC Q76329;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interactin.
GN ABPD.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96365468; PubMed=9700162;
RA Rivero F.J., Kuspa A., Brokamp R., Matzner M., Noegel A.A.;
RT "Interactin, an actin-binding protein of the alpha-actinin superfamily
RT in Dictyostelium discoideum, is developmentally and CAMP-regulated and
RT associates with intracellular membrane compartments.";
RL J. Cell Biol. 142:735-750(1998).
DR EMBL; AF057019; AAC34582.1;
DR PIR; T14867; T14867.
DR HSSP; P46939; IQAG.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR001589; Actbind_actinin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR001990; Grainin.
DR InterPro; IPR001451; Hexaped_transf.
DR InterPro; IPR02017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR SMART; SMO0033; CH; 2.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
DR PROSITE; PS00422; GRANINS_1; 1.
DR PROSITE; PS00101; HEXAPEP_TRANSFERSSES; 1.
SQ SEQUENCE 1738 AA, 204457 MW, 577A99D28C79AF5C CRC64;
Query Match 6.3%; Score 132; DB 5; Length 1738;
Best Local Similarity 18.4%; Pred. No. 5.2; Indels 129; Gaps 18;
Matches 78; Conservative 79; Mismatches 129; Indels 138; Gaps 18;
QY 23 LNTSDTEGFLGVEKGAENKSIQSDQMDV-----EYVYITDI--QKTYPCYQ-----LF 71
DB 466 LSTWQATNSELMEKI--GGLNMDLTDIPQDIKEKDEIANKIESEKNLKFQDDFNALQ 524
QY 72 SFYNSGSEVNEQ--ALKILSNVKNVGMVKKFRHSDDIMFRRERLHKNIQEHHSNQ 128
DB 525 SRYSLTLEQTSQODRLKQILNEIQERDDKFIETNSSNSQSLDNQAVIQLTNE--KQ 581
QY 129 DLVEFLITPSITTESGSTRLEHSLYEPQKGLFHRVPLVAVANIGMSEQLGYTVSGSCWS 188
DB 582 SITQLQDDQDIKK-----EFQFEKQ--LISQDISITT----- 615
QY 189 TGFRAVQTHSSKFF-----FEEDGS-----KEVHKINEMVAYSLQELKSIKKV 233
DB 616 -----IQEYODKFNNIQGFNTQCTLNQOETRLTQQLVQINTDINEKQTQLQS---EI 666
QY 224 EDSEQAVDKLVQVNRLLKREIERKGAQIQAAEKKNIQKDPOENIFLCQALRTFFPNSF 293

```
Db 667 KDNQINBQNLKQSEKDEIKLSNQEQQDEK----- 701
QY 294 LHSQWSLKQNRHVSKSSCNYNHLLDVNDLTLMEHTDIPKASPASTPOLIKKALDD 353
Db 702 -----INNLLLEIKKCC-LIERINOQLENN-IDLNS 731
QY 354 RMO-----FKRSRLDPTQDKRSKANTGSSNODKASKMSPTDEIEKKK-----GFG 401
Db 732 KYQQLLEFENFKLNSKEKENQNLFLQSKQDERFQNLN---DEKLEKQLOQSTIEDEFN 788
QY 402 EYSR 405
Db 789 QYKQ 792

RESULT 15
ID 081L22 PRELIMINARY; PRT; 4405 AA.
AC 081L22;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN PF14_0101.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2235705; PubMed=12368664;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., K.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.W., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RT Nature 419:498-511 (2002).
RL EMBL: AB014817; FAN36713.1;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPRO02068; Aldehyde dehydr.
DR InterPro; IPRO01179; FKBP_Priase.
DR InterPro; IPRO01680; WD40.
DR Pfam; PF00400; WD40; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00453; FKBP_PRIASE_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Hypothetical protein.
SQ SEQUENCE 4405 AA; 526726 MW; 982E03E716161797 CRC64;

Query Match 6.3%; Score 132; DB 5; Length 4405;
Best Local Similarity 19.4%; Pred. No.15;
Matches 80; Conservative 67; Mismatches 141; Indels 124; Gaps 16;

QY 24 NTDSDEGFLGVKGEAKSITDSQMDVEVVYITDIQKIYFCYQLFSFYNSSGEVNEQ 83
Db 2287 NTQKRNKTLQDDKRGK--NKIENDEMD-----HKID-----DNIKENDEM 2326
QY 84 ALKKIISNVKQNVGVGKFRHSDDQIMTFRERLHK--NLQEHFSNQLVFLLLTPSII 140
Db 2327 KDKHIDNIIKEN--NEKKDKHIDNIIKENDEMDKHIDNIIKENNEMKD----- 2373
QY 141 TEGSCTHRLHESLYKQKGLFHRVPLVNLGMSQQLGYKTVSGSCMSTGFSRAVQTHSS 200
Db 2374 -----HKIDNIIKENDEMDKHID-----DNIIENDEM 2401
```

```
QY 201 KFFPEDSLKE-----VHKINEMAYSLQBELKSIQCKVEDSEQAVDVKVDVNRK----- 251
Db 2402 KDKHIDNIIKENDEMDKHID-----NIIKDEKDKHIDNIIKENDNIIKDNFI 2451
QY 252 ---REIEKRRGAQIOARERKNIQKDPQENIFLCOALRTPF-----PNSSEFLHSCVM 299
Db 2452 LEBQNLSEQR-TLIMINKEDDIDDKKQNESEQNIIEYFCQKNESENNLANSYACFM 2510
QY 300 SLKRRHVSKSSCNYNHLLDVNDLTLMEHTDIPKASPASTPOLIKKALDDRRQ--- 356
Db 2511 ELNNKXNDNKCICYDEHRYNE-----TEKENIKNTIPKENEI---NTIMLDEKYNNSI 2562
QY 357 -----FKRSRLDPTQDKRSKANTGSSNODKASKM-----SSPTDEIE 395
Db 2563 IENKENSISKSSYDWDYDSYSSISNGSDNLSMDNNEFFYFSSSECSCE 2614
```

Search completed: April 16, 2004, 10:15:57
Job time : 48 secs

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 20

PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254

PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGFVYALAFQHLNTPDSTEGFLGGEVYGEAKNSITDSQMDPVEVYITD 60
DB 1 MEGESTSAVLSGFVYALAFQHLNTPDSTEGFLGGEVYGEAKNSITDSQMDPVEVYITD 60
QY 61 IOKYIPCYQLFSFYNSSGEVEQALKILSNVKNVGVYKFRHRSDQIMTFREELHKN 120
DB 61 IOKYIPCYQLFSFYNSSGEVEQALKILSNVKNVGVYKFRHRSDQIMTFREELHKN 120
QY 121 LOEHSNQDLVLLTPSLITTESCSTHLEHSLYKPGQGLFHRVPLVVAANGMSQGLGX 180

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 18

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C22
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTAVLSGFTVGAIAFQHLNTDPTGFLGVEYGEAKNSITDSQMDVETITD 60
DB 1 MEGESTAVLSGFTVGAIAFQHLNTDPTGFLGVEYGEAKNSITDSQMDVETITD 60
QY 61 IOKYIPCYQLPSEFYNSGSEVNBQALKILSNVKNVVMYKFRHSDIMTFREBLHKN 120
DB 61 IOKYIPCYQLPSEFYNSGSEVNBQALKILSNVKNVVMYKFRHSDIMTFREBLHKN 120
QY 121 LOEHFNSODLVFLITPSIITTESCSTHRLSHSLYKPOKGLFHRVPLVYANIGMSEQLGYK 180
DB 121 LOEHFNSODLVFLITPSIITTESCSTHRLSHSLYKPOKGLFHRVPLVYANIGMSEQLGYK 180
QY 181 TVSGSCMTGFSRAVQHTSSKFEEDGSLKVEYKINENYASIOELKSIKCKVEDSEQAV 240
DB 181 TVSGSCMTGFSRAVQHTSSKFEEDGSLKVEYKINENYASIOELKSIKCKVEDSEQAV 240
QY 241 DCLVNDVNRKLKEIKERGAQIOAREKNIQKDPENIPLCOALTFPENSEFLHSCYMS 300
DB 241 DCLVNDVNRKLKEIKERGAQIOAREKNIQKDPENIPLCOALTFPENSEFLHSCYMS 300
QY 301 LKNRIVSSSCVYNHLLVNDLTLMVEHTDIPASPASTQIHKKALDIDDRWQFES 360
DB 301 LKNRIVSSSCVYNHLLVNDLTLMVEHTDIPASPASTQIHKKALDIDDRWQFES 360
QY 361 RLIDTQDKRSKANTGSSNQDKASKYSPETDEIEIKMGFGSEYSSPTF 409
DB 361 RLIDTQDKRSKANTGSSNQDKASKYSPETDEIEIKMGFGSEYSSPTF 409

RESULT 11
US-09-990-456-158
Sequence 158, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Ferrata, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerltzen, Mary E.

PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-180;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSTSAVLSGFLGALAFQHLNTSDTEGFLGVEYGAKNISITDSQMDVEVYITD 60
 DB 1 MEGSTSAVLSGFLGALAFQHLNTSDTEGFLGVEYGAKNISITDSQMDVEVYITD 60
 QY 61 IQXTIPCYOLFSEFYNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRILHKN 120
 DB 61 IQXTIPCYOLFSEFYNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRILHKN 120
 QY 121 LOEHSNODVFLITTSITTESCSTHRLSHSLYKPOKGLFHRVPLVVALGSEBOLGK 180
 DB 121 LOEHSNODVFLITTSITTESCSTHRLSHSLYKPOKGLFHRVPLVVALGSEBOLGK 180
 QY 181 TVSSGCMSTGFSRAVQTHSSKFEEDGSLKXVKINEMVYASLOEBLSICKVDESEQAV 240
 DB 181 TVSSGCMSTGFSRAVQTHSSKFEEDGSLKXVKINEMVYASLOEBLSICKVDESEQAV 240
 QY 241 DKLVKYNRLKRELEKRGQIQARERKNQKPOENIFCOLRTPFSESLHSCWVS 300
 DB 241 DKLVKYNRLKRELEKRGQIQARERKNQKPOENIFCOLRTPFSESLHSCWVS 300
 QY 301 LKKNHVKSSSCNVNHLVDVNLTLWVEHTDIPASASTPQILKHALDLDRWQFKS 360
 DB 301 LKKNHVKSSSCNVNHLVDVNLTLWVEHTDIPASASTPQILKHALDLDRWQFKS 360
 QY 361 RLDDTQKRSKANTGSSNODYASMSSEPTDESELEKKGGEYSRPTF 409
 DB 361 RLDDTQKRSKANTGSSNODYASMSSEPTDESELEKKGGEYSRPTF 409

RESULT 10
 US-09-993-604-158
 Sequence 158; Application US/09993604
 Patent No. US20020137075A1

GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Deeneyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gutney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C25
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 14

PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090662
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;

Best Local Similarity 100.0%; Pred. No. 3.2e-180; Indels 0; Gaps 0;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTAVLSGFTVAGALAFQHLNTSDTEGFLGGEVKGAKNSITDSQMDVEVVYTIID 60
DB 1 MEGESTAVLSGFTVAGALAFQHLNTSDTEGFLGGEVKGAKNSITDSQMDVEVVYTIID 60

QY 61 IQKTIPTCYQLFSFYNSSGEVNEQALKLLSNVKNVGVNMYKFRHSDQIMTFRRRLHKH 120
DB 61 IQKTIPTCYQLFSFYNSSGEVNEQALKLLSNVKNVGVNMYKFRHSDQIMTFRRRLHKH 120
QY 121 LOEHFNSQDLVFLILTPSIIITESCTHREHSLYKPKQGLFHRVPLVYVANGSEOLGYK 180
DB 121 LOEHFNSQDLVFLILTPSIIITESCTHREHSLYKPKQGLFHRVPLVYVANGSEOLGYK 180
QY 181 TVSGSCMSTGSPRAVQTHSSKPFEDGSLKEVHKINEMVYASLOERLKSICKVDSBPAY 240
DB 181 TVSGSCMSTGSPRAVQTHSSKPFEDGSLKEVHKINEMVYASLOERLKSICKVDSBPAY 240
QY 241 DCLVADVNRILKREIEKRRGAQIOAREKNIOKDPQENIFLCQALRTPFPNSEPLHSCVMS 300
DB 241 DCLVADVNRILKREIEKRRGAQIOAREKNIOKDPQENIFLCQALRTPFPNSEPLHSCVMS 300
QY 301 LKNRHSVSSCNYNHHLDVNDLTMVHTDIPASPASTQIILKXKALDIDDRWQFGRS 360
DB 301 LKNRHSVSSCNYNHHLDVNDLTMVHTDIPASPASTQIILKXKALDIDDRWQFGRS 360
QY 361 RLDTQDKRSKXANTSSNQDKASXKSPETDEIEKMGFGEYRSPTF 409
DB 361 RLDTQDKRSKXANTSSNQDKASXKSPETDEIEKMGFGEYRSPTF 409

RESULT 9
US-09-991-163-158

Sequence 158, Application US/09991163
Patent No. US20020132253A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin J.
APPLICANT: Kjaavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

Db 301 LKRWKSSCNVHLDVNDLTVNWEHTDIPASASPTPOIKKALDLDRWPKRS 360
OY 361 RLDTQKRSKANTGSSNQDKASWSSPFTDEIEKKKGFGEYSRSPFT 409
Db 361 RLDTQKRSKANTGSSNQDKASWSSPFTDEIEKKKGFGEYSRSPFT 409

RESULT 8
US-09-990-442-158
Sequence 158, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C8
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/990,442
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088367
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 12

PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTAVLSGFTVGLAFOHNTDPTBGFLLGBVYGEAKNSITDSOMDVEVYTTID 60
DB 1 MEGESTAVLSGFTVGLAFOHNTDPTBGFLLGBVYGEAKNSITDSOMDVEVYTTID 60
QY 61 IQXVPCYQULFSFYNSSGEVNEQALKILSNVKNVGVYFRHSDQIMTFRRLLHKN 120
DB 61 IQXVPCYQULFSFYNSSGEVNEQALKILSNVKNVGVYFRHSDQIMTFRRLLHKN 120
QY 121 LOEHFSNODLVFLLTPTBILITESGSTRLEHSLYKPKQGFHRVPLVYVANGMSBOLGYK 180
DB 121 LOEHFSNODLVFLLTPTBILITESGSTRLEHSLYKPKQGFHRVPLVYVANGMSBOLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSKFPEEDSLKXVKHINEMVYSLQEBLSICKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSKFPEEDSLKXVKHINEMVYSLQEBLSICKVEDSEQAV 240
QY 241 DKLVDVNRLLKRETEKRRGAQIOAREKNTOKDQENIFLQOALRTFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKRETEKRRGAQIOAREKNTOKDQENIFLQOALRTFPNSEFLHSCVMS 300
QY 301 LKNRNVSKSCNVYHHLDDVVDNLTLMVHTDIPSPASPTQIITKHALDLIDRMOFKRS 360
DB 301 LKNRNVSKSCNVYHHLDDVVDNLTLMVHTDIPSPASPTQIITKHALDLIDRMOFKRS 360

PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-180;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESNSAVSGVLTGALAFQHLNTSDPTDEGELLGVEKGEAKNSITDSQMDVVEVYTTD 60
 DB 1 MEGESNSAVSGVLTGALAFQHLNTSDPTDEGELLGVEKGEAKNSITDSQMDVVEVYTTD 60
 QY 61 IOKYIPCYQLFSEFNSSGVEVQALKKILSNVKNVGVWYKFRHSDDQIMTFPERLLHKN 120
 DB 61 IOKYIPCYQLFSEFNSSGVEVQALKKILSNVKNVGVWYKFRHSDDQIMTFPERLLHKN 120
 QY 121 LOEHFNSQDVLFLITPSITTESCSTHRLHSLYKQKGLFHRVPLVAVNLGMSBOLGYK 180
 DB 121 LOEHFNSQDVLFLITPSITTESCSTHRLHSLYKQKGLFHRVPLVAVNLGMSBOLGYK 180
 QY 181 TVSGSCSTGFSRAVQVHSHSKFPEEDQSLKEVKINEMVASLQEEKLSCKKVEDEBQAV 240
 DB 181 TVSGSCSTGFSRAVQVHSHSKFPEEDQSLKEVKINEMVASLQEEKLSCKKVEDEBQAV 240
 QY 241 DKLVDVNRLEKREIEKRGAGQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVNS 300
 DB 241 DKLVDVNRLEKREIEKRGAGQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVNS 300
 QY 301 LKORHVSCKSNVNHLDVVDNLTLMVEHTDIPBASPTPOIKKHALDLDRWQFKRS 360
 DB 301 LKORHVSCKSNVNHLDVVDNLTLMVEHTDIPBASPTPOIKKHALDLDRWQFKRS 360
 QY 361 RLIDTODKRSKANTGSSNQDKASKMSPEIDEEIEKKKGFGEYSRSPTF 409
 DB 361 RLIDTODKRSKANTGSSNQDKASKMSPEIDEEIEKKKGFGEYSRSPTF 409

RESULT 7
 US-09-991-073-158
 Sequence 158, Application US/09991073
 Patent No. US20020127576A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Denoyers, Luc

APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Geritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Guiney, Austin L.
 APPLICANT: KJavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zenlin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C1S
 CURRENT APPLICATION NUMBER: US/09/991,073
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 10

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089559
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544

PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3, 2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSTSAVLGFTLGAALAFQHLNTSDTSGFLGVEYKGEAKNSITDSQMDVZEVYTTID 60
DB 1 MEGSTSAVLGFTLGAALAFQHLNTSDTSGFLGVEYKGEAKNSITDSQMDVZEVYTTID 60
QY 61 IQXTIPCYQLFSSFYNSGGEVNEQALKILSNVXKNVGVTKFRHSDQIMTFRRRLHKX 120
DB 61 IQXTIPCYQLFSSFYNSGGEVNEQALKILSNVXKNVGVTKFRHSDQIMTFRRRLHKX 120
QY 121 LOEHPNODLVFLLTTSITTESCTRLHSLYKPKQGFPHRYPLVYANLGMSEQLGYK 180
DB 121 LOEHPNODLVFLLTTSITTESCTRLHSLYKPKQGFPHRYPLVYANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDDSLKEVHKINEMYASLOELKSIQKVDSDQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEDDSLKEVHKINEMYASLOELKSIQKVDSDQAV 240
QY 241 DKLVDVNRLLKRELEKRGAGIOAAREKNIOXDQENIFLCOALRTFPPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKRELEKRGAGIOAAREKNIOXDQENIFLCOALRTFPPNSEFLHSCVMS 300
QY 301 LKNRHSKSCNVMHHLDDVVDNLTLNVEHTDIPASPASTPQIIKXALDLDDSWQPKRS 360
DB 301 LKNRHSKSCNVMHHLDDVVDNLTLNVEHTDIPASPASTPQIIKXALDLDDSWQPKRS 360
QY 361 RLDTQDRSKAANTGSSNQDPAKSSPDTDELEKXKGFGEYRSRSTP 409
DB 361 RLDTQDRSKAANTGSSNQDPAKSSPDTDELEKXKGFGEYRSRSTP 409

RESULT 6

US-09-989-732-158
Sequence 158, Application US/09989732

Patent No. US20020123463A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.

QY 1 MEGESTASAVLSGFLVGLALFQHLNTSDTDEGFLIGVEYGEAKNSITDSQMDVEVYVYITD 60
Db 1 MEGESTASAVLSGFLVGLALFQHLNTSDTDEGFLIGVEYGEAKNSITDSQMDVEVYVYITD 60
QY 61 IOKTIPCYOLFSPFNSSGVEVEQALKKILSNVKKAVGVGWKFRHSDQITFPERLLHKN 120
Db 61 IOKTIPCYOLFSPFNSSGVEVEQALKKILSNVKKAVGVGWKFRHSDQITFPERLLHKN 120
QY 121 LOEHFNSQDVLFLITFSITTESCSTRLEHSLYKPKXGIFHRVPLVYANLGMSEQLGYX 180
Db 121 LOEHFNSQDVLFLITFSITTESCSTRLEHSLYKPKXGIFHRVPLVYANLGMSEQLGYX 180
QY 181 TVSSGCMSTGFSRAVQVHSSKFEEDGSLKEVHKINMYASLOELKSIKCKVEDSEQAV 240
Db 181 TVSSGCMSTGFSRAVQVHSSKFEEDGSLKEVHKINMYASLOELKSIKCKVEDSEQAV 240
QY 241 DKLVCVYNR.LKREIEKRGAGIQAREKNIQKPOENIFLQALRTFEPNSEFLHSCVMS 300
Db 241 DKLVCVYNR.LKREIEKRGAGIQAREKNIQKPOENIFLQALRTFEPNSEFLHSCVMS 300
QY 301 LKNHVSCKSCNVNHLVDVNLTLNWEHTDIPASPASTPQIIKHALDLDRMQPKRS 360
Db 301 LKNHVSCKSCNVNHLVDVNLTLNWEHTDIPASPASTPQIIKHALDLDRMQPKRS 360
QY 361 RLJDTQPKRSKANTGSSNQDKASHMSPEUDEEIEKKKGFGEYSRSPTE 409
Db 361 RLJDTQPKRSKANTGSSNQDKASHMSPEUDEEIEKKKGFGEYSRSPTE 409
RESULT 5
US-09-989-731-158
Sequence 158, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC70
CURRENT APPLICATION NUMBER: US/09/989,731
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770

PROR FILING DATE: 1997-11-24
PROR APPLICATION NUMBER: 60/075945
PROR FILING DATE: 1998-02-25
PROR APPLICATION NUMBER: 60/076910
PROR FILING DATE: 1998-03-20
PROR APPLICATION NUMBER: 60/083322
PROR FILING DATE: 1998-04-28
PROR APPLICATION NUMBER: 60/084600
PROR FILING DATE: 1998-05-07
PROR APPLICATION NUMBER: 60/087106
PROR FILING DATE: 1998-05-28
PROR APPLICATION NUMBER: 60/087607
PROR FILING DATE: 1998-06-02
PROR APPLICATION NUMBER: 60/087609
PROR FILING DATE: 1998-06-02
PROR APPLICATION NUMBER: 60/087759
PROR FILING DATE: 1998-06-02
PROR APPLICATION NUMBER: 60/087827
PROR FILING DATE: 1998-06-03
PROR APPLICATION NUMBER: 60/088021
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088025
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088026
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088028
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088029
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088030
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088033
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088326
PROR FILING DATE: 1998-06-04
PROR APPLICATION NUMBER: 60/088167
PROR FILING DATE: 1998-06-05
PROR APPLICATION NUMBER: 60/088202
PROR FILING DATE: 1998-06-05
PROR APPLICATION NUMBER: 60/088212
PROR FILING DATE: 1998-06-05
PROR APPLICATION NUMBER: 60/088217
PROR FILING DATE: 1998-06-05
PROR APPLICATION NUMBER: 60/088655
PROR FILING DATE: 1998-06-09
PROR APPLICATION NUMBER: 60/088734
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088738
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088742
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088810
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088824
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088826
PROR FILING DATE: 1998-06-10
PROR APPLICATION NUMBER: 60/088858
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/088861
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/088876
PROR FILING DATE: 1998-06-11
PROR APPLICATION NUMBER: 60/089105
PROR FILING DATE: 1998-06-12
PROR APPLICATION NUMBER: 60/089440
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089512
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089514
PROR FILING DATE: 1998-06-16
PROR APPLICATION NUMBER: 60/089532
PROR FILING DATE: 1998-06-17

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 7

PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947

PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3,2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/030431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3.2e-180;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSVLSGFLVGAFAHMLNDSTBEGFLGVEYKGAKNISITDSOMDVEVVTID 60
 DB 1 MEGESTSVLSGFLVGAFAHMLNDSTBEGFLGVEYKGAKNISITDSOMDVEVVTID 60
 QY 1 IOKYIPCYQLFSPYNSGEVNEQALKILSNVKNVGVWYFRHSDQIMTFRERLIHN 120
 DB 61 IOKYIPCYQLFSPYNSGEVNEQALKILSNVKNVGVWYFRHSDQIMTFRERLIHN 120
 QY 121 LOEHNSNDIVFLITPSITTESCTHLESLVKKPOKGFHRVPIVAVNAGMSEOLGYK 180
 DB 121 LOEHNSNDIVFLITPSITTESCTHLESLVKKPOKGFHRVPIVAVNAGMSEOLGYK 180
 QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINENYASLQELKSI CKVDESDQAV 240
 DB 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINENYASLQELKSI CKVDESDQAV 240

QY 241 DLYVDVNRLEKREIEKRRGAIOIARREKNIOKDPOENTFLCOALRTFPPNSEFLHSCVMS 300
 DB 241 DLYVDVNRLEKREIEKRRGAIOIARREKNIOKDPOENTFLCOALRTFPPNSEFLHSCVMS 300
 QY 301 LKNRHSVSKSCNVNHLDVDNLTLMWZHTDIPASPASTPOIHKRALDUDRWQFKRS 360
 DB 301 LKNRHSVSKSCNVNHLDVDNLTLMWZHTDIPASPASTPOIHKRALDUDRWQFKRS 360
 QY 361 RLDTQDGRSKANTGSSNODKASKSSPPTDEIEKMGFGESRSPTE 409
 DB 361 RLDTQDGRSKANTGSSNODKASKSSPPTDEIEKMGFGESRSPTE 409

RESULT 4
 US-09-989-727-158
 Sequence 158, Application US/09989727
 Patent No. US20020072497A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Geider, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC65
 CURRENT APPLICATION NUMBER: US/09/989,727
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075845
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 4

PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3,2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGTVGALAFQHLNLTDSYEGHLLGEVYGEANSTLTDSDMDVEVYITD 60
DB 1 MEGESTSAVLSGTVGALAFQHLNLTDSYEGHLLGEVYGEANSTLTDSDMDVEVYITD 60
QY 61 IQKILPCYQLFSPVNSSGEYNEQALKLISNKKVAVGMYKFRHSDDQIMFRERLHKN 120
DB 61 IQKILPCYQLFSPVNSSGEYNEQALKLISNKKVAVGMYKFRHSDDQIMFRERLHKN 120
QY 121 LQHFNSODLVFLLTPSIITTESCSTHRLHSLYKPKGLFHRVPLVANNLQMSQOLGYK 180
DB 121 LQHFNSODLVFLLTPSIITTESCSTHRLHSLYKPKGLFHRVPLVANNLQMSQOLGYK 180
QY 181 TVSGSCMSTGFSAAVOTHSKPEEDGSLKEYHKNEMVYASIOEELKSLCKVEDESEQAV 240
DB 181 TVSGSCMSTGFSAAVOTHSKPEEDGSLKEYHKNEMVYASIOEELKSLCKVEDESEQAV 240
QY 241 DKLVDVNRLEKREIKRGAQIOAAREKNIQXDPQENITLCOALRTFFNSEFLHSCVNS 300
DB 241 DKLVDVNRLEKREIKRGAQIOAAREKNIQXDPQENITLCOALRTFFNSEFLHSCVNS 300
QY 301 LKRRHYSKSCNHNLDVVDNLTWVEHTDIPASPASTPOLIKKALDLDROWQFORS 360
DB 301 LKRRHYSKSCNHNLDVVDNLTWVEHTDIPASPASTPOLIKKALDLDROWQFORS 360
QY 361 RLDDQKRSKANTGSSNODKASKMSPTDEEIEKMGGEYSRSPTF 409
DB 361 RLDDQKRSKANTGSSNODKASKMSPTDEEIEKMGGEYSRSPTF 409

RESULT 3
US-09-989-279-158
; Sequence 158, Application US/09989279
; Patent No. US20020072496A1

PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3.2e-180;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSTSAVLSGFTLGAFOHINTSDTEGFLGVEYKSAKSIITDSQMDVEVYTTD 60
 DB 1 MEGSTSAVLSGFTLGAFOHINTSDTEGFLGVEYKSAKSIITDSQMDVEVYTTD 60
 QY 61 IQXTIPCYQFSPFNSSGVEVEQALKKILSNVKKVGVYKFRHSDQIMTFRRLLHKN 120
 DB 61 IQXTIPCYQFSPFNSSGVEVEQALKKILSNVKKVGVYKFRHSDQIMTFRRLLHKN 120
 QY 121 LOEHSNODVFLTLTSSITTESGSTRLEHSLYKPKGKPHVPLVYALGMSBQLGYK 180
 DB 121 LOEHSNODVFLTLTSSITTESGSTRLEHSLYKPKGKPHVPLVYALGMSBQLGYK 180
 QY 181 TVSSGCSGTFSRAVQTHSSKFFEDDGLKEVKNINEMVYALOBELKISCKYVEDSQAV 240
 DB 181 TVSSGCSGTFSRAVQTHSSKFFEDDGLKEVKNINEMVYALOBELKISCKYVEDSQAV 240
 QY 241 DKLYDVNRLKREIEKRGAGIOAAREKNIQKPOENIFICOALRTFFPSSEFLHSCWVS 300
 DB 241 DKLYDVNRLKREIEKRGAGIOAAREKNIQKPOENIFICOALRTFFPSSEFLHSCWVS 300
 QY 301 LKKNHVSCKSNVYHHLVDVNTLTMVEHTDIPASASTPQIILKHALDLDRMOKFS 360
 DB 301 LKKNHVSCKSNVYHHLVDVNTLTMVEHTDIPASASTPQIILKHALDLDRMOKFS 360
 QY 361 RLDDTODKRSKANTGSSNODKASWSSPEFDEIEKKKGFGEYSRSTPF 409
 DB 361 RLDDTODKRSKANTGSSNODKASWSSPEFDEIEKKKGFGEYSRSTPF 409

RESULT 2
 US-09-989-723-158
 Sequence 158, Application US/09989723
 Patent No. US20020072092A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eilat, Dan L.
 APPLICANT: Ferrata, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gottlieb, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Goddard, Paul J.
 APPLICANT: Grimaldi, V. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavich, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C62
 CURRENT APPLICATION NUMBER: US/09/989,723
 PRIOR APPLICATION NUMBER: 60/045787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:13:35 ; Search time 48 Seconds

(without alignments)
2348.965 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109

Sequence: 1 MEGESTSAVLSGFVLCALAF.....TDEIEIKMKGFGEYSRSPFR 409

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2109	100.0	409	9	US-09-989-722-158 Sequence 158, App
2	2109	100.0	409	9	US-09-989-723-158 Sequence 158, App
3	2109	100.0	409	9	US-09-989-279-158 Sequence 158, App
4	2109	100.0	409	9	US-09-989-727-158 Sequence 158, App
5	2109	100.0	409	9	US-09-989-731-158 Sequence 158, App
6	2109	100.0	409	9	US-09-989-732-158 Sequence 158, App
7	2109	100.0	409	9	US-09-991-073-158 Sequence 158, App
8	2109	100.0	409	9	US-09-990-442-158 Sequence 158, App
9	2109	100.0	409	9	US-09-991-153-158 Sequence 158, App
10	2109	100.0	409	9	US-09-993-604-158 Sequence 158, App
11	2109	100.0	409	9	US-09-990-456-158 Sequence 158, App
12	2109	100.0	409	9	US-09-989-721-158 Sequence 158, App
13	2109	100.0	409	9	US-09-992-598-158 Sequence 158, App
14	2109	100.0	409	9	US-09-989-293A-158 Sequence 158, App
15	2109	100.0	409	9	US-09-989-735-158 Sequence 158, App

15	2109	100.0	409	9	US-09-990-444-158 Sequence 158, App
17	2109	100.0	409	9	US-09-991-181-158 Sequence 158, App
18	2109	100.0	409	9	US-09-989-730-158 Sequence 158, App
19	2109	100.0	409	9	US-09-990-436-158 Sequence 158, App
20	2109	100.0	409	9	US-09-993-687-158 Sequence 158, App
21	2109	100.0	409	10	US-09-989-734-158 Sequence 158, App
22	2109	100.0	409	10	US-09-997-653-158 Sequence 158, App
23	2109	100.0	409	10	US-09-993-667-158 Sequence 158, App
24	2109	100.0	409	10	US-09-997-428-158 Sequence 158, App
25	2109	100.0	409	10	US-09-997-666-158 Sequence 158, App
26	2109	100.0	409	10	US-09-990-458-158 Sequence 158, App
27	2109	100.0	409	10	US-09-990-562-158 Sequence 158, App
28	2109	100.0	409	10	US-09-990-711-158 Sequence 158, App
29	2109	100.0	409	10	US-09-989-726-158 Sequence 158, App
30	2109	100.0	409	10	US-09-998-156-158 Sequence 158, App
31	2109	100.0	409	10	US-09-990-437-158 Sequence 158, App
32	2109	100.0	409	10	US-09-991-157-158 Sequence 158, App
33	2109	100.0	409	10	US-09-997-514-158 Sequence 158, App
34	2109	100.0	409	10	US-09-997-573-158 Sequence 158, App
35	2109	100.0	409	10	US-09-991-172-158 Sequence 158, App
36	2109	100.0	409	10	US-09-990-726-158 Sequence 158, App
37	2109	100.0	409	10	US-09-997-559-158 Sequence 158, App
38	2109	100.0	409	10	US-09-997-601-158 Sequence 158, App
39	2109	100.0	409	10	US-09-990-443-158 Sequence 158, App
40	2109	100.0	409	10	US-09-991-854-158 Sequence 158, App
41	2109	100.0	409	10	US-09-997-628-158 Sequence 158, App
42	2109	100.0	409	10	US-09-997-683-158 Sequence 158, App
43	2109	100.0	409	10	US-09-989-729A-158 Sequence 158, App
44	2109	100.0	409	10	US-09-997-349-158 Sequence 158, App
45	2109	100.0	409	10	US-09-997-440-158 Sequence 158, App

ALIGNMENTS

RESULT 1
US-09-989-722-158
Sequence 158, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

Db 121 LOEHFNSODLVFLLPSTITTESCSTRLEHSLYKFOKGLFHRVPLVANLGMSEGLGYK 180
 Qy 181 TVGSGCMSTGFSFSAVQCHSKSFEEDGSLKEVHKINEMVASIOEELKSTCKYVEDSEOKAV 240
 Db 181 TVGSGCMSTGFSFSAVQCHSKSFEEDGSLKEVHKINEMVASIOEELKSTCKYVEDSEOKAV 240
 Qy 241 DKLVKQVNRKREIEKRGAGQIOAAREKNIQKDPQENIFLQCALRFFPNSEFLHSCVMS 300
 Db 241 DKLVKQVNRKREIEKRGAGQIOAAREKNIQKDPQENIFLQCALRFFPNSEFLHSCVMS 300
 Qy 301 LKRRHVSCKSCNNHHLVDVNDLTLVWEHTDIPASASTPQIIRKALDLDROQFKRS 360
 Db 301 LKRRHVSCKSCNNHHLVDVNDLTLVWEHTDIPASASTPQIIRKALDLDROQFKRS 360
 Qy 361 RLIDTQDKSGSKANTGSSNODKASKMSPTDEIEIKMGFGSEYSRSPTE 409
 Db 361 RLIDTQDKSGSKANTGSSNODKASKMSPTDEIEIKMGFGSEYSRSPTE 409

RESULT 13

US-09-92-598-158
 / Sequence 158, Application US/09992598
 / Patent No. US20020160384A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnovers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerltsen, Mary E.
 / APPLICANT: Goddard, Audrey J.
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Kijavlin, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Matanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: P2730PLC20
 / CURRENT APPLICATION NUMBER: US/09/992,598
 / PRIOR FILING DATE: 2001-11-14
 / PRIOR APPLICATION NUMBER: 60/049787
 / PRIOR FILING DATE: 1997-06-16
 / PRIOR APPLICATION NUMBER: 60/062250
 / PRIOR FILING DATE: 1997-10-17
 / PRIOR APPLICATION NUMBER: 60/065186
 / PRIOR FILING DATE: 1997-11-12
 / PRIOR APPLICATION NUMBER: 60/065311
 / PRIOR FILING DATE: 1997-11-13
 / PRIOR APPLICATION NUMBER: 60/066770
 / PRIOR FILING DATE: 1997-11-24
 / PRIOR APPLICATION NUMBER: 60/075945
 / PRIOR FILING DATE: 1998-02-25
 / PRIOR APPLICATION NUMBER: 60/078910
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/083322
 / PRIOR FILING DATE: 1998-04-28
 / PRIOR APPLICATION NUMBER: 60/084600
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 22

PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3, 2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSTGVLSGFLGALAQHNTDSDTGFLLGVEYKGAIXSITSDQMDVYVTTID 60
DB 1 MEGSTSAVLSGFLGALAQHNTDSDTGFLLGVEYKGAIXSITSDQMDVYVTTID 60
QY 61 IQXTIPCYQLFSFYNSGGEVNEQALKITLSNVKKNVGVYKFRHSQDQMTFRRLHKN 120
DB 61 IQXTIPCYQLFSFYNSGGEVNEQALKITLSNVKKNVGVYKFRHSQDQMTFRRLHKN 120
QY 121 LOEHFSNODLVFLLLTPTSIITTESCTYRLHSLYKPOKGLPHRVPLVYANLGSBQJGYK 180
DB 121 LOEHFSNODLVFLLLTPTSIITTESCTYRLHSLYKPOKGLPHRVPLVYANLGSBQJGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINMYASLQEBLKSICKYEDSBOAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINMYASLQEBLKSICKYEDSBOAV 240
QY 241 DKLVDVNRLLKREIEKRGQAQIQAREKNIQKDPQENIFLQALRTFFPSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRGQAQIQAREKNIQKDPQENIFLQALRTFFPSEFLHSCVMS 300
QY 301 LKRNHVSXSSCNVYHLDVVDNLTLMWEHNDIEBASASTPOLIKKALDLDKRWPKRS 360
DB 301 LKRNHVSXSSCNVYHLDVVDNLTLMWEHNDIEBASASTPOLIKKALDLDKRWPKRS 360
QY 361 RLDDTQDKRSKANTGSSNODKASRMSSPETDEIEKKKGGEYSRSPTE 409
DB 361 RLDDTQDKRSKANTGSSNODKASRMSSPETDEIEKKKGGEYSRSPTE 409

RESULT 14
US-09-989-293A-158
Sequence 158, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16

1	PRIOR APPLICATION NUMBER: 60/062255
2	PRIOR FILING DATE: 1997-10-17
3	PRIOR APPLICATION NUMBER: 60/065186
4	PRIOR FILING DATE: 1997-11-12
5	PRIOR APPLICATION NUMBER: 60/065311
6	PRIOR FILING DATE: 1997-11-13
7	PRIOR APPLICATION NUMBER: 60/066770
8	PRIOR FILING DATE: 1997-11-24
9	PRIOR APPLICATION NUMBER: 60/075945
10	PRIOR FILING DATE: 1998-02-25
11	PRIOR APPLICATION NUMBER: 60/078910
12	PRIOR FILING DATE: 1998-03-20
13	PRIOR APPLICATION NUMBER: 60/083322
14	PRIOR FILING DATE: 1998-04-28
15	PRIOR APPLICATION NUMBER: 60/084600
16	PRIOR FILING DATE: 1998-05-07
17	PRIOR APPLICATION NUMBER: 60/087106
18	PRIOR FILING DATE: 1998-05-28
19	PRIOR APPLICATION NUMBER: 60/087607
20	PRIOR FILING DATE: 1998-06-02
21	PRIOR APPLICATION NUMBER: 60/087759
22	PRIOR FILING DATE: 1998-06-02
23	PRIOR APPLICATION NUMBER: 60/087827
24	PRIOR FILING DATE: 1998-06-03
25	PRIOR APPLICATION NUMBER: 60/088021
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088025
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088026
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088028
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088029
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088030
36	PRIOR FILING DATE: 1998-06-04
37	PRIOR APPLICATION NUMBER: 60/088033
38	PRIOR FILING DATE: 1998-06-04
39	PRIOR APPLICATION NUMBER: 60/088326
40	PRIOR FILING DATE: 1998-06-04
41	PRIOR APPLICATION NUMBER: 60/088167
42	PRIOR FILING DATE: 1998-06-05
43	PRIOR APPLICATION NUMBER: 60/088202
44	PRIOR FILING DATE: 1998-06-05
45	PRIOR APPLICATION NUMBER: 60/088212
46	PRIOR FILING DATE: 1998-06-05
47	PRIOR APPLICATION NUMBER: 60/088217
48	PRIOR FILING DATE: 1998-06-05
49	PRIOR APPLICATION NUMBER: 60/088655
50	PRIOR FILING DATE: 1998-06-05
51	PRIOR APPLICATION NUMBER: 60/088734
52	PRIOR FILING DATE: 1998-06-10
53	PRIOR APPLICATION NUMBER: 60/088738
54	PRIOR FILING DATE: 1998-06-10
55	PRIOR APPLICATION NUMBER: 60/088742
56	PRIOR FILING DATE: 1998-06-10
57	PRIOR APPLICATION NUMBER: 60/088810
58	PRIOR FILING DATE: 1998-06-10
59	PRIOR APPLICATION NUMBER: 60/088824
60	PRIOR FILING DATE: 1998-06-10
61	PRIOR APPLICATION NUMBER: 60/088826
62	PRIOR FILING DATE: 1998-06-10
63	PRIOR APPLICATION NUMBER: 60/088858
64	PRIOR FILING DATE: 1998-06-11
65	PRIOR APPLICATION NUMBER: 60/088861
66	PRIOR FILING DATE: 1998-06-11
67	PRIOR APPLICATION NUMBER: 60/088766
68	PRIOR FILING DATE: 1998-06-11
69	PRIOR APPLICATION NUMBER: 60/089105
70	PRIOR FILING DATE: 1998-06-12
71	PRIOR APPLICATION NUMBER: 60/089440

PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/0895512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089532
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089538
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089598
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090439
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090676
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090650
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090654
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090655
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090656
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090662
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090682

PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3,2e-180; Indels 0; Gaps 0;
Matches 409; Conservative 0; Mismatches 0;

QY 1 MEGSTSAVLGFLVGLAFQHLNTDSDTEGFLGVEYGEAKNSITDSQMDVEVYTIID 60
DB 1 MEGSTSAVLGFLVGLAFQHLNTDSDTEGFLGVEYGEAKNSITDSQMDVEVYTIID 60
QY 61 IQXIPCVQLPSFVNSGEVNEQALKILSNVKNVGVNMYFRHSQIMFRRLHKN 120
DB 61 IQXIPCVQLPSFVNSGEVNEQALKILSNVKNVGVNMYFRHSQIMFRRLHKN 120
QY 121 LOEHNSNDVFLTLTPSITTESCTHLEHSLVYKQKGLHFRVPLVANIGSEQLGYK 180
DB 121 LOEHNSNDVFLTLTPSITTESCTHLEHSLVYKQKGLHFRVPLVANIGSEQLGYK 180
QY 121 LOEHNSNDVFLTLTPSITTESCTHLEHSLVYKQKGLHFRVPLVANIGSEQLGYK 180
DB 121 LOEHNSNDVFLTLTPSITTESCTHLEHSLVYKQKGLHFRVPLVANIGSEQLGYK 180
QY 181 TVSGSCMSTGFRRAVQHTSSKFFEDGSLKEVHKINEMVYASLOELKSIQKVEDSEQAV 240
DB 181 TVSGSCMSTGFRRAVQHTSSKFFEDGSLKEVHKINEMVYASLOELKSIQKVEDSEQAV 240
QY 241 DKLVDVNRLEKREIKRGAQIOAREKNIOKDPENITFLCOARTFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLEKREIKRGAQIOAREKNIOKDPENITFLCOARTFPNSEFLHSCVMS 300
QY 301 LKNRNVKSSCYNVNHLDVNDLTLMEHTDIPKASPASTQIIRKALDIDDERQPKRS 360
DB 301 LKNRNVKSSCYNVNHLDVNDLTLMEHTDIPKASPASTQIIRKALDIDDERQPKRS 360
QY 361 RLDDQDKRSKANTGSSNODKSKMSPETDEIEKMGFGYRSPTF 409
DB 361 RLDDQDKRSKANTGSSNODKSKMSPETDEIEKMGFGYRSPTF 409

RESULT 15

US-09-989-735-158
Sequence 158, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi U.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Wally E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090576
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090662
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGVPGALAFQHLNDSDEGFLGSGVGEAKSITDSQMDVEVYITD 60
DB 1 MEGESTSAVLGSGVPGALAFQHLNDSDEGFLGSGVGEAKSITDSQMDVEVYITD 60
QY 61 IQKXIPCYQLFSFYNSSGEVNEQALKILSNVKKVNVGWYKFRRSDDQIMFRERLHK 120
DB 61 IQKXIPCYQLFSFYNSSGEVNEQALKILSNVKKVNVGWYKFRRSDDQIMFRERLHK 120
QY 121 LOHFNSQDLVFLLLTPSITTSCTHRLHSLYRQKLFRRVPLVYANLQMSROLGYK 180
DB 121 LOHFNSQDLVFLLLTPSITTSCTHRLHSLYRQKLFRRVPLVYANLQMSROLGYK 180
QY 121 LOHFNSQDLVFLLLTPSITTSCTHRLHSLYRQKLFRRVPLVYANLQMSROLGYK 180
DB 121 LOHFNSQDLVFLLLTPSITTSCTHRLHSLYRQKLFRRVPLVYANLQMSROLGYK 180
QY 181 TVSGSCMSTGFSRAVOTHSKFFEDGSLKEVHKINEMVYASIQEELKSI CKVEDESEQAV 240
DB 181 TVSGSCMSTGFSRAVOTHSKFFEDGSLKEVHKINEMVYASIQEELKSI CKVEDESEQAV 240
QY 241 DKLVQVNFUKREIERKRAQIOAAREKNOIQDPQENTLCOALRTFFNSSEFLSCVNS 300
DB 241 DKLVQVNFUKREIERKRAQIOAAREKNOIQDPQENTLCOALRTFFNSSEFLSCVNS 300
QY 301 LKRRHVS KSCVNHLDVVDNLTLMVHTDIPEASPASTPOLIKKALDLDROQFKS 360
DB 301 LKRRHVS KSCVNHLDVVDNLTLMVHTDIPEASPASTPOLIKKALDLDROQFKS 360
QY 361 RLDDTDKSKSKANTGSSNODKASKWSPEPTDEIEKMGFGYRSPTF 409
DB 361 RLDDTDKSKSKANTGSSNODKASKWSPEPTDEIEKMGFGYRSPTF 409

Search completed: April 16, 2004, 10:17:33
Job time : 50 secs

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 26

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 ; Search time 23 Seconds

(without alignments)
918.044 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109
Sequence: 1 MEGESTSAVLGSGFVGLALAF.....TDEIEIKMKGFGEYSRSPTE 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents Aa.*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778	36.9	151	4	US-09-621-976-3917
2	122	5.8	1087	4	US-09-914-259-12
3	122	5.8	2482	1	US-08-328-254-6
4	122	5.8	3248	1	US-08-353-700-1
5	122	5.8	3248	5	PCT-US95-16216-1
6	111.5	5.3	1038	4	US-08-334-179A-2
7	111.5	5.3	1038	4	US-09-908-500A-2
8	111	5.3	1972	4	US-08-875-435B-4
9	110.5	5.2	1038	3	US-09-541-782-4
10	110.5	5.2	1038	4	US-09-723-820-4
11	110.5	5.2	1038	4	US-10-270-085-4
12	110	5.2	530	4	US-08-979-608A-8
13	110	5.2	530	4	US-09-517-849-8
14	110	5.2	530	4	US-09-616-289-8
15	110	5.2	546	4	US-09-616-289-8
16	109.5	5.2	1038	4	US-08-334-179A-8
17	109	5.2	1972	4	US-08-875-435B-3
18	108.5	5.1	1257	4	US-08-049-783-2
19	108.5	5.1	1257	1	US-08-158-232-6
20	108.5	5.1	1257	1	US-08-304-625-6
21	108.5	5.1	1257	1	US-08-316-301A-6
22	108.5	5.1	1257	2	US-08-611-928-6
23	108.5	5.1	1257	3	US-09-173-891-6
24	108.5	5.1	1257	3	US-09-076-137-6
25	108.5	5.1	1257	3	US-09-738-363-6
26	108.5	5.1	1257	5	PCT-US92-03624-6
27	108.5	5.1	2652	4	US-09-595-684B-31

28	108	5.1	557	4	US-08-979-608A-5	Sequence 5, Appl1
29	108	5.1	557	4	US-09-517-849-5	Sequence 5, Appl1
30	108	5.1	557	4	US-09-616-289-5	Sequence 5, Appl1
31	108	5.1	2954	4	US-09-150-867-1	Sequence 1, Appl1
32	106.5	5.0	558	1	US-08-285-440-6	Sequence 6, Appl1
33	106.5	5.0	558	1	US-08-330-349-6	Sequence 6, Appl1
34	106.5	5.0	1111	4	US-09-914-259-28	Sequence 28, Appl1
35	105.5	5.0	582	4	US-08-334-179A-4	Sequence 4, Appl1
36	105.5	5.0	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
37	105.5	5.0	1251	3	US-09-080-855-2	Sequence 2, Appl1
38	105.5	5.0	1251	4	US-09-566-076-2	Sequence 2, Appl1
39	105.5	5.0	3878	4	US-09-914-259-11	Sequence 11, Appl1
40	105	5.0	352	4	US-09-543-681A-6618	Sequence 6618, Ap
41	105	5.0	1969	4	US-09-418-710-72	Sequence 72, Appl1
42	105	5.0	1972	4	US-09-418-710-21	Sequence 21, Appl1
43	104.5	5.0	2329	3	US-08-755-587-16	Sequence 16, Appl1
44	104.5	5.0	3418	2	US-08-639-501-2	Sequence 2, Appl1
45	104.5	5.0	3418	2	US-08-603-753D-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-621-976-3917
Sequence 3917, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OR INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621, 976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3917
LENGTH: 151
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
US-09-621-976-3917

Query Match 36.9%; Score 778; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGESTSAVLGSGFVGLALAFQHLNTSDTEGFLGVEYKSAKNSITDSQMDVEVYTTID	60
DB	1	MEGESTSAVLGSGFVGLALAFQHLNTSDTEGFLGVEYKSAKNSITDSQMDVEVYTTID	60
QY	61	IQRTIPCYOLFSEYNSGSEVNEQALKILSNVKKNVGWYKFRHSDQITPFRRLHKX	120
DB	61	IQRTIPCYOLFSEYNSGSEVNEQALKILSNVKKNVGWYKFRHSDQITPFRRLHKX	120
QY	121	LOEHFSNODLVFLTPSITTESCSTRLEH	151
DB	121	LOEHFSNODLVFLTPSITTESCSTRLEH	151

RESULT 2
US-09-914-259-12
Sequence 12, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999

CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1087
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-914-259-12

Query Match
Best Local Similarity 19.8%; Score 122; DB 4; Length 1087;
Pred. No. 0.024; Indels 94; Gaps 13;
Matches 68; Conservative 59; Mismatches 122;

79 EVNEQALKKILSNVKNVGVYKFRHSDQIMTFRRRLAKNVLQEHFNSODLVFLLLTPS 138
205 EVQLQERDAIDRKEKEITNL-----EQLEQFRELELNKKEEVQLHMQLE----- 251
139 ITTESGSTRLL-----EHSLYPKQKGLFHRVPLVYANLGMSSQLGYKTVSGSCMSTGFSR 193
252 -IQKESTTRLOELEGENKLFKDE-----MKTGFALKESDAVSPDQO 294
194 AVQTHSSKFEEDGSLKEVHKINEMVYASIQEELKSIQKVEDSEQAVDKLVQVNRKRE 253
295 VIFGKFAQIHE--KEVELDRLEQIILKQQLKITD-----KVTLEKKELLRD 343
254 IEXRGAQIQV--AREKNIQKPOENIFLCALRTFFPENSEFLHSCVMSLKNR----- 304
344 LE---AQIECLMSDQERVRKREBEI-----EQINLVIEKLOQELANIDOK 386
305 -----HVKSSCNVNHLDVVDNLTLMVEH--TDIPEASPASTPQIIRKALDDLD----- 353
387 TSWDPSLSLEBDSLKHQDLKVIKTAELALEHOVETTNEMATKXVLKETNKVMQLTOE 446
354 -----RWQFKSRLLDTQDKRSKANTGSSNQKASRMSSPETD 391
447 LSLKRREREMERIQSVPEKSVMSVGDLSKDK-----PEWD 483

RESULT 3
US-08-328-254-6
Sequence 6, Application US/08328254
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CU 1191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-254-6

Query Match
Best Local Similarity 20.7%; Score 122; DB 1; Length 2482;
Pred. No. 0.081;
Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;

36 EVKGEAKNS-ITDSQMDVVEVYITDIQYI-----PCYQFSPYNSGGEVNEQALKKI 88
185 EADQSPKNSAILONRYDSLK--FSLSQKMSDLOKQCEELVQI--KGEIENLMK-- 237
89 LSNVKNVGVYKFRHSDQIMTFRE--RLHKVNLQEH--FENODLVFLLLTPSITTES 143
238 AEQMHQSFWA-----ETSQRIKQLQEDTSAHQVVAETLSALENKEKQLDLNDKYEETQ 292
144 C-----STHRLHSLYKQKGLFHRVPLVYANLGMSSQLGYKTVSGSCMSTGFSRAVQ 196
293 AEIQELKSNHLLSDSLKEHQL-----LSETLSEKKEKMSIISLNKREIE 338
197 THSKFEEDGSLKEVHKINEMVYASIQEELKSIQKVEDSEQAVDKLVQVNRKREIEK 256
339 ---ELQENGTLKEIN-----ASLNQEKNNLIQSESFANYIDERSKISLSQYKQ 388
257 RRGAIQVAREK-NIQKPOENIFLCALRTFFPENSE--FLHSCVMSLKNRHYSSCN 312
389 EKILLQRCGETGNAVEDLSQYKAAQ-----KNSKLECLINECTSLCENRANELEQLK 443
313 ---YNNHLDVVDNLTLMVEHTDIPKASPASTPQIIRKALDDLDNRQFRSRLLDQDKR 369
444 EAPAKEHQEFLTKLAPAEEN-----QNLMLLETVOALRSEMTDQON-N 488
370 SKANTGSSNQ-----DKASKMSSPETD--EEIEKM 397
489 SKSEAGGLKQELMTLKEQNKMKQKVEDLQENQEL 524

RESULT 4
US-08-353-700-1
Sequence 1, Application US/08353700
Patent No. 5599919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE:

TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
US-08-353-700-1

Query Match 5.8%; Score 122; DB 1; Length 3248;
Best Local Similarity 20.7%; Pred. No. 0.12;
Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;

36 EVKGEAKNS-ITDSQMDVVEVYTTIDQYI-----PCYOLFSPYNSGGEVNEQALKKI 88
817 EADSPKNSAIIQNRVDSLE--FSLESQKQMSDLDQKCEELVQI--KGEIENLMK-- 869
89 LSNVKNVGVYKFRHRSQDQIMTFRE-RLAHKQLQEH---FSNODLVFLILTPSITTES 143
870 AEQHQSFVA-----ETSORISKLOEDTSAHQNVVAETLSALBNKEKEQLDLNDKYTEQ 924
144 C-----STHRLHSLYKQKGLFHRVPLVAVNLGMSQDQKTVSGSCMSTGSPRAVQ 196
925 AEIQELKSNHLLBDSLKELQI-----LSETLSLEKEMSSITSLNKRRIE 970
197 THSKFEEDSLKEVHKINEMVYASIQEELKSIKCKVEDESOAVDKLVQVNLKREIEK 256
971 ----ELTQENGTLKEIN-----ASLNQEKMLIQKSESPANYIDEREKSISELSDQYKQ 1020
257 RRGQIQAREK-NIQDPOENIFLCQALRTFFPNS---FLHSCVMSLKNRHVSSSCN 312
1021 EKLILQRCETGNAYEDLSQYKKAQE-----KNSKLECLINECTSLCENRQNELEQLK 1075
313 ----YNNHLDVVNLTLVNEHTDIPKASPASTPQIIRKALDLDDBQFRRSLDTPQDKR 369
1076 EAPAKHQEFLTKLAFABERN-----QNLMLLETVOQALRSEMTDNQ-N 1120
370 SKANTGSSNQ-----DKASKMSPEPTD--EEIEK 397
1121 SKSBAGLKQEIIMTLKEQNKQKQEVNDILOENEOL 1156

RESULT 5
PCT-US95-16216-1

Sequence 1, Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Ratner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochores Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-16216-1

Query Match 5.8%; Score 122; DB 5; Length 3248;
Best Local Similarity 20.7%; Pred. No. 0.12;
Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;

36 EVKGEAKNS-ITDSQMDVVEVYTTIDQYI-----PCYOLFSPYNSGGEVNEQALKKI 88
817 EADSPKNSAIIQNRVDSLE--FSLESQKQMSDLDQKCEELVQI--KGEIENLMK-- 869
89 LSNVKNVGVYKFRHRSQDQIMTFRE-RLAHKQLQEH---FSNODLVFLILTPSITTES 143
870 AEQHQSFVA-----ETSORISKLOEDTSAHQNVVAETLSALBNKEKEQLDLNDKYTEQ 924
144 C-----STHRLHSLYKQKGLFHRVPLVAVNLGMSQDQKTVSGSCMSTGSPRAVQ 196
925 AEIQELKSNHLLBDSLKELQI-----LSETLSLEKEMSSITSLNKRRIE 970
197 THSKFEEDSLKEVHKINEMVYASIQEELKSIKCKVEDESOAVDKLVQVNLKREIEK 256
971 ----ELTQENGTLKEIN-----ASLNQEKMLIQKSESPANYIDEREKSISELSDQYKQ 1020
257 RRGQIQAREK-NIQDPOENIFLCQALRTFFPNS---FLHSCVMSLKNRHVSSSCN 312
1021 EKLILQRCETGNAYEDLSQYKKAQE-----KNSKLECLINECTSLCENRQNELEQLK 1075
313 ----YNNHLDVVNLTLVNEHTDIPKASPASTPQIIRKALDLDDBQFRRSLDTPQDKR 369
1076 EAPAKHQEFLTKLAFABERN-----QNLMLLETVOQALRSEMTDNQ-N 1120
370 SKANTGSSNQ-----DKASKMSPEPTD--EEIEK 397
1121 SKSBAGLKQEIIMTLKEQNKQKQEVNDILOENEOL 1156

RESULT 6
US-08-334-179A-2

Sequence 2, Application US/08334179A
Patent No. 6306622
GENERAL INFORMATION:
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: NOHNO, TSUTOMU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11810 EAST MIAHT RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: US
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,179A
FILING DATE: 04-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONSTANCE, BEAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5473
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-2858
TELEFAX: 513-627-0260
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-334-179A-2

```

```

Query Match      5.3%; Score 111.5; DB 4; Length 1038;
Best Local Similarity 19.3%; Pred. No. 0.21;
Matches 100; Conservative 66; Mismatches 147; Indels 205; Gaps 22;

QY 5 STSAVLGFLGALAFQHLNTSDTEGFLGEGVKGAKNSITDSQMDVYVYTIIDIKY 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 SYLAIVL-----IVALCTGYRMLTGDRKQGLHSMNMMEALASPSLDLNLKLELIGRGY 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 IPCY-----QLFSFYNSGGEVNEQALKTI-----LSNYKKNVGVYKFRHSDDI 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 GAVYKGLSDERPVAVKVFSPANRQNFINEKNIYRVFLMEHDNIARFIVG-----DER 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 MTPRERLHKNLQEHNSNOLV--FILLTPSIITSGSTRLEHSL----- 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 VTADGRMEYLLVMEYIPNSGLCKYLSLHTSDWVSSC--RLASVTRGLAYHTELPGRD 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 154 -YKPKGLFHRVPLVVAANLGMSEOLGYKTV-----SGSCMSTGFSRAVQTHSKPF-----E 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 HYKP--AISHR-----DLNSRNVLVKNGDQCVISDPGLSMRLTGNRLVPRGEE 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 EDGSLKEVHKINEMVSLQE-----ELKSLCKYKVE----- 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 370 DNAAISEVGTIRYMADEVLEGAVNLRCBSALKQVDMVALGLIYWEIFNRCITDLFPGESEV 429
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 -----DSEQAVDKLVKDVN----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 430 PEYQMAFQTEVGNHPTFEDMQVLVSRKQRPKPEAKMKENSLAVRLKETIEDCWDQDAE 489
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -RLKREIERKRGAIQIQAAREKTIQKDPQENIFLCALRTFFPNSEFLHSCVMSLKNRAYS 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 ARLTAQCAERMAELMWIRKNSVSPVYN-----PMSTAMQENRNL-----HNRKVP 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 K-----SSCNV-----NHLD--VVDNLTLMVHTDIPKASPASTPQIIKHKALDLDDRW 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 KIGPYDYSSSYIEDSIHTDSIVKNIS-----SEHMSNSTLTLTIGK----- 582
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 356 QPKRSRLDTPQDKRSKANTGSSN---QDKASKMSPEPT 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 583 -----NNSINRYERQAQARIPSPET 603
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 7
US-08-908-500A-2
Sequence 2, Application US/09908500A
Patent No. 6642002
GENERAL INFORMATION:
APPLICANT: James Loyd
APPLICANT: Kirk B. Lane
APPLICANT: John A. Phillips, III
TITLE OF INVENTION: METHOD OF DIAGNOSING PULMONARY
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 22000.010803
CURRENT APPLICATION NUMBER: US/09/908,500A

```

```

CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 60/218,740
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/220,133
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1038
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-908-500A-2

```

```

Query Match      5.3%; Score 111.5; DB 4; Length 1038;
Best Local Similarity 19.3%; Pred. No. 0.21;
Matches 100; Conservative 66; Mismatches 147; Indels 205; Gaps 22;

QY 5 STSAVLGFLGALAFQHLNTSDTEGFLGEGVKGAKNSITDSQMDVYVYTIIDIKY 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 SYLAIVL-----IVALCTGYRMLTGDRKQGLHSMNMMEALASPSLDLNLKLELIGRGY 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 IPCY-----QLFSFYNSGGEVNEQALKTI-----LSNYKKNVGVYKFRHSDDI 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 GAVYKGLSDERPVAVKVFSPANRQNFINEKNIYRVFLMEHDNIARFIVG-----DER 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 MTPRERLHKNLQEHNSNOLV--FILLTPSIITSGSTRLEHSL----- 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 VTADGRMEYLLVMEYIPNSGLCKYLSLHTSDWVSSC--RLASVTRGLAYHTELPGRD 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 154 -YKPKGLFHRVPLVVAANLGMSEOLGYKTV-----SGSCMSTGFSRAVQTHSKPF-----E 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 HYKP--AISHR-----DLNSRNVLVKNGDQCVISDPGLSMRLTGNRLVPRGEE 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 EDGSLKEVHKINEMVSLQE-----ELKSLCKYKVE----- 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 370 DNAAISEVGTIRYMADEVLEGAVNLRCBSALKQVDMVALGLIYWEIFNRCITDLFPGESEV 429
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 -----DSEQAVDKLVKDVN----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 430 PEYQMAFQTEVGNHPTFEDMQVLVSRKQRPKPEAKMKENSLAVRLKETIEDCWDQDAE 489
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -RLKREIERKRGAIQIQAAREKTIQKDPQENIFLCALRTFFPNSEFLHSCVMSLKNRAYS 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 ARLTAQCAERMAELMWIRKNSVSPVYN-----PMSTAMQENRNL-----HNRKVP 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 K-----SSCNV-----NHLD--VVDNLTLMVHTDIPKASPASTPQIIKHKALDLDDRW 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 KIGPYDYSSSYIEDSIHTDSIVKNIS-----SEHMSNSTLTLTIGK----- 582
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 356 QPKRSRLDTPQDKRSKANTGSSN---QDKASKMSPEPT 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 583 -----NNSINRYERQAQARIPSPET 603
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 8
US-08-875-435B-4
Sequence 4, Application US/08875435B
Patent No. 6593304
GENERAL INFORMATION:
APPLICANT: Haesegawa, Kazuhide
APPLICANT: Arahawa, Eml
APPLICANT: Oda, Shoji
APPLICANT: Matsuda, Yuzuru
APPLICANT: Takahashi, Katsuhito
APPLICANT: Sugahara, Michihito
APPLICANT: Ishiyama, Haruo
TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
TITLE OF INVENTION: VECTOR DNA, MICROORGANISM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
FILE REFERENCE: 07898-013001
CURRENT APPLICATION NUMBER: US/08/875,435B

```

```

: CURRENT FILING DATE: 1997-07-25
: PRIOR APPLICATION NUMBER: PCT/JP96/00134
: PRIOR FILING DATE: 1996-01-25
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 1972
: TYPE: PRT
: ORGANISM: Oryctolagus cuniculus
: OS-08-875-435B-4

```

Query Match	Score	DB	Length
5.3%;	111;	4;	1972;
17.8%;	90;	0;	0;

[illegible]

```

RESULT 9
US-09-541-782-4
Sequence 4, Application US/03541782
Patient No. 6284480
GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Betaud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FaalSeq for Windows Version 4.0.0
SEQ ID NO: 4
LENGTH: 1038
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-541-782-4

```

```

Query Match: 5.2%; Score 110.5; DB 3, Length 1038;
Best local similarity 20.1%; Pred. No. 0.267;
Matches 76; Conservative 67; Mismatches 139; Indels 97; Gaps 18;

QY      21  CHLNDSTGEFLGVGVGAKNSITDSQDVP-----EYVYTIIDIOKTYPCQLSFSF--- 73
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
      360  QEFHITNMEGNTLQ-KGLKHROVASITKNDDSSRHTPTITLYKKHQ-DELFRISKM 417
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
OY      74  -----YNSGVEVNEQA-----LKLITLSNVKKNVGVWYKFRHSDQIITFERLLH 118

```

[illegible]

```

RESULT 10
US-09-723-820-4
; Sequence 4, Application US/09723820
; Patent No. 6468760
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sawicz, Roman
; APPLICANT: Beroud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/723,820
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-723-820-4

```

[illegible]

QY 310 SCNYNHLDPVDN--LTLN 326
DB 696 ETNIGPNLDMIKNEVLTLN 714

RESULT 11

US-10-270-085-4
Sequence 4, Application US/10270085
Patent No. 6627408
GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Bernard, Christophe
TITLE OF INVENTION: Antifungal Aseay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/10/270,085
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1038
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-270-085-4

Query Match 5.2%; Score 110.5; DB 4; Length 1038;
Best Local Similarity 20.1%; Pred. No. 0.26;
Matches 76; Conservative 67; Mismatches 139; Indels 97; Gaps 18;

QY 21 QHNTSDPTBGLGVEKGEAKNSITDSQMDV---EYVYTIIDIOKXIPCYQLSPF--- 73
DB 360 QEHITNMEGMLNLLD-KGLKRRQVASTKNDPSSRSHITFTITLYKKHQ-DELRISKY 417
QY 74 ---YNSGGEVNEQA---LKKILSNVKNVGVYKFRHSQDQMTFRRLH 118
DB 418 NIVDLASERINSGALNQRKAGSINSLSLIGVINALVDKSH---IPFRESKLT 473
QY 119 KNIQEHPSNODLVFLILT--PSITT--EESCT---HRLHSLYKPKGLFHRVPLVYAN 170
DB 474 RLIDQSDIGNTKTLATISPAKYTSEETCSTLEVASKAKNIKPKQLGSFTMKDILVKN 533
QY 171 LGM-----SEOLGYTVSGSCMSTGFSRAVOTHSKFEEDGSLK-EVHKINEMYASL- 222
DB 534 ITHELAKISDLSLTSKSGIYSDHYKNINSDLSEYNGVOECKREIESLTSKALLV 593
QY 223 QEELKSI CKKVEDSEAVDKLVQDVNRLKREIEKRRGAQIOAREKN-IOKDPQENIFLC 281
DB 594 KDKLKS-KETIQSONCQIESLKTITIDLPALDKCHKEIEISDFNNKLQK----- 643
QY 282 QALRTFEPNSEFHSQVMSLKNR-----HVSK-----S 309
DB 644 -----LTEVQWALHDYKKEELDNLQKFEKHITKIKLSITFLQJLNTMOQESLIQ 695
QY 310 SCNYNHLDPVDN--LTLN 326
DB 696 ETNIGPNLDMIKNEVLTLN 714

RESULT 12

US-08-979-608A-8
Sequence 8, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NOV-2000 6355451-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-979-608A-8
Query Match 5.2%; Score 110; DB 4; Length 530;
Best Local Similarity 18.7%; Pred. No. 0.11;
Matches 56; Conservative 62; Mismatches 118; Indels 64; Gaps 12;

QY 1 MEGESTSAVTSGLYALAA--FOHNTSDPTBGLGVEKGEAKNSITDS---QMDVEY 55
DB 211 LRGEHSRAVLARSKLTLELRELQHNRSLSKEGVQAREEERKREKVTSHFOYTLNDIQL 270
QY 56 VYTIIDIOKXIPCYQLSFEYNSGGEVNEQA-LKKILSNVKNVGVYKFR-RHSQDQMTFRE 114
DB 271 -----QMEHNRNRSKLRQENNE--LAERLKLIIQYELREHIDKVRK--- 312
QY 115 RLHKNIQEHPSNODLVFLITPSITTESCTRLHSLYKPKGLFHRVPLVYANLIGMS 174
DB 313 ---HKDLQOQILDVAK---LQQAQEMLKEAERQRKEDFLKKE-----AVEQQRMC 357
QY 175 EQLGYTVSGSCMSTGFSRAVOTHSKFEEDGSLKEVHKINEMYASLOELKSI CKVE 234
DB 358 ELNKKQO-----ETHKQQLALYTEKFEFOYTLN---KSSVFTTFKQEMKMKTKIK 407
QY 235 DSEQAVDKLVQDVNRLKREIEKRRGAQIOAREKNIOKDPQENI-----FLQQLART 286
DB 408 -----KLREKETTMRSRWESSNKKALLEVAEKETVRDKELQGLQVYIQRLKLCRALQT 460

RESULT 13

US-09-517-849-8
Sequence 8, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:15 ; Search time 59 seconds

(without alignments)
1958.677 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109
Sequence: 1 MEGESTSAVLGFGVIGALAF.....TDEIEKMGKGFGRSPTF 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2109	100.0	409	3	AAy66666 Membrane-
2	2109	100.0	409	4	AAU29090 Human PRO
3	2109	100.0	409	4	AAAB7536 Human PRO
4	2109	100.0	409	4	AAAB5189 Human PRO
5	2109	100.0	409	5	ABG95861 Human sec
6	2109	100.0	409	6	ABUS8466 Human PRO
7	2109	100.0	409	6	ABUS8804 Novel hum
8	2109	100.0	409	6	ABU84329 Human sec
9	2109	100.0	409	6	ABR66203 Human sec
10	2109	100.0	409	6	ABR55953 Human sec
11	2109	100.0	409	6	ABU99533 Human PRO
12	2109	100.0	409	6	ABUS5802 Novel hum
13	2109	100.0	409	6	ABUS5902 Human sec
14	2109	100.0	409	6	ABUS2554 Human sec
15	2109	100.0	409	6	ABUS2554 Human sec
16	2109	100.0	409	6	ABUS2772 Human PRO
17	2109	100.0	409	6	ABUS8953 Novel hum
18	2109	100.0	409	6	ABR68142 Human sec
19	2109	100.0	409	6	ABU96195 Novel hum
20	2109	100.0	409	6	ABUS2626 Human sec
21	2109	100.0	409	6	ABUS2626 Human sec
22	2109	100.0	409	6	ABO02755 Human sec
23	2109	100.0	409	6	ABR74909 Human sec
24	2109	100.0	409	6	ABR94671 Human sec
25	2109	100.0	409	6	ABU13895 Human PRO

26	2109	100.0	409	6	ABUS5644 Human PRO
27	2109	100.0	409	6	ABUS8804 Novel hum
28	2109	100.0	409	6	ABU98019 Novel hum
29	2109	100.0	409	6	ABU91725 Novel hum
30	2109	100.0	409	6	ABUS9418 Human PRO
31	2109	100.0	409	6	ABUS6259 Human sec
32	2109	100.0	409	6	ABUS7472 Human sec
33	2109	100.0	409	6	ABUS0500 Human PRO
34	2109	100.0	409	6	ABU72460 Novel hum
35	2109	100.0	409	6	ABU90866 Human sec
36	2109	100.0	409	6	ABO33945 Human sec
37	2109	100.0	409	6	ABR99418 Human sec
38	2109	100.0	409	6	ABR98808 Human sec
39	2109	100.0	409	6	ABO16331 Human sec
40	2109	100.0	409	6	ABR92231 Human sec
41	2109	100.0	409	6	ABO18872 Human sec
42	2109	100.0	409	6	ABR78293 Human sec
43	2109	100.0	409	6	ABU71962 Novel hum
44	2109	100.0	409	6	ABUS5029 Novel hum
45	2109	100.0	409	6	ABO00168 Novel hum

ALIGNMENTS

RESULT 1					
AAy66666	AAy66666 standard; protein; 409 AA.				
ID	AAy66666				
XX	AAy66666				
AC	AAy66666				
DT	05-APR-2000 (first entry)				
XX	05-APR-2000				
DE	Membrane-bound protein PRO1013.				
XX	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;				
KW	pharmaceutical; receptor immunoadhesin; gene mapping.				
XX					
OS	Homo sapiens.				
XX					
PN	WO9963088-A2.				
XX					
PD	09-DEC-1999.				
XX					
PF	02-JUN-1999;	99WO-US012252.			
XX					
PR	02-JUN-1998;	98US-0087607P.			
PR	02-JUN-1998;	98US-0087609P.			
PR	02-JUN-1998;	98US-0087759P.			
PR	03-JUN-1998;	98US-0087827P.			
PR	04-JUN-1998;	98US-0088021P.			
PR	04-JUN-1998;	98US-0088025P.			
PR	04-JUN-1998;	98US-0088028P.			
PR	04-JUN-1998;	98US-0088032P.			
PR	04-JUN-1998;	98US-0088033P.			
PR	04-JUN-1998;	98US-0088032P.			
PR	04-JUN-1998;	98US-0088326P.			
PR	05-JUN-1998;	98US-0088167P.			
PR	05-JUN-1998;	98US-0088202P.			
PR	05-JUN-1998;	98US-0088212P.			
PR	05-JUN-1998;	98US-0088217P.			
PR	05-JUN-1998;	98US-0088655P.			
PR	09-JUN-1998;	98US-0088722P.			
PR	10-JUN-1998;	98US-0088730P.			
PR	10-JUN-1998;	98US-0088734P.			
PR	10-JUN-1998;	98US-0088738P.			
PR	10-JUN-1998;	98US-0088740P.			
PR	10-JUN-1998;	98US-0088741P.			
PR	10-JUN-1998;	98US-0088742P.			
PR	10-JUN-1998;	98US-0088810P.			
PR	10-JUN-1998;	98US-0088811P.			
PR	10-JUN-1998;	98US-0088824P.			
PR	10-JUN-1998;	98US-0088825P.			

PR	10-JUN-1998	9.8US-00888826P	9.8US-00888826P
PR	11-JUN-1998	9.8US-00888859P	9.8US-00888859P
PR	11-JUN-1998	9.8US-00888611P	9.8US-00888611P
PR	11-JUN-1998	9.8US-00888632P	9.8US-00888632P
PR	11-JUN-1998	9.8US-0088876P	9.8US-0088876P
PR	12-JUN-1998	9.8US-00890090P	9.8US-00890090P
PR	12-JUN-1998	9.8US-0089105P	9.8US-0089105P
PR	16-JUN-1998	9.8US-00894402P	9.8US-00894402P
PR	16-JUN-1998	9.8US-00895112P	9.8US-00895112P
PR	16-JUN-1998	9.8US-00895114P	9.8US-00895114P
PR	17-JUN-1998	9.8US-00895332P	9.8US-00895332P
PR	17-JUN-1998	9.8US-00895388P	9.8US-00895388P
PR	17-JUN-1998	9.8US-00895928P	9.8US-00895928P
PR	17-JUN-1998	9.8US-00895939P	9.8US-00895939P
PR	17-JUN-1998	9.8US-0089600P	9.8US-0089600P
PR	17-JUN-1998	9.8US-00896533P	9.8US-00896533P
PR	18-JUN-1998	9.8US-00896601P	9.8US-00896601P
PR	18-JUN-1998	9.8US-00896907P	9.8US-00896907P
PR	18-JUN-1998	9.8US-00899088P	9.8US-00899088P
PR	19-JUN-1998	9.8US-00899447P	9.8US-00899447P
PR	19-JUN-1998	9.8US-00899448P	9.8US-00899448P
PR	19-JUN-1998	9.8US-00899522P	9.8US-00899522P
PR	22-JUN-1998	9.8US-0090246P	9.8US-0090246P
PR	22-JUN-1998	9.8US-00902522P	9.8US-00902522P
PR	22-JUN-1998	9.8US-00902542P	9.8US-00902542P
PR	23-JUN-1998	9.8US-0090349P	9.8US-0090349P
PR	23-JUN-1998	9.8US-00903555P	9.8US-00903555P
PR	24-JUN-1998	9.8US-00904229P	9.8US-00904229P
PR	24-JUN-1998	9.8US-00904331P	9.8US-00904331P
PR	24-JUN-1998	9.8US-00904335P	9.8US-00904335P
PR	24-JUN-1998	9.8US-0090444P	9.8US-0090444P
PR	24-JUN-1998	9.8US-00904452P	9.8US-00904452P
PR	24-JUN-1998	9.8US-00904612P	9.8US-00904612P
PR	24-JUN-1998	9.8US-00904722P	9.8US-00904722P
PR	24-JUN-1998	9.8US-00905335P	9.8US-00905335P
PR	24-JUN-1998	9.8US-00905388P	9.8US-00905388P
PR	24-JUN-1998	9.8US-0090557P	9.8US-0090557P
PR	24-JUN-1998	9.8US-0090576P	9.8US-0090576P
PR	25-JUN-1998	9.8US-0090678P	9.8US-0090678P
PR	25-JUN-1998	9.8US-0090688P	9.8US-0090688P
PR	25-JUN-1998	9.8US-00906903P	9.8US-00906903P
PR	25-JUN-1998	9.8US-0090691P	9.8US-0090691P
PR	25-JUN-1998	9.8US-0090694P	9.8US-0090694P
PR	25-JUN-1998	9.8US-0090695P	9.8US-0090695P
PR	25-JUN-1998	9.8US-0090696P	9.8US-0090696P
PR	26-JUN-1998	9.8US-00908632P	9.8US-00908632P
PR	26-JUN-1998	9.8US-00908636P	9.8US-00908636P
PR	01-JUL-1998	9.8US-0091358P	9.8US-0091358P
PR	01-JUL-1998	9.8US-0091360P	9.8US-0091360P
PR	02-JUL-1998	9.8US-0091478P	9.8US-0091478P
PR	02-JUL-1998	9.8US-0091486P	9.8US-0091486P
PR	02-JUL-1998	9.8US-0091519P	9.8US-0091519P
PR	02-JUL-1998	9.8US-0091544P	9.8US-0091544P
PR	02-JUL-1998	9.8US-0091626P	9.8US-0091626P
PR	02-JUL-1998	9.8US-0091628P	9.8US-0091628P
PR	02-JUL-1998	9.8US-0091633P	9.8US-0091633P
PR	02-JUL-1998	9.8US-0091646P	9.8US-0091646P
PR	02-JUL-1998	9.8US-0091673P	9.8US-0091673P
PR	07-JUL-1998	9.8US-0091978P	9.8US-0091978P
PR	07-JUL-1998	9.8US-0091982P	9.8US-0091982P
PR	09-JUL-1998	9.8US-0092182P	9.8US-0092182P
PR	10-JUL-1998	9.8US-0092472P	9.8US-0092472P
PR	10-JUL-1998	9.8US-0093339P	9.8US-0093339P
PR	30-JUL-1998	9.8US-0094651P	9.8US-0094651P
PR	04-AUG-1998	9.8US-0095282P	9.8US-0095282P
PR	04-AUG-1998	9.8US-0095285P	9.8US-0095285P
PR	04-AUG-1998	9.8US-0095302P	9.8US-0095302P
PR			

```

YY      1 MEGESTSVLGGFVIGALAFQHLNLTDSPTBGFLLGEVVGKXNSITDSQMDDVEVVYTIID    60
DB      1 MEGESTSVLVGCVFVLGNALFPQHNLNTDSTBTBFLLGEVVGKXNSITDSQMDDVEVVYTIID    60

Query Match          100.0%; Score 2109; DB 3; Length 409;
Best Local Similarity 100.0%; Freq. No. 1,Se-175; Indels 0; Gaps 0;
Matches 409; Conservative 0; Mismatches 0;

XX      WPI: 2000-072883/06.
XX      DR N-PSDB; AAZ64999.
XX      PT Membrane-bound proteins and related nucleotide sequences.
XX      PS Claim 12; Fig 95; 822pp; English.
XX      CC The invention provides membrane-bound PRO polypeptides and
XX      CC polymucleotides encoding them. The PRO sequences of the invention were
XX      CC identified based on extracellular domain homology screening. The PRO
XX      CC sequences have homology with proteins including LDL receptors, TIE
XX      CC ligands and various enzymes. The membrane-bound proteins and receptor
XX      CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX      CC immunoadhesins, for instance, can be used as therapeutic agents to block
XX      CC receptor-ligand interactions. The membrane-bound proteins can also be
XX      CC employed for screening of potential peptide or small molecule inhibitors
XX      CC of the relevant receptor/ligand interaction. The PRO encoding sequences
XX      CC are useful as hybridization probes, in chromosome and gene mapping and in
XX      CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX      CC also be useful for the preparation of PRO polypeptides, especially by
XX      CC recombinant techniques
XX      SQ Sequence 409 AA;

PR 10-AUG-1998; 98US-0055329P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096339P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0086949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097218P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097651P.
PR 26-AUG-1998; 98US-0087951P.
PR 26-AUG-1998; 98US-0087952P.
PR 26-AUG-1998; 98US-0087952P.
PR 26-AUG-1998; 98US-0087954P.
PR 26-AUG-1998; 98US-0087955P.
PR 26-AUG-1998; 98US-0087971P.
PR 26-AUG-1998; 98US-0087974P.
PR 26-AUG-1998; 98US-0087978P.
PR 26-AUG-1998; 98US-0087979P.
PR 26-AUG-1998; 98US-0087986P.
PR 26-AUG-1998; 98US-0088014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX      PA (GETH ) GENENTECH INC.
XX      PI Baker K, Chan J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX      P1 Wood WI, Yuan J;
XX      XX WPI: 2000-072883/06.
XX      DR N-PSDB; AAZ64999.
XX      PT Membrane-bound proteins and related nucleotide sequences.
XX      PS Claim 12; Fig 95; 822pp; English.
XX      CC The invention provides membrane-bound PRO polypeptides and
XX      CC polymucleotides encoding them. The PRO sequences of the invention were
XX      CC identified based on extracellular domain homology screening. The PRO
XX      CC sequences have homology with proteins including LDL receptors, TIE
XX      CC ligands and various enzymes. The membrane-bound proteins and receptor
XX      CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX      CC immunoadhesins, for instance, can be used as therapeutic agents to block
XX      CC receptor-ligand interactions. The membrane-bound proteins can also be
XX      CC employed for screening of potential peptide or small molecule inhibitors
XX      CC of the relevant receptor/ligand interaction. The PRO encoding sequences
XX      CC are useful as hybridization probes, in chromosome and gene mapping and in
XX      CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX      CC also be useful for the preparation of PRO polypeptides, especially by
XX      CC recombinant techniques
XX      SQ Sequence 409 AA;


```

QY 61 IOKYIPCYQLFSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFERRLHKX 120
Db 61 IOKYIPCYQLFSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFERRLHKX 120
QY 121 LOEHFSNODLVFLLTPSITTESCTHRLHSLYKPKGLFHRVPLVYVANGMEQOLGYK 180
Db 121 LOEHFSNODLVFLLTPSITTESCTHRLHSLYKPKGLFHRVPLVYVANGMEQOLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOEELKSIKCKYDESEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOEELKSIKCKYDESEQAV 240
QY 241 DKLVDVNRLLKREIERKRGAOIQARREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVDVNRLLKREIERKRGAOIQARREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHSVSKSCNYNHLVDVNLTMVHTDIPKASPASTQIILKXALDDDDWQPKRS 360
Db 301 LKNRHSVSKSCNYNHLVDVNLTMVHTDIPKASPASTQIILKXALDDDDWQPKRS 360
QY 361 RLDDTQDKRSKANTGSSNODKASKMSPEDEBEIKMGKGFYSRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNODKASKMSPEDEBEIKMGKGFYSRSPTF 409
RESULT 2
AAU29090
ID AAU29090 standard; protein; 409 AA.
XX
AC AAU29090;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #67.
XX
KM PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186368P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192855P.
PR 29-MAR-2000; 2000US-0193032P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194499P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195875P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.

PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GENTH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR N-PSDB; AAS45991.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 11, Fig 134; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours, and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 409 AA;
Query Match 100.0%; Score 2109; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLISGVLALAFQHLNTSDPTEGFLIGVKEBAKNSINDSQMDVYVYTTID 60
Db 1 MEGESTSAVLISGVLALAFQHLNTSDPTEGFLIGVKEBAKNSINDSQMDVYVYTTID 60
QY 61 IOKYIPCYQLFSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFERRLHKX 120
Db 61 IOKYIPCYQLFSFYNSGGEVNEQALKKILSNVKNVGVWYKFRHSDQIMTFERRLHKX 120
QY 121 LOEHFSNODLVFLLTPSITTESCTHRLHSLYKPKGLFHRVPLVYVANGMEQOLGYK 180
Db 121 LOEHFSNODLVFLLTPSITTESCTHRLHSLYKPKGLFHRVPLVYVANGMEQOLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOEELKSIKCKYDESEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVYASLOEELKSIKCKYDESEQAV 240
QY 241 DKLVDVNRLLKREIERKRGAOIQARREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVDVNRLLKREIERKRGAOIQARREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300

QY 301 LKNRHVSKSCNYYNHLVDVNDLTLMEHTDIPEASPASTPQIIKHKALDLDNRQFKS 360
Db 301 LKNRHVSKSCNYYNHLVDVNDLTLMEHTDIPEASPASTPQIIKHKALDLDNRQFKS 360
QY 361 RLDTQDKRSKANTGSSNQDKASKMSSPTDEIEIKMGFGGEYSRPTF 409
Db 361 RLDTQDKRSKANTGSSNQDKASKMSSPTDEIEIKMGFGGEYSRPTF 409

RESULT 3

AAB87536
ID AAB87536 standard; protein; 409 AA.

AC AAB87536;

DT 15-MAY-2001 (first entry)

DE Human PRO1013.

KM Human; PRO protein; mapping.

OS Homo sapiens.

PN WO200116318-A2.

PD 08-MAR-2001.

PF 24-AUG-2000; 2000WO-US023328.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99US-0169495P.

PR 07-DEC-1999; 99US-0169495P.

PR 09-DEC-1999; 99US-0170262P.

PR 11-JAN-2000; 2000US-0175481P.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 01-MAR-2000; 2000WO-US005601.

PR 03-MAR-2000; 2000US-0187202P.

PR 21-MAR-2000; 2000US-0191007P.

PR 30-MAR-2000; 2000WO-US008439.

PR 25-APR-2000; 2000US-0199397P.

PR 22-MAY-2000; 2000WO-US014042.

PR 05-JUN-2000; 2000US-0209832P.

XX (GETH) GENENTECH INC.

XX PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CU, Gurney AL, Watanabe CK, Wood WI;

XX DR WPI; 2001-183260/18.

XX N-PSDB; AAF92068.

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

XX PT biology, including use as hybridization probes, and in chromosome and

XX PT gene mapping.

XX PS Claim 12; Fig 22; 278pp; English.

XX CC The present sequence is a human PRO polypeptide (secreted and

XX CC transmembrane) The PRO protein, and PRO agonists, PRO antagonists or

XX CC anti-PRO antibodies are useful for preparation of a medicament useful in

XX CC the treatment of a condition which is responsive to the PRO protein.

XX CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be

XX CC employed as molecular weight markers for protein electrophoresis. The PRO

XX CC coding sequence has applications in molecular biology, including use as

XX CC hybridisation probes, and in chromosome and gene mapping

XX CC Sequence 409 AA;

XX Query Match 100.0%; Score 2109; DB 4; Length 409;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-175; Indels 0; Gaps 0;

XX Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGFVIGALAFQHLNTSDTREGFLGEGYKGEAKNSITDSQMDVVEVYITD 60
Db 1 MEGESTSAVLGSGFVIGALAFQHLNTSDTREGFLGEGYKGEAKNSITDSQMDVVEVYITD 60
QY 61 IOKYICCYOLFSPYNSGGEVNEQALKILSNYKKNVGVYKFRHSDQINTERERLLHN 120
Db 61 IOKYICCYOLFSPYNSGGEVNEQALKILSNYKKNVGVYKFRHSDQINTERERLLHN 120
QY 121 LOHFENODIVFLITPSIITBSCTHRLHSHLYPOKGLFRRVPLVYANLQMSDGLYK 180
Db 121 LOHFENODIVFLITPSIITBSCTHRLHSHLYPOKGLFRRVPLVYANLQMSDGLYK 180
QY 181 TVSGSCMSTGFSFAVOTHSKPFEEBDSLKEVHKINEMVYASIQEELKSI CKVDESEQAV 240
Db 181 TVSGSCMSTGFSFAVOTHSKPFEEBDSLKEVHKINEMVYASIQEELKSI CKVDESEQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIQAAERKNIQKDPENIFLQALRTFFPNSSEFLHCVMS 300
Db 241 DKLVDVNRLLKREIEKRRGAQIQAAERKNIQKDPENIFLQALRTFFPNSSEFLHCVMS 300
QY 301 LKNRHVSKSCNYYNHLVDVNDLTLMEHTDIPEASPASTPQIIKHKALDLDNRQFKS 360
Db 301 LKNRHVSKSCNYYNHLVDVNDLTLMEHTDIPEASPASTPQIIKHKALDLDNRQFKS 360
QY 361 RLDTQDKRSKANTGSSNQDKASKMSSPTDEIEIKMGFGGEYSRPTF 409
Db 361 RLDTQDKRSKANTGSSNQDKASKMSSPTDEIEIKMGFGGEYSRPTF 409

RESULT 4

AAB65189
ID AAB65189 standard; protein; 409 AA.

AC AAB65189;

DT 02-APR-2001 (first entry)

DE Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.

XX Human; secreted and transmembrane protein; PRO; cytosatic; cell death;

XX KW cancer; chromosomal mapping; gene mapping; tissue typing;

XX OS diagnostic assay.

XX XX Homo sapiens.

XX PN WO200073454-A1.

XX PD 07-DEC-2000.

XX PF 30-MAR-2000; 2000WO-US008439.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 23-JUN-1999; 99US-0141037P.

XX PR 07-JUL-1999; 99US-0143048P.

XX PR 20-JUL-1999; 99US-0144758P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 28-JUL-1999; 99US-0146222P.

XX PR 17-AUG-1999; 99US-0149396P.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 08-OCT-1999; 99US-0158663P.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 16-DEC-1999; 99WO-US030095.

XX PR 20-DEC-1999; 99WO-US030911.

XX PR 05-JAN-2000; 2000WO-US000376.

XX PR 11-FEB-2000; 2000WO-US003365.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 24-FEB-2000; 2000WO-US004914.

XX PR 24-FEB-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841.
15-MAR-2000; 2000WO-US005884.
20-MAR-2000; 2000WO-US007377.
(GETH) GENENTECH INC.
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers I, Eaton DL;
Ferrara N, Fong S, Geher H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi CJ, Gurey AL, Kijavini IU, Napier MA, Pan U, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2001-032160/04.
N-PSDB; AAF44145.
PRO polynucleotides used to produce polypeptides used to target bioactive
molecules such as toxins, radiolabels or antibodies, to specific cells,
to cause targeted cell death.
Claim 12; Fig 95; 9359p; English.
The present invention describes human secreted and transmembrane PRO
protein. The PRO proteins have cytosolic activity. The PRO proteins can
be used for targeted delivery of bioactive molecules, such as toxins,
radiolabels or antibodies, that cause cell death. PRO nucleotide
sequences, and their fragments, can be used as hybridisation probes, in
chromosomal and gene mapping, and in the generation of anti-sense RNA and
DNA. They may also be used to produce transgenic animals which are used
to develop and screen therapeutically useful reagents. The PRO nucleotide
and protein sequence can be used for tissue typing and in treating
cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
AAF44470 represent PCR primers and hybridisation probes used in the
isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
AAF65300 represent human PRO polynucleotide and protein sequences given
in the exemplification of the present invention
Sequence 409 AA;
SQ
Query Match 100.0%; Score 2109; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1,5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESISATLSGVLGALAFQHLNDSDEGFLGHEVKEAENSTIDSQMDVEVYITD 60
DB 1 MEGESISATLSGVLGALAFQHLNDSDEGFLGHEVKEAENSTIDSQMDVEVYITD 60
QY 61 IQKIFCYOLFSPYSSGGEVNEQALKKISNVKXNVGVYKFRRSDDIMTFRERLAKN 120
DB 61 IQKIFCYOLFSPYSSGGEVNEQALKKISNVKXNVGVYKFRRSDDIMTFRERLAKN 120
QY 121 LOHFSNODLVPLLTPTSIITSCSTRLEHSLYKPKQLFHRVPLVYANLMSQOLGYK 180
DB 121 LOHFSNODLVPLLTPTSIITSCSTRLEHSLYKPKQLFHRVPLVYANLMSQOLGYK 180
QY 181 TVSGSGMSGTFSAVQVTHSSKPFEEBDSLKEYAKINEMVASQEBELKSCCKVESEQAV 240
DB 181 TVSGSGMSGTFSAVQVTHSSKPFEEBDSLKEYAKINEMVASQEBELKSCCKVESEQAV 240
QY 241 DKLVKDVNRLKEIEKRRGAQIOAAREKNIQKDPQENIFLCALRTFFPNSFFLHSCVMS 300
DB 241 DKLVKDVNRLKEIEKRRGAQIOAAREKNIQKDPQENIFLCALRTFFPNSFFLHSCVMS 300
QY 301 LKRRHVSASSCNVNHLDVVDNLTLMVEHTDIPEASPASTPOLIKHKLDDDRQPKRS 360
DB 301 LKRRHVSASSCNVNHLDVVDNLTLMVEHTDIPEASPASTPOLIKHKLDDDRQPKRS 360
QY 361 RLIDTODKSKANTGSSNODKASKVSSPTDEIEIKMKFGYSRSPTR 409
DB 361 RLIDTODKSKANTGSSNODKASKVSSPTDEIEIKMKFGYSRSPTR 409

ABG95861 standard; protein; 409 AA.
ABG95861;
10-DEC-2002 (first entry)
Human secreted/transmembrane protein PRO1013.
Human; secreted protein; transmembrane protein; antirheumatic;
antiarthritic; osteopathic; sports-related joint problem;
articular cartilage defect; osteoarthritis; rheumatoid arthritis.
Homo sapiens.
US2002119130-A1.
29-AUG-2002.
06-DEC-2001; 2001US-00006867.
29-OCT-1997; 97US-0063435P.
29-OCT-1997; 97US-0064215P.
22-APR-1998; 98US-0082737P.
29-APR-1998; 98US-0083495P.
15-MAY-1998; 98US-0085579P.
02-JUN-1998; 98US-0087759P.
04-JUN-1998; 98US-0088021P.
04-JUN-1998; 98US-0088030P.
10-JUN-1998; 98US-0088734P.
10-JUN-1998; 98US-0088740P.
10-JUN-1998; 98US-0088811P.
10-JUN-1998; 98US-0088824P.
10-JUN-1998; 98US-0088825P.
11-JUN-1998; 98US-0088863P.
12-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089653P.
19-JUN-1998; 98US-0089952P.
22-JUN-1998; 98US-0090246P.
24-JUN-1998; 98US-0090444P.
25-JUN-1998; 98US-0090688P.
25-JUN-1998; 98US-0090689P.
26-JUN-1998; 98US-0090862P.
02-JUL-1998; 98US-0091628P.
10-AUG-1998; 98US-0096012P.
17-AUG-1998; 98US-0096757P.
18-AUG-1998; 98US-0096949P.
18-AUG-1998; 98US-0096959P.
26-AUG-1998; 98US-0097954P.
26-AUG-1998; 98US-0097971P.
26-AUG-1998; 98US-0097979P.
01-SEP-1998; 98US-0098749P.
10-SEP-1998; 98US-0099741P.
10-SEP-1998; 98US-0099763P.
10-SEP-1998; 98US-0099792P.
10-SEP-1998; 98US-0099812P.
10-SEP-1998; 98US-0099815P.
16-SEP-1998; 98US-0100627P.
16-SEP-1998; 98US-0100662P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100683P.
17-SEP-1998; 98US-0100684P.
17-SEP-1998; 98US-0100930P.
22-SEP-1998; 98US-0101279P.
23-SEP-1998; 98US-0101475P.
24-SEP-1998; 98US-0101738P.
24-SEP-1998; 98US-0101743P.
24-SEP-1998; 98US-0101916P.
30-SEP-1998; 98US-0102570P.
06-OCT-1998; 98US-0103449P.
08-MAR-1999; 99WO-US005028.
14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021099.
 PR 15-SEP-1999; 99WO-US021199.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 (GENT) GENENTECH INC.
 Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
 MPI: 2002-731348/79.
 N-PSDB; AB674388.
 New isolated secreted and transmembrane PRO polypeptide useful for
 modulating biological activity of a cell, or for treating sports-related
 joint problems, osteoarthritis or rheumatoid arthritis.
 Claim 20; Fig 22; 399pp; English.
 The invention relates to an isolated secreted and transmembrane PRO
 polypeptide having 80 + sequence identity to a sequence appearing as
 ABG5851-ABG59334 or their associated signal peptide, or a sequence of an
 extracellular domain of the proteins with their associated signal peptide
 or lacking its associated signal peptide. Also included are the nucleic
 acids encoding the proteins, vectors, host cells, fusion proteins and
 antibodies which specifically bind to the proteins. The proteins are
 useful for detecting a polypeptide designated as A, B, C or D in a sample
 suspected of containing A, B, C or D polypeptide, by contacting the
 sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 conjugate in the sample, where the formation of the conjugate is
 indicative of the presence of an A, B, C or D polypeptide in the sample,
 where A is a PRO10772 polypeptide, B is a PRO20110 polypeptide, C is a
 PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 H or I polypeptide is labeled with a detectable label or is attached to a
 solid support. The proteins are useful for linking a bioactive molecule
 to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 H or I. The bioactive molecule is a toxin, a radiolabel, or an antibody.
 The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 or I, or antibodies against them are useful for modulating a biological
 activity of a cell expressing a polypeptide designated as A, B, C or D or
 E, F, G, H, or I. The cell is killed. The proteins are useful for
 identifying agonists or antagonists, for the preparation of a medicament
 useful in the treatment of a condition which is responsive to the
 proteins, as molecular weight markers for protein electrophoresis
 purposes, and as therapeutic agents for treating sports-related joint
 problems, articular cartilage defects, osteoarthritis or rheumatoid
 arthritis. Nucleic acids encoding the proteins are useful as
 hybridisation probes, in chromosome and gene mapping, in the generation
 of anti-sense RNA and DNA, for the preparation of the proteins, to

CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention.
 CC
 CC
 XX Sequence 409 AA;
 SQ
 Query Match 100.0%; Score 2109; DB 5; Length 409;
 Best Local Similarity 100.0%; Pred No. 1.5e-175;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEGESTSAVLGSGFVLGALAFQHLNTDSDTEGFLGSGKEAKNSITDSQMDVEVYTTD 60
 Db 1 MEGESTSAVLGSGFVLGALAFQHLNTDSDTEGFLGSGKEAKNSITDSQMDVEVYTTD 60
 QY 61 IQKTIPTCYQLFSFYNSGSEVNEQALKKILSNYKQNVGVYKFFRHSDDQMTFRERLLHKX 120
 Db 61 IQKTIPTCYQLFSFYNSGSEVNEQALKKILSNYKQNVGVYKFFRHSDDQMTFRERLLHKX 120
 QY 121 LOEHFSNQDVLVFLITPSITTESCSTRLEHSLYKPOKGLFRRVPLVYVNLGNSQLGYK 180
 Db 121 LOEHFSNQDVLVFLITPSITTESCSTRLEHSLYKPOKGLFRRVPLVYVNLGNSQLGYK 180
 QY 181 TVSGSCMSTGSPRAVQTHSKFEEPDGSLKEVYKINEMVASLOELKSTCKYEDSEQAV 240
 Db 181 TVSGSCMSTGSPRAVQTHSKFEEPDGSLKEVYKINEMVASLOELKSTCKYEDSEQAV 240
 QY 241 DKLVDVNRLLKRELEKRGAGQIQAREKNIQKPOENIFLQALRTFFPNSSEJHSQVMS 300
 Db 241 DKLVDVNRLLKRELEKRGAGQIQAREKNIQKPOENIFLQALRTFFPNSSEJHSQVMS 300
 QY 301 LKNRHSKSSCNTNHLVDVNTLTVEHTDITBASPASTPQIIKKKALDIDRMQFKRS 360
 Db 301 LKNRHSKSSCNTNHLVDVNTLTVEHTDITBASPASTPQIIKKKALDIDRMQFKRS 360
 QY 361 RLIDTQKRSKANTGSSNQDKASMSPEETDEIEKKAGGEYSRSPTE 409
 Db 361 RLIDTQKRSKANTGSSNQDKASMSPEETDEIEKKAGGEYSRSPTE 409
 RESULT 6
 ID ABUS8466 standard; protein: 409 AA.
 XX
 AC ABUS8466;
 DT 15-APR-2003 (first entry)
 XX
 DE Human PRO polypeptide #67.
 XX
 KM Human; PRO: cytosolic; tumour; cancer; breast; lung; stomach; liver;
 KM dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
 KM antibody-dependent enzyme mediated prodrug therapy.
 OS Homo sapiens.
 XX
 PN US2003027272-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 21-JUN-2002; 2002US-00176492.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 XX
 PR 18-SEP-1997; 97US-0059266P.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 XX
 PR 21-OCT-1997; 97US-0063486P.
 XX
 PR 24-OCT-1997; 97US-0063120P.
 XX
 PR 24-OCT-1997; 97US-0063121P.
 XX
 PR 28-OCT-1997; 97US-0063540P.
 XX
 PR 28-OCT-1997; 97US-0063541P.

PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGSGVIGALAFQHLINTDSTEGFLGEVKEANSITDSQMDVAVYITD 60
DB 1 MEGESTSAVLGSGVIGALAFQHLINTDSTEGFLGEVKEANSITDSQMDVAVYITD 60
QY 61 IQKVTICCYOLFSPYNSGGEVNOALKKILSNVKNVGVYKRRSDQIMTFRRLHK 120
DB 61 IQKVTICCYOLFSPYNSGGEVNOALKKILSNVKNVGVYKRRSDQIMTFRRLHK 120
QY 121 LOEHFENODLVPLLTPTSITTESCSTRLEHSLYKPKGLFHRVPLVANIGMSQOLGYK 180
DB 121 LOEHFENODLVPLLTPTSITTESCSTRLEHSLYKPKGLFHRVPLVANIGMSQOLGYK 180
QY 181 TVSGSCMSGTGFSNAVTGSHSKFFREDGSLKEYHKINEMWASIOEELKSCCKVEDEQAV 240
DB 181 TVSGSCMSGTGFSNAVTGSHSKFFREDGSLKEYHKINEMWASIOEELKSCCKVEDEQAV 240
QY 241 DKLKQVNRRLKREIEKRGQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLKQVNRRLKREIEKRGQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKRRHYSKSCSNVNHLDVVDNLTLMVEHTDTPAEPASTPQIKKALDLDROFKRS 360
DB 301 LKRRHYSKSCSNVNHLDVVDNLTLMVEHTDTPAEPASTPQIKKALDLDROFKRS 360
QY 361 RLDDTODKRSKANTGSSNODKASMGSPETDEIEIEKMGFGESRSPTF 409
DB 361 RLDDTODKRSKANTGSSNODKASMGSPETDEIEIEKMGFGESRSPTF 409

RESULT 7
ABU88014
ID ABU88014 standard; protein; 409 AA.
XX
AC ABU88014;
DT 07-JUL-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO1013.
DE Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
XX chondrocyte proliferation; chondrocyte differentiation; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
OS Homo sapiens.
PN US2003032127-A1.
XX
XX 13-FEB-2003.
PD
PF 26-JUN-2002; 2002US-00183012.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063544P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080154P.
PR 01-APR-1998; 98US-0080337P.
PR 01-APR-1998; 98US-0080337P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0082588P.
PR 21-APR-1998; 98US-0082589P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083499P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086332P.
PR 22-MAY-1998; 98US-0086466P.
PR 28-MAY-1998; 98US-0087038P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088555P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 15-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089538P.
PR 18-JUN-1998; 98US-0089563P.
PR 18-JUN-1998; 98US-0089568P.
PR 19-JUN-1998; 98US-0089582P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095598P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.

PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 15-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 18-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101766P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102685P.
PR 06-OCT-1998; 98US-0103258P.

Query Match 100.0%; Score 2109; DB 6; Length 409;

Best Local Similarity 100.0%; Pred. No. 1,5e-175;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MEGSTAVLSGFLGALAFCHNTDSDTEGFLGVEYKGAKSITDSOMDVEVYITID 60
DB 1 MEGSTAVLSGFLGALAFCHNTDSDTEGFLGVEYKGAKSITDSOMDVEVYITID 60
CY 61 IOKYIPCYOLFSEFNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRELLHKN 120
DB 61 IOKYIPCYOLFSEFNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRELLHKN 120
CY 121 LOEHFSNODLVFLLTTSITTESGSTRLEHSLYKPKGKLFHVPVLANLGMSQGYK 180
DB 121 LOEHFSNODLVFLLTTSITTESGSTRLEHSLYKPKGKLFHVPVLANLGMSQGYK 180
CY 121 LOEHFSNODLVFLLTTSITTESGSTRLEHSLYKPKGKLFHVPVLANLGMSQGYK 180
DB 121 LOEHFSNODLVFLLTTSITTESGSTRLEHSLYKPKGKLFHVPVLANLGMSQGYK 180
CY 181 TVSGSCMSTGSPRAVQTHSSKFEEDGSLKEVHKINEMVYASLOBELSKICKYEDSEQAV 240
DB 181 TVSGSCMSTGSPRAVQTHSSKFEEDGSLKEVHKINEMVYASLOBELSKICKYEDSEQAV 240
CY 241 DKLIVDVNRLKRELEKRGQIOAAREKNIQKPOENIFLCQALRTFFPNSFFLHSCVMS 300
DB 241 DKLIVDVNRLKRELEKRGQIOAAREKNIQKPOENIFLCQALRTFFPNSFFLHSCVMS 300
CY 301 LKNRHVSKSCNVYHHDVDVNDLTLMVEHTDIPASASTPQIHKKALDLDROWQPKRS 360
DB 301 LKNRHVSKSCNVYHHDVDVNDLTLMVEHTDIPASASTPQIHKKALDLDROWQPKRS 360
CY 361 RLDDTOKRSKANTGSSNODKASRMSSPFTDEIEKKKGGGEYSRSTP 409

Db 361 RLLDTRDKRSKANTSSNODKASKSSPFLDEIEHMKGFYSNPT 409

RESULT 8
ABU84329
ID ABU84329 standard; protein; 409 AA.
XX
AC ABU84329;
XX

DT 02-AUG-2003 (first entry)

XX Human secreted/transmembrane protein (PRO) #67.

XX Human; secreted and transmembrane protein; PRO; TNF-alpha;
KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM tissue typing.

XX Homo sapiens.

PN US2003032112-A1.

PD 13-FEB-2003.

XX 21-JUN-2002; 2002US-00176756.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065111P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 11-DEC-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 20-MAR-1998; 98US-0077649P.

PR 20-MAR-1998; 98US-0078866P.

PR 27-MAR-1998; 98US-0079639P.

PR 27-MAR-1998; 98US-0079664P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.

PR 15-MAY-1998; 98US-0085582P.

PR 18-MAY-1998; 98US-0085700P.

PR 22-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 26-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087088P.

PR 28-MAY-1998; 98US-0087208P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088366P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088863P.

PR 12-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089080P.

PR 16-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089512P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089538P.

PR 18-JUN-1998; 98US-0089653P.

PR 19-JUN-1998; 98US-0089952P.

PR 22-JUN-1998; 98US-0090246P.

PR 22-JUN-1998; 98US-0090252P.

PR 22-JUN-1998; 98US-0090254P.

PR 24-JUN-1998; 98US-0090439P.

PR 24-JUN-1998; 98US-0090439P.

PR 24-JUN-1998; 98US-0090444P.

PR 24-JUN-1998; 98US-0090461P.

PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.

PR 25-JUN-1998; 98US-0090676P.

PR 25-JUN-1998; 98US-0090678P.

PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090690P.

PR 25-JUN-1998; 98US-0090694P.

PR 25-JUN-1998; 98US-0090695P.

PR 25-JUN-1998; 98US-0090696P.

PR 26-JUN-1998; 98US-0090699P.

PR 26-JUN-1998; 98US-0090704P.

PR 26-JUN-1998; 98US-0090863P.

PR 26-JUN-1998; 98US-0090863P.

PR 26-JUN-1998; 98US-0091010P.

PR 01-JUL-1998; 98US-0091359P.

PR 01-JUL-1998; 98US-0091544P.

PR 02-JUL-1998; 98US-0091478P.

PR 02-JUL-1998; 98US-0091486P.

PR 02-JUL-1998; 98US-0091626P.

PR 02-JUL-1998; 98US-0091628P.

PR 02-JUL-1998; 98US-0091632P.

PR 02-JUL-1998; 98US-0091632P.

PR 04-AUG-1998; 98US-0095282P.

PR 10-AUG-1998; 98US-0095998P.
PR 17-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096157P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096952P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098602P.
PR 10-SEP-1998; 98US-0098741P.
PR 10-SEP-1998; 98US-0098754P.
PR 10-SEP-1998; 98US-0098763P.
PR 10-SEP-1998; 98US-0098812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101922P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102685P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103258P.
PR 07-OCT-1998; 98US-00168976.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Beet Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTASVLSGFGVLAGALAFQHLNTSDTEGFLGGEVKGAKNSITDSQMDVAVVYTIID 60
DB 1 MEGESTASVLSGFGVLAGALAFQHLNTSDTEGFLGGEVKGAKNSITDSQMDVAVVYTIID 60
QY 61 IQXVLPVQLPFFNNSGGEVNEQALKLISNVKKNVGVWYKFRHSDDIMTFRRLLHKN 120
DB 61 IQXVLPVQLPFFNNSGGEVNEQALKLISNVKKNVGVWYKFRHSDDIMTFRRLLHKN 120

QY 121 LOEHFNSODLVFLLLTPSIITBESCSTRLEHSLYKPOKGLFHRVPLVVAANTGMSBOLGYK 180
DB 121 LOEHFNSODLVFLLLTPSIITBESCSTRLEHSLYKPOKGLFHRVPLVVAANTGMSBOLGYK 180
QY 181 TVSGSCMSGSPSAVQTHSKPFEEGSLKEVYKIMEMVASIOEELKSLCKYDESEQAV 240
DB 181 TVSGSCMSGSPSAVQTHSKPFEEGSLKEVYKIMEMVASIOEELKSLCKYDESEQAV 240
QY 241 DKLVDVNLKREIEKRGQAIQAAEKXIOKPOENIFLQALRTFFNSEFLHSCVMS 300
DB 241 DKLVDVNLKREIEKRGQAIQAAEKXIOKPOENIFLQALRTFFNSEFLHSCVMS 300
QY 301 LKNRHVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPOLIKKALDLDROMQFKS 360
DB 301 LKNRHVSKSCNHNHLDVVDNLTLMVEHTDIPASPASTPOLIKKALDLDROMQFKS 360
QY 361 RLIDTDKSKANTGSSNODKASKMSPEDEIEKMGFGESRSPTF 409
DB 361 RLIDTDKSKANTGSSNODKASKMSPEDEIEKMGFGESRSPTF 409

RESULT 9
ABR66203 standard; protein; 409 AA.

AC ABR66203;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1013, SEQ ID NO:134.

XX Human; PRO; secreted protein; transmembrane protein;

KM extracellular domain; tumour necrosis factor- α ; TNF- α ;

KM chondrocyte; proliferation; differentiation; cartilage disorder;

KM bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

KM adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

KM liver; drug screening; transgenic animal; genetic analysis;

KM antithrombotic; vulnerability; gene therapy.

XX Homo sapiens.

XX US2003027278-A1.

PD 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176987.

PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063546P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.

PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-008269P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-008359P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-008580P.
PR 15-MAY-1998; 98US-008582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-008759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089608P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090439P.
PR 24-JUN-1998; 98US-009043P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00905413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-009159P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 04-JUL-1998; 98US-009406P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-009598P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-009691P.
PR 17-AUG-1998; 98US-0096997P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-009884P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-010151P.
PR 16-SEP-1998; 98MO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1,5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGESESTAVLSGVTALAFQHLNLTSDTBGFLGVEKGAOKSITDSQMDVVEVYITD 60
DB 1 MGESESTAVLSGVTALAFQHLNLTSDTBGFLGVEKGAOKSITDSQMDVVEVYITD 60
QY 61 IQKXTCYOLFSPYNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLHK 120
DB 61 IQKXTCYOLFSPYNSSGEVNEQALKKILSNVKNVGVYKFRHSDQIMTFRERLHK 120
QY 121 LQHFENODIVFLTLTPSIITTESCSTRLEHSLYKQKLFHRVPIVANLGMSEQLGYK 180
DB 121 LQHFENODIVFLTLTPSIITTESCSTRLEHSLYKQKLFHRVPIVANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSFSAVOTHSKFEEDGSLKEVHKINEMVYASIQEELKSI CKKVEDSEQAV 240
DB 181 TVSGSCMSTGFSFSAVOTHSKFEEDGSLKEVHKINEMVYASIQEELKSI CKKVEDSEQAV 240
QY 241 DKLVDVNRLEKREIEKRGNOIQAREKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLEKREIEKRGNOIQAREKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300
QY 301 LKRRHYSKSCNNHLDVVDNLTLMVEHTDIPRASPASTPQIKKALDLDROQFKRS 360
DB 301 LKRRHYSKSCNNHLDVVDNLTLMVEHTDIPRASPASTPQIKKALDLDROQFKRS 360
QY 361 RLIDTODKRSKANTGSSNODKASKMSPETDEIEIKMGFGESRSPTF 409
DB 361 RLIDTODKRSKANTGSSNODKASKMSPETDEIEIKMGFGESRSPTF 409
RESULT 10
ID ABR65593 standard; protein; 409 AA.
AC ABR65593;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0018773.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0068335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078868P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080134P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086032P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087509P.
PR 02-JUN-1998; 98US-0087559P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088036P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089512P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091526P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096871P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097032P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099744P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099912P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.

PR 16-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 29-SEP-1998; 98US-0102467P.
PR 30-SEP-1998; 98US-0102467P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSTSAVLSGFLGALAFQHLNTDSDTEGFLGVEYKGAKNISITDSQMDVEVYTTID 60
DB 1 MEGSTSAVLSGFLGALAFQHLNTDSDTEGFLGVEYKGAKNISITDSQMDVEVYTTID 60

QY 61 IQKTI PCYQLPSPFNSSGGEVNEQALKILSNKKNVGVYKFFRHSQINTFFERLIHN 120
DB 61 IQKTI PCYQLPSPFNSSGGEVNEQALKILSNKKNVGVYKFFRHSQINTFFERLIHN 120

QY 121 LOEHFSNODLVFLLTPTSITTESCTRLHSHLYKPKQGFHRYPLVAVANIGMSEQLGYK 180
DB 121 LOEHFSNODLVFLLTPTSITTESCTRLHSHLYKPKQGFHRYPLVAVANIGMSEQLGYK 180

QY 181 TVSGSCWSTGFSRAVQTHSSKFFEDGSLXEVKINEMVYASLOELKSIKKYEDSEQAV 240
DB 181 TVSGSCWSTGFSRAVQTHSSKFFEDGSLXEVKINEMVYASLOELKSIKKYEDSEQAV 240

QY 241 DKLVTQVNRRLKRETEKRGAGIOAREKNIQKPOENIFCOALRTFFPNSFFLHSCVMS 300
DB 241 DKLVTQVNRRLKRETEKRGAGIOAREKNIQKPOENIFCOALRTFFPNSFFLHSCVMS 300

QY 301 LKNRHVSKSCNVYVHDLVDVNTLTWVETDIPASPASTPQIHKRALDLDPRWQFKRS 360
DB 301 LKNRHVSKSCNVYVHDLVDVNTLTWVETDIPASPASTPQIHKRALDLDPRWQFKRS 360

QY 361 RLIDTQDKRSKANTGSSNODKASWSSPPTDEIEKKMGGEYSRSPTE 409
DB 361 RLIDTQDKRSKANTGSSNODKASWSSPPTDEIEKKMGGEYSRSPTE 409

RESULT 11
ABU99533
ID ABU99533 standard; protein; 409 AA.
XX ABU99533;
XX 09-AUG-2003 (first entry)
DE Human secreted/transmembrane protein (PRO) #67.
XX Human, secreted and transmembrane protein; PRO; TNF-alpha;
KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX Homo sapiens.
OS US2003040070-A1.
XX
XX

PD 27-FEB-2003.
XX 27-JUN-2002; 2002US-00184627.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 13-NOV-1997; 97US-0064103P.
PR 21-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086233P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086396P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087098P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089030P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089588P.
PR 18-JUN-1998; 98US-0089633P.
PR 19-JUN-1998; 98US-0089982P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096881P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 01-SEP-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.

PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102584P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1,5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSCFVLGALAFQHLMTDSDTGEFLGEGKEANKSITDSQMDVEVYITID 60
1 MEGESTSAVLSCFVLGALAFQHLMTDSDTGEFLGEGKEANKSITDSQMDVEVYITID 60
Db 1 MEGESTSAVLSCFVLGALAFQHLMTDSDTGEFLGEGKEANKSITDSQMDVEVYITID 60
QY 61 IQKTYICQYQFSPYNSGGEVNEQALKKILSNVKKVGVGKRRHSDQINTFRRLHKN 120
61 IQKTYICQYQFSPYNSGGEVNEQALKKILSNVKKVGVGKRRHSDQINTFRRLHKN 120
Db 61 IQKTYICQYQFSPYNSGGEVNEQALKKILSNVKKVGVGKRRHSDQINTFRRLHKN 120
QY 121 LQHFANQDVLFFLLTPSITTESCSTRLEHSLYKPOKGLFHRVPLVLANLGASEQLGYX 180
121 LQHFANQDVLFFLLTPSITTESCSTRLEHSLYKPOKGLFHRVPLVLANLGASEQLGYX 180
Db 121 LQHFANQDVLFFLLTPSITTESCSTRLEHSLYKPOKGLFHRVPLVLANLGASEQLGYX 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASJOEBELKSJCKEYBSEQAV 240
181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASJOEBELKSJCKEYBSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMVASJOEBELKSJCKEYBSEQAV 240
QY 241 DKLVKDVNRLKREIEKRGAKIQABREKNIQKDPENIFLCOALRTFPENSEFLHSQVMS 300
241 DKLVKDVNRLKREIEKRGAKIQABREKNIQKDPENIFLCOALRTFPENSEFLHSQVMS 300
Db 241 DKLVKDVNRLKREIEKRGAKIQABREKNIQKDPENIFLCOALRTFPENSEFLHSQVMS 300
QY 301 LKQRHVSKSSCNTNHHLDVVDNLTLMVERTDIPASPASTPQIITKHALDLDDRWQFKKS 360
301 LKQRHVSKSSCNTNHHLDVVDNLTLMVERTDIPASPASTPQIITKHALDLDDRWQFKKS 360
Db 301 LKQRHVSKSSCNTNHHLDVVDNLTLMVERTDIPASPASTPQIITKHALDLDDRWQFKKS 360
QY 361 RLIDTODKRSKANTGSSNODKASKMSSPETDEIEIKMKGGEYSRSPTF 409
361 RLIDTODKRSKANTGSSNODKASKMSSPETDEIEIKMKGGEYSRSPTF 409
Db 361 RLIDTODKRSKANTGSSNODKASKMSSPETDEIEIKMKGGEYSRSPTF 409

RESULT 12

ABUS8004
ID ABUS8004 standard; protein; 409 AA.
XX
AC ABUS8004;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #36.
XX
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADPEPT;
KW antibody-dependent enzyme mediated prodng therapy.
XX
CS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PE 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083342P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088036P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088862P.
PR 11-JUN-1998; 98US-0088868P.
PR 11-JUN-1998; 98US-0088868P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089589P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.

PR	22-JUN-1998	98US-00896962
PR	22-JUN-1998	98US-00902522
PR	22-JUN-1998	98US-00902522
PR	22-JUN-1998	98US-00902542
PR	23-JUN-1998	98US-00903439
PR	23-JUN-1998	98US-00903552
PR	24-JUN-1998	98US-00904292
PR	24-JUN-1998	98US-00904315
PR	24-JUN-1998	98US-00904451
PR	24-JUN-1998	98US-00904444
PR	24-JUN-1998	98US-00904444
PR	24-JUN-1998	98US-00904678
PR	25-JUN-1998	98US-00906502
PR	25-JUN-1998	98US-00906502
PR	25-JUN-1998	98US-00906549
PR	25-JUN-1998	98US-00906552
PR	25-JUN-1998	98US-00906562
PR	26-JUN-1998	98US-00908622
PR	26-JUN-1998	98US-00908632
PR	01-JUL-1998	98US-00913602
PR	01-JUL-1998	98US-00915442
PR	02-JUL-1998	98US-00914782
PR	02-JUL-1998	98US-00915192
PR	02-JUL-1998	98US-00916262
PR	02-JUL-1998	98US-00916282
PR	02-JUL-1998	98US-00916332
PR	02-JUL-1998	98US-00916462
PR	02-JUL-1998	98US-00916732
PR	07-JUL-1998	98US-00919782
PR	07-JUL-1998	98US-00919822
PR	09-JUL-1998	98US-00921822
PR	10-JUL-1998	98US-00924722
PR	10-JUL-1998	98US-00933392
PR	30-08-1998	98US-00946512
PR	04-AUG-1998	98US-00952822
PR	04-AUG-1998	98US-00952852
PR	04-AUG-1998	98US-00953012
PR	04-AUG-1998	98US-00953022
PR	04-AUG-1998	98US-00953182
PR	04-AUG-1998	98US-00953212
PR	04-AUG-1998	98US-00953252
PR	10-AUG-1998	98US-00959162
PR	10-AUG-1998	98US-00960122
PR	11-AUG-1998	98US-00961432
PR	11-AUG-1998	98US-00961462
PR	12-AUG-1998	98US-00963392
PR	17-AUG-1998	98US-00965762
PR	17-AUG-1998	98US-00967662
PR	17-AUG-1998	98US-00967682
PR	17-AUG-1998	98US-00967732
PR	17-AUG-1998	98US-00967712
PR	17-AUG-1998	98US-00968672
PR	17-AUG-1998	98US-00968812
PR	17-AUG-1998	98US-00968842
PR	17-AUG-1998	98US-00968852
PR	17-AUG-1998	98US-00969872
PR	18-AUG-1998	98US-00969832
PR	18-AUG-1998	98US-00969502
PR	18-AUG-1998	98US-00969532
PR	18-AUG-1998	98US-00969602
PR	18-AUG-1998	98US-00970222
PR	19-AUG-1998	98US-00971412
PR	20-AUG-1998	98US-00972182
PR	24-AUG-1998	98US-00976612
PR	26-AUG-1998	98US-00979522
PR	26-AUG-1998	98US-00979542
PR	26-AUG-1998	98US-00979552

PR	26-AUG-1998	98US-0097971P
PR	26-AUG-1998	98US-0097974P
PR	26-AUG-1998	98US-0097978P
PR	26-AUG-1998	98US-0097979P
PR	26-AUG-1998	98US-0097986P
PR	26-AUG-1998	98US-0098014P
PR	31-AUG-1998	98US-0098652P
PR	16-SEP-1998	98US-0100634P
PR	17-SEP-1998	98US-0100658P
PR	17-SEP-1998	98US-0100658P
PR	17-SEP-1998	98US-0100658P
PR	07-OCT-1998	98US-0100658P
PR	07-OCT-1998	98US-0100658P
PR	01-DEC-1998	98US-0100658P
PR	01-DEC-1998	98US-0100658P
PR	05-JAN-1999	98US-0100658P
PR	05-JAN-1999	98US-0100658P
PR	12-MAR-1999	98US-0100658P
PR	12-MAR-1999	98US-0100658P
PR	02-JUN-1999	98US-0100658P
PR	02-JUN-1999	98US-0100658P
PR	23-JUN-1999	98US-0100658P
PR	23-JUN-1999	98US-0100658P
PR	07-JUL-1999	98US-0100658P
PR	07-JUL-1999	98US-0100658P
PR	26-JUL-1999	98US-0100658P
PR	26-JUL-1999	98US-0100658P
PR	18-AUG-1999	98US-0100658P
PR	18-AUG-1999	98US-0100658P
PR	15-SEP-1999	98US-0100658P
PR	15-SEP-1999	98US-0100658P
PR	08-OCT-1999	98US-0100658P
PR	30-NOV-1999	98US-0100658P
PR	01-DEC-1999	98US-0100658P
PR	01-DEC-1999	98US-0100658P
PR	16-DEC-1999	98US-0100658P
PR	20-DEC-1999	98US-0100658P
PR	05-JAN-2000	98US-0100658P
PR	05-JAN-2000	98US-0100658P
PR	10-MAR-2000	98US-0100658P
PR	10-MAR-2000	98US-0100658P
PR	15-MAR-2000	98US-0100658P
PR	15-MAR-2000	98US-0100658P
PR	30-MAR-2000	98US-0100658P
PR	30-MAR-2000	98US-0100658P
PR	17-MAY-2000	98US-0100658P
PR	22-MAY-2000	98US-0100658P
PR	22-MAY-2000	98US-0100658P
PR	02-JUN-2000	98US-0100658P
PR	02-JUN-2000	98US-0100658P
PR	28-JUL-2000	98US-0100658P
PR	28-JUL-2000	98US-0100658P
PR	11-AUG-2000	98US-0100658P
PR	11-AUG-2000	98US-0100658P
PR	24-AUG-2000	98US-0100658P
PR	24-AUG-2000	98US-0100658P
PR	07-SEP-2000	98US-0100658P

Query Match	Similarity	100.0%;	Score 2109;	DB 6;	Length 409;
Best Local	Similarity	100.0%;	Pred. No. 1,5e-175;		
Matches	Conservative	0;	Mismatches	0;	Indels
				Gaps	0;
QY	1	MEGESTAVLSGFLGALAFQHLNTDSDTEGFLIGEVKGEAKNSITDSQMDDEVEVTTID	60		
Db	1	MEGESTAVLSGFLGALAFQHLNTDSDTEGFLIGEVKGEAKNSITDSQMDDEVEVTTID	60		
QY	1	IQRTIPCTOLFSPNNSGGEVNEBQALKILSNVKNVGNWTKYKPRRHSQIMTFRRLIHN	120		
Db	61	IQRTIPCTOLFSPNNSGGEVNEBQALKILSNVKNVGNWTKYKPRRHSQIMTFRRLIHN	120		
QY	121	LQEHFNODLVFLLLTSSITTESCSTRLEHSLYKPKQGLFHRVPLVAVAMIGSEQLGYK	180		
Db	121	LQEHFNODLVFLLLTSSITTESCSTRLEHSLYKPKQGLFHRVPLVAVAMIGSEQLGYK	180		
QY	181	TVSGSCMSGTGSRVAVQTHSSKFEEDSDLKEVHKINEMVASLOEBELKICKYVDSEQAV	240		

Db 181 TVSGSMSGSTGFSAVTGHSSKFFEEEDGSLNEVHKINEMVASIQEELKSIQCKVEDESEQAV 240
 Qy 241 DKLVKQVNRKREIERKRRGQIQAREKNIQKDPQENIFLQALRTFFNSFELSCVWS 300
 Db 241 DKLVKQVNRKREIERKRRGQIQAREKNIQKDPQENIFLQALRTFFNSFELSCVWS 300
 Qy 301 LKRRHVSQSCVNNHLDVVDNLTLMVEHTDIPASPASTPQIIRKALDLDPRQFKRS 360
 Db 301 LKRRHVSQSCVNNHLDVVDNLTLMVEHTDIPASPASTPQIIRKALDLDPRQFKRS 360
 Qy 361 RLDDTQDKRSKANTGSSNQKASMSPEDEEIEKMGKFGEXRSRPTF 409
 Db 361 RLDDTQDKRSKANTGSSNQKASMSPEDEEIEKMGKFGEXRSRPTF 409
 RESULT 13
 ABUS9082 standard; protein; 409 AA.
 ID ABUS9082
 AC ABUS9082;
 XX
 DT 28-APR-2003 (first entry)
 XX
 XX Novel human secreted or transmembrane protein PRO1013.
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumor; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpesiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 KW
 OS Homo sapiens.
 XX
 XX US2002132252-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 14-NOV-2001; 2001US-00990442.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR

PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089582P.
 PR 17-JUN-1998; 98US-0089592P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US0050106.
 PR 08-MAR-1999; 99WO-US0050504.
 PR 02-JUN-1999; 99WO-US021252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US0000219.
 PR 06-JAN-2000; 2000WO-US0000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US020166.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941392.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara NJ, Fong S, Garber H, Gerlitsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Kijavlin ID, Napier MA, Pan J, Paoni NF,
 PI Roy RA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;

XX WPI; 2003-247083/24.
 DR N-PSDB; ABX80226.
 XX
 XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.

XX Claim 12; Fig 95; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO813, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or Crohn's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein

XX Sequence 409 AA;

XX Query Match 100.0%; Score 2109; DB 6; Length 409;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-175;
 XX Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGVLGALAFQHLNDSPTGFLGVEGKGNKSTDSQMDVYVYITD 60
 DB 1 MEGESTSAVLSGVLGALAFQHLNDSPTGFLGVEGKGNKSTDSQMDVYVYITD 60
 QY 61 IQKXICYOYLFYNSGGEVNEQALKKILSNYKKNVGVYKPRRSDQWTFREKLLHN 120
 DB 61 IQKXICYOYLFYNSGGEVNEQALKKILSNYKKNVGVYKPRRSDQWTFREKLLHN 120
 QY 61 IQKXICYOYLFYNSGGEVNEQALKKILSNYKKNVGVYKPRRSDQWTFREKLLHN 120
 DB 61 IQKXICYOYLFYNSGGEVNEQALKKILSNYKKNVGVYKPRRSDQWTFREKLLHN 120
 QY 121 LOHFSNODLVFLITPSITTESCSYHLESLYKPKQLFRRVPLVYANLMSQGLGX 180
 DB 121 LOHFSNODLVFLITPSITTESCSYHLESLYKPKQLFRRVPLVYANLMSQGLGX 180
 QY 121 LOHFSNODLVFLITPSITTESCSYHLESLYKPKQLFRRVPLVYANLMSQGLGX 180
 DB 121 LOHFSNODLVFLITPSITTESCSYHLESLYKPKQLFRRVPLVYANLMSQGLGX 180
 QY 181 TVSGSGMSGTGSAVQVTHSSKPEEDGSLKEYHKINEMVASYOELKSCCKVEDEBQAV 240
 DB 181 TVSGSGMSGTGSAVQVTHSSKPEEDGSLKEYHKINEMVASYOELKSCCKVEDEBQAV 240
 QY 181 TVSGSGMSGTGSAVQVTHSSKPEEDGSLKEYHKINEMVASYOELKSCCKVEDEBQAV 240
 DB 181 TVSGSGMSGTGSAVQVTHSSKPEEDGSLKEYHKINEMVASYOELKSCCKVEDEBQAV 240
 QY 241 DKLVKDVNLIKREIERKGAQIOAAREKNIQKDPQENIFLCALRTFFPNSFLLSCVWS 300
 DB 241 DKLVKDVNLIKREIERKGAQIOAAREKNIQKDPQENIFLCALRTFFPNSFLLSCVWS 300
 QY 301 LKRRHVSXSSCNVNHLDVVDNLTWVEHTDIPKAPASTPOIKKKALDLDKROPKRS 360
 DB 301 LKRRHVSXSSCNVNHLDVVDNLTWVEHTDIPKAPASTPOIKKKALDLDKROPKRS 360
 QY 361 RLIDTODKRSKANTGSSNODKASKWSPEETDEEIEKMKGFGEYSRSPTF 409
 DB 361 RLIDTODKRSKANTGSSNODKASKWSPEETDEEIEKMKGFGEYSRSPTF 409

DB 361 RLIDTODKRSKANTGSSNODKASKWSPEETDEEIEKMKGFGEYSRSPTF 409

RESULT 14
 ID AB082594
 ID AB082594 standard; protein; 409 AA.

AC AB082594;

DT 26-JUN-2003 (first entry)

DE Human secreted/transmembrane protein PRO1013.

XX Human; PRO; secreted protein; transmembrane protein; healing;
 XX cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosa; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.

OS Homo sapiens.

PN US2003032023-A1.

PD 13-FEB-2003.

PF 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.
 XX 17-OCT-1997; 97US-0062250P.
 XX 05-NOV-1997; 97MO-US020069.
 XX 12-NOV-1997; 97US-0065186P.
 XX 13-NOV-1997; 97US-0065311P.
 XX 24-NOV-1997; 97US-0066770P.
 XX 25-FEB-1998; 98US-0075945P.
 XX 20-MAR-1998; 98US-0078912P.
 XX 28-APR-1998; 98US-0083322P.
 XX 07-MAY-1998; 98US-0084600P.
 XX 28-MAY-1998; 98US-0087106P.
 XX 02-JUN-1998; 98US-0087607P.
 XX 02-JUN-1998; 98US-0087609P.
 XX 02-JUN-1998; 98US-0087759P.
 XX 03-JUN-1998; 98US-0087827P.
 XX 04-JUN-1998; 98US-0088021P.
 XX 04-JUN-1998; 98US-0088025P.
 XX 04-JUN-1998; 98US-0088026P.
 XX 04-JUN-1998; 98US-0088028P.
 XX 04-JUN-1998; 98US-0088029P.
 XX 04-JUN-1998; 98US-0088030P.
 XX 04-JUN-1998; 98US-0088033P.
 XX 05-JUN-1998; 98US-0088136P.
 XX 05-JUN-1998; 98US-0088167P.
 XX 05-JUN-1998; 98US-0088202P.
 XX 05-JUN-1998; 98US-0088212P.
 XX 05-JUN-1998; 98US-0088217P.
 XX 09-JUN-1998; 98US-0088655P.
 XX 10-JUN-1998; 98US-0088734P.
 XX 10-JUN-1998; 98US-0088738P.
 XX 10-JUN-1998; 98US-0088742P.
 XX 10-JUN-1998; 98US-0088824P.
 XX 10-JUN-1998; 98US-0088826P.
 XX 11-JUN-1998; 98US-0088858P.
 XX 11-JUN-1998; 98US-0088861P.
 XX 11-JUN-1998; 98US-0088876P.
 XX 12-JUN-1998; 98US-0089105P.
 XX 16-JUN-1998; 98US-0089440P.
 XX 16-JUN-1998; 98US-0089512P.
 XX 16-JUN-1998; 98US-0089514P.
 XX 17-JUN-1998; 98US-0089532P.
 XX 17-JUN-1998; 98US-0089538P.
 XX 17-JUN-1998; 98US-0089587P.
 XX 17-JUN-1998; 98US-0089595P.

PR	17-JUN-1998;	98US-0089600P.	PR	18-AUG-1998;	98US-0097022P.
PR	17-JUN-1998;	98US-0088653P.	PR	19-AUG-1998;	98US-0097141P.
PR	18-JUN-1998;	98US-0088801P.	PR	20-AUG-1998;	98US-0097218P.
PR	18-JUN-1998;	98US-0088907P.	PR	24-AUG-1998;	98US-0097611P.
PR	18-JUN-1998;	98US-0088908P.	PR	26-AUG-1998;	98US-0097952P.
PR	19-JUN-1998;	98US-0088947P.	PR	26-AUG-1998;	98US-0097954P.
PR	19-JUN-1998;	98US-0088948P.	PR	26-AUG-1998;	98US-0097955P.
PR	19-JUN-1998;	98US-0088952P.	PR	26-AUG-1998;	98US-0097971P.
PR	22-JUN-1998;	98US-0090245P.	PR	26-AUG-1998;	98US-0097974P.
PR	22-JUN-1998;	98US-0090252P.	PR	26-AUG-1998;	98US-0097978P.
PR	23-JUN-1998;	98US-0090349P.	PR	26-AUG-1998;	98US-0097986P.
PR	23-JUN-1998;	98US-0090355P.	PR	26-AUG-1998;	98US-0098014P.
PR	24-JUN-1998;	98US-0090429P.	PR	31-AUG-1998;	98US-0098525P.
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090435P.	PR	16-SEP-1998;	98MO-US019330.
PR	24-JUN-1998;	98US-0090444P.	PR	17-SEP-1998;	98US-0100858P.
PR	24-JUN-1998;	98US-0090445P.	PR	17-SEP-1998;	98MO-US019437.
PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98MO-US021141.
PR	24-JUN-1998;	98US-0090535P.	PR	01-DEC-1998;	98MO-US025108.
PR	24-JUN-1998;	98US-0090540P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	99MO-US000106.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	99MO-US005028.
PR	25-JUN-1998;	98US-0090676P.	PR	12-MAR-1999;	99US-0123957P.
PR	25-JUN-1998;	98US-0090678P.	PR	02-JUN-1999;	99MO-US012252.
PR	25-JUN-1998;	98US-0090690P.	PR	23-JUN-1999;	99US-0141037P.
PR	25-JUN-1998;	98US-0090694P.	PR	07-JUL-1999;	99US-0143048P.
PR	25-JUN-1998;	98US-0090695P.	PR	20-JUL-1999;	99US-0144758P.
PR	26-JUN-1998;	98US-0090862P.	PR	26-JUL-1999;	99US-0145698P.
PR	26-JUN-1998;	98US-0090863P.	PR	28-JUL-1999;	99US-0146322P.
PR	01-JUL-1998;	98US-0091360P.	PR	17-AUG-1999;	99US-0149396P.
PR	01-JUL-1998;	98US-0091544P.	PR	15-SEP-1999;	99MO-US021090.
PR	02-JUL-1998;	98US-0091478P.	PR	15-SEP-1999;	99MO-US021547.
PR	02-JUL-1998;	98US-0091519P.	PR	08-OCT-1999;	99US-0158663P.
PR	02-JUL-1998;	98US-0091626P.	PR	30-NOV-1999;	99MO-US028313.
PR	02-JUL-1998;	98US-0091632P.	PR	01-DEC-1999;	99MO-US028301.
PR	02-JUL-1998;	98US-0091633P.	PR	01-DEC-1999;	99MO-US028634.
PR	02-JUL-1998;	98US-0091646P.	PR	16-DEC-1999;	99MO-US030095.
PR	02-JUL-1998;	98US-0091673P.	PR	20-DEC-1999;	99MO-US030911.
PR	07-JUL-1998;	98US-0091678P.	PR	05-JAN-2000;	2000MO-US000219.
PR	07-JUL-1998;	98US-0091982P.	PR	06-JAN-2000;	2000MO-US000376.
PR	09-JUL-1998;	98US-0092182P.	PR	11-FEB-2000;	2000MO-US003565.
PR	10-JUL-1998;	98US-00932472P.	PR	18-FEB-2000;	2000MO-US004414.
PR	20-JUL-1998;	98US-0093339P.	PR	22-FEB-2000;	2000MO-US004914.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	2000MO-US005004.
PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	2000MO-US005841.
PR	04-AUG-1998;	98US-0095301P.	PR	10-MAR-2000;	2000MO-US006519.
PR	04-AUG-1998;	98US-0095302P.	PR	15-MAR-2000;	2000MO-US006884.
PR	04-AUG-1998;	98US-0095318P.	PR	20-MAR-2000;	2000MO-US007377.
PR	04-AUG-1998;	98US-0095321P.	PR	30-MAR-2000;	2000MO-US008439.
PR	10-AUG-1998;	98US-0095916P.	PR	15-MAY-2000;	2000MO-US013358.
PR	10-AUG-1998;	98US-0095929P.	PR	17-MAY-2000;	2000MO-US013705.
PR	11-AUG-1998;	98US-0096012P.	PR	22-MAY-2000;	2000MO-US014042.
PR	11-AUG-1998;	98US-0096143P.	PR	30-MAY-2000;	2000MO-US014841.
PR	12-AUG-1998;	98US-0096146P.	PR	02-JUN-2000;	2000MO-US015264.
PR	17-AUG-1998;	98US-0096329P.	PR	23-JUN-2000;	2000US-0213637P.
PR	17-AUG-1998;	98US-0096766P.	PR	28-JUL-2000;	2000MO-US020710.
PR	17-AUG-1998;	98US-0096768P.	PR	11-AUG-2000;	2000MO-US022031.
PR	17-AUG-1998;	98US-0096773P.			
PR	17-AUG-1998;	98US-0096771P.			
PR	17-AUG-1998;	98US-0096867P.			
PR	17-AUG-1998;	98US-0096881P.			
PR	17-AUG-1998;	98US-0096884P.			
PR	17-AUG-1998;	98US-0096895P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096949P.			
PR	18-AUG-1998;	98US-0096950P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0096960P.			

Query Match 100.0%; Score 2109; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1,5e-175;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGEISAVLGGFLGALAFQHLNTSDTREGFLGVEYKGAJNSITDSQMDVVEVYTTID	60
DB	1	MEGEISAVLGGFLGALAFQHLNTSDTREGFLGVEYKGAJNSITDSQMDVVEVYTTID	60
QY	61	IQKTIPTCYOLFSEFNSGGEFNEQALKKILSNVKKNVGVGKKFRHSQDITPFRRLHKH	120
DB	61	IQKTIPTCYOLFSEFNSGGEFNEQALKKILSNVKKNVGVGKKFRHSQDITPFRRLHKH	120
QY	121	LOEHRSNQDVLFLILNPSITTESCSTRLEHSLYKQKGLFHRVPLVYANLGSBOLGYK	180

Db 121 LQHFNSQDVLVLLTPSLITTESCSYHLEHSLYKQKLFHVPVLVNLDMSSQLGK 180
Qy 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMTASIQEELKSI CKKVEDEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMTASIQEELKSI CKKVEDEQAV 240
Qy 241 DKLVCVNLKREIERBRGQIOAREKNIQDPCENITLQALRFFPNSFLLSCVMS 300
Db 241 DKLVCVNLKREIERBRGQIOAREKNIQDPCENITLQALRFFPNSFLLSCVMS 300
Qy 301 LKNRHVSKSCVNNHLLDVNLLTLMVEHTDIPKASPASTPOLIKKALDLDRLQFKRS 360
Db 301 LKNRHVSKSCVNNHLLDVNLLTLMVEHTDIPKASPASTPOLIKKALDLDRLQFKRS 360
Qy 361 RLIDTQDKRSKANTGSSNODKASKSSPETDEIEKMGFGYSRSPPT 409
Db 361 RLIDTQDKRSKANTGSSNODKASKSSPETDEIEKMGFGYSRSPPT 409

RESULT 15
ABU82772
ID ABU82772 standard; protein; 409 AA.
XX ABU82772;
AC 27-JUN-2003 (first entry)
DT 27-JUN-2003 (first entry)
XX
XX Human PRO polypeptide #67.
KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX chromosome mapping; gene mapping; cytosolic.
OS Homo sapiens.
XX
XX US2003032113-A1.
XX
XX 13-FEB-2003.
PD 20-JUN-2002; 2002US-00176911.
XX
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.

PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083455P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 05-MAY-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086033P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086466P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088039P.
PR 04-JUN-1998; 98US-0088177P.
PR 05-JUN-1998; 98US-0088177P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088867P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089658P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090536P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.

PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-00105413.
 PR 26-JUN-1998; 98US-0090862P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 26-JUN-1998; 98US-0091010P.
 PR 01-JUL-1998; 98US-0091359P.
 PR 01-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091632P.
 PR 24-JUL-1998; 98US-0094006P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 10-AUG-1998; 98US-0095988P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096867P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 18-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097022P.
 PR 26-AUG-1998; 98US-0097522P.
 PR 26-AUG-1998; 98US-0097554P.
 PR 26-AUG-1998; 98US-0097555P.
 PR 26-AUG-1998; 98US-0097711P.
 PR 26-AUG-1998; 98US-0097747P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 09-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 16-SEP-1998; 98MO-US019310.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101739P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101922P.
 PR 25-SEP-1998; 98US-0101786P.
 PR 25-SEP-1998; 98US-010207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.

PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98US-0103395P.
 Query Match 100.0%; Score 2109; DB 6; Length 409;
 Best Local Similarity 100.0%; Pred.No.1.5e-175; Indels 0; Gaps 0;
 Matches 409; Conservative 0; Mismatches 0;
 QY 1 MEGSTSAVLGFLGALAFQHLNTSDTEGLGKGEAKNSITDSQMDVEVYITID 60
 DB 1 MEGSTSAVLGFLGALAFQHLNTSDTEGLGKGEAKNSITDSQMDVEVYITID 60
 QY 61 IQXIPCYOLFSPYNSGVEVNEQALKKILSNVKNVGVYKPRRSDQMTFRERLHN 120
 DB 61 IQXIPCYOLFSPYNSGVEVNEQALKKILSNVKNVGVYKPRRSDQMTFRERLHN 120
 QY 121 LOEHFSNQDLVFLITPISITTESCSTRLEHSLYKFOKGFHRVPLVANTGMSQGLGX 180
 DB 121 LOEHFSNQDLVFLITPISITTESCSTRLEHSLYKFOKGFHRVPLVANTGMSQGLGX 180
 QY 181 TVSGSCMTGFSRAVQTHSKFPEEDGSLKEVAKINEMTASLOEELKSICTKYEDSEQV 240
 DB 181 TVSGSCMTGFSRAVQTHSKFPEEDGSLKEVAKINEMTASLOEELKSICTKYEDSEQV 240
 QY 241 DKLVDVNRLLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSFTHSCVMS 300
 DB 241 DKLVDVNRLLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSFTHSCVMS 300
 QY 301 LKRRHVSXSCNTHHLDVVDNLTLYVEHTDLEBASPAPQIHKKALDLDNRQFKS 360
 DB 301 LKRRHVSXSCNTHHLDVVDNLTLYVEHTDLEBASPAPQIHKKALDLDNRQFKS 360
 QY 361 RLDPDQRKANTGSSNODKASMSPEDEIEKMGKGEYSRSPTE 409
 DB 361 RLDPDQRKANTGSSNODKASMSPEDEIEKMGKGEYSRSPTE 409

Search completed: April 16, 2004, 10:13:32
 Job time : 63 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:16 ; Search time 18 Seconds

(without alignments)
1183.150 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109
Sequence: 1 MEGESTSAVLGSGVGLALAF.....TDEIEKKKGFGEYSRPTF 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129.5	6.1	531	1 CALD_RAT	Q62736 rattus norv
2	123	5.8	8797	1 SNEI_HUMAN	Q8n591 homo sapien
3	122	5.8	1087	1 AKG9_RABIT	Q28628 coryctolagus
4	122	5.8	3210	1 CENF_HUMAN	P49454 homo sapien
5	121	5.7	993	1 SCPI_MOUSE	Q62209 mus musculu
6	121	5.7	5327	1 MACF_MOUSE	Q9qz20 mus musculu
7	121	5.7	5430	1 MACF_HUMAN	Q9qz23 homo sapien
8	118.5	5.6	866	1 RASO_ARCFU	Q29230 archaeoglob
9	117.5	5.6	875	1 ZIPI_YEAST	P31111 saccharomyc
10	117.5	5.6	1163	1 SBCC_CLOAB	Q14789 clostridium
11	117.5	5.6	3258	1 GOSI_HUMAN	Q58687 pyrococcus
12	116	5.5	879	1 RASO_PYRHO	Q86up2 homo sapien
13	115.5	5.5	1357	1 KTN1_HUMAN	Q8ra76 thermoaer
14	115	5.5	288	1 ISPH_THETN	Q09779 schizosacch
15	115	5.5	1628	1 YATE_SCHPO	Q9pct7 xenopus lae
16	114.5	5.4	1360	1 CING_XENTIA	Q93410 rattus norv
17	114	5.4	997	1 SCPI_RAT	P25386 saccharomyc
18	114	5.4	1790	1 USOI_YEAST	P46875 arabidopsis
19	113.5	5.4	754	1 ATK3_ARATH	P52519 human herpe
20	113.5	5.4	1526	1 P100_HSVJ7	Q9u5u6 schizosacch
21	113	5.4	1875	1 MYSD_SCHPO	Q02445 saccharomyc
22	113	5.4	1875	1 ABFI_HUMAN	Q15911 homo sapien
23	113	5.4	3703	1 MYSP_DROME	P35415 drosophila
24	112.5	5.3	879	1 MYHB_CHICK	P10587 gallus gall
25	112.5	5.3	1398	1 MYHB_YEAST	P43688 saccharomyc
26	112	5.3	1038	1 BMR2_HUMAN	Q13873 homo sapien
27	111.5	5.3	1972	1 MYHB_RABIT	Q13878 oryctolagus
28	110.5	5.2	1038	1 C1N8_YEAST	P271895 saccharomyc
29	110.5	5.2	1193	1 YPER_BACSU	P54199 bacillus su
30	110.5	5.2	2116	1 MYSD2_DICDI	P48799 dictyostel
31	110	5.2	1518	1 KKK1_YEAST	P43244 saccharomyc
32	110	5.2	2022	1 ANTI1_ONCVO	P21249 onchocerca
33	110	5.2	2022	1 ANTI1_ONCVO	P21249 onchocerca

34	109.5	5.2	866	1 RASO_SULAC	Q33600 sulfobolus
35	109.5	5.2	1038	1 BMR2_MOUSE	Q35607 mus musculu
36	109.5	5.2	1243	1 SMCA_MICAR	Q98r55 microtus ar
37	109	5.2	862	1 CSP2_MACFA	Q9852 macaca fasc
38	109	5.2	1583	1 GCC2_HUMAN	Q81w72 homo sapien
39	109	5.2	1972	1 MYHB_MOUSE	Q08638 mus musculu
40	109	5.2	2867	1 RBP2_PLAIV	Q00799 plasmidium
41	108.5	5.1	747	1 KEF3_HUMAN	Q15066 homo sapien
42	108.5	5.1	845	1 SCPI_MESAU	Q60563 mesocricetu
43	108.5	5.1	1257	1 CCA1_BACTU	Q45754 bacillus th
44	108.5	5.1	1938	1 MYB_ABOIR	P24773 aequiptecten
45	108.5	5.1	2663	1 CENF_HUMAN	Q02224 homo sapien

ALIGNMENTS

RESULT 1
ID CALD_RAT STANDARD; PRT; 531 AA.
AC Q62736;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Non-muscle caldesmon (CDM) (L-caldesmon).
GN CALD1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., MUTAGENESIS, AND PHOSPHORYLATION SITES.
RC TISSUE=Liver;
RX MEDLINE=95181370; PubMed=7876150;
RA Yamashiro S., Yamakita Y., Yoshida K.-S., Takiguchi K., Matsumura F.;
RT "Characterization of the COOH terminus of non-muscle caldesmon
mutants lacking mitosis-specific phosphorylation sites.";
RL J. Biol. Chem. 270:4023-4030(1995).
RN [2]
RP PHOSPHORYLATION BY CDC2.
RX MEDLINE=91095023; PubMed=1986309;
RA Yamashiro S., Yamakita Y., Hosoya H., Matsumura F.;
RT "Phosphorylation of non-muscle caldesmon by p34cdc2 kinase during
mitosis.";
RL Nature 348:169-172(1993).
CC -!- FUNCTION: Actin- and myosin-binding protein implicated in the
regulation of actomyosin interactions in smooth muscle and
nonmuscle cells (could act as a bridge between myosin and actin
filaments). Stimulates actin binding of tropomyosin which
increases the stabilization of actin filament structure. In muscle
tissues, inhibits the actomyosin ATPase by binding to F-actin.
This inhibition is attenuated by calcium-calmodulin and is
potentiated by tropomyosin. Interacts with actin, myosin, two
molecules of tropomyosin and with calmodulin. Also play an
essential role during cellular mitosis and receptor coupling.
CC -!- SUBCELLULAR LOCATION: On thin filaments in smooth muscle and on
stress fibers in fibroblasts (nonmuscle) (By similarity).
CC -!- TISSUE SPECIFICITY: High-molecular-weight caldesmon (h-caldesmon)
is predominantly expressed in smooth muscles, whereas low-
molecular-weight caldesmon (l-caldesmon) is widely distributed in
non-muscle tissues and cells. Not expressed in skeletal muscle or
heart (By similarity).
CC -!- DOMAIN: The N-terminal part seems to be a myosin/calmodulin-
binding domain, and the C-terminal a tropomyosin/actin/calmodulin-
binding domain. These two domains are separated by a central
helical region in the smooth-muscle form.
CC -!- PTM: In non-muscle cells, phosphorylation by CDC2 during mitosis
causes caldesmon to dissociate from microfilaments.
CC Phosphorylation reduces caldesmon binding to actin, myosin, and
calmodulin as well as its inhibition of actomyosin ATPase
activity. Phosphorylation also occurs in both quiescent and
dividing smooth muscle cells with similar effects on the
interaction with actin and calmodulin and on microfilaments

CC reorganization.
 CC -1- SIMILARITY: Belongs to the caldesmon family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U88419; AA56852.1; -
 CC FTR; A55887; A55887.
 CC DR InterPro: IPR006017; Caldesmon.
 CC DR InterPro: IPR006018; Caldesmon_LSP.
 CC DR Pfam: PF02029; Caldesmon.1.
 CC DR PRINTS: PR01076; CALDBSMON.
 CC KM Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
 CC Alternative splicing.
 CC FT DOMAIN 20 200
 FT 303 360 MYOSIN AND CALMODULIN-BINDING (BY
 FT 402 412 SIMILARITY).
 FT 392 424 TROPOMYOSIN-BINDING (POTENTIAL).
 FT 454 460 STRONG ACTIN-BINDING (BY SIMILARITY).
 FT 506 531 CALMODULIN-BINDING (BY SIMILARITY).
 FT 33 40 WEAK ACTIN-BINDING (BY SIMILARITY).
 FT 180 189 POLY-ARG.
 FT 279 282 POLY-GLU.
 FT 319 322 POLY-ARG.
 FT 336 339 POLY-GLU.
 FT 249 249 PHOSPHORYLATION (BY CDC2).
 FT 462 462 PHOSPHORYLATION (BY CDC2).
 FT 468 468 PHOSPHORYLATION (BY CDC2).
 FT 491 491 PHOSPHORYLATION (BY CDC2).
 FT 497 497 PHOSPHORYLATION (BY CDC2).
 FT 527 527 PHOSPHORYLATION (BY CDC2).
 FT 249 249 S->A: DECREASES STRONGLY PHOSPHORYLATION-
 FT MUTAGEN 527 527 DEPENDENT ACTIN BINDING.
 FT 462 462 S->A: DECREASES PHOSPHORYLATION-DEPENDENT
 FT MUTAGEN 462 462 ACTIN BINDING.
 FT 468 468 T->A: DECREASES PHOSPHORYLATION-DEPENDENT
 FT MUTAGEN 468 468 ACTIN BINDING.
 FT 491 491 S->A: DECREASES PHOSPHORYLATION-DEPENDENT
 FT MUTAGEN 491 491 ACTIN BINDING.
 FT 497 497 S->A: DECREASES PHOSPHORYLATION-DEPENDENT
 FT MUTAGEN 497 497 ACTIN BINDING.
 FT 527 527 S->A: DOES NOT DECREASE PHOSPHORYLATION-
 FT MUTAGEN 527 527 DEPENDENT ACTIN BINDING.
 SQ SEQUENCE 531 AA; 60584 MW; CBEC50271A23829 CRC64;
 Query Match 6.1%; Score 129.5; DB 1; Length 531;
 Best Local Similarity 24.0%; Pred. No. 0.48;
 Matches 85; Conservative 54; Mismatches 122; Indels 93; Gaps 21;
 QY 35 GEVKGAKNSITSDQMDVEVYITDIQKTYPCYQLFSPYNSG-----EVEQAK 86
 DB 143 GEEKGESRSG--RYEMETEYVIT-----SYQKNYSYDADADKXKEKEEKEEKEK 192
 QY 87 KIISNVKKNVGVKFPFRH---SDQIMTFRRLHKHQLGHFNODLVFLLTPSITTS 143
 DB 193 G--GNLGENQIKDKIKDKKPEKVEVNFIDR--KKGFTF--VKAQNEFH----- 237
 QY 144 CSTHRLF--HSLVYPOKQ-----LFHRYPLVANLGMSEQLGYKTVSGSCMGTGFSR 193
 DB 238 --TETLKQTEVAFSPSPSGRAGDKEAGAPVEAKRLIE--LRRRGTESESEFEK 292
 QY 194 AVQCHSKRFPEDSLKVEHKINMYASLOEELKSIQKYVEDSOAVDKLVKVNPLKE 253
 DB 293 LKQOQOEALIE---LEELKKKREKRVLESEQRKQEDADKRAFE--EKRLKHE 346
 QY 254 IEKRRGAQIQARERKTIQKPOENI-----FLCQALRTFF-----NSFPHSCV 298

DB 347 IERRRA---EAAERK--QKMPEDGLSEDKKFFKC-----FTPGSSUKIEERAEFL----- 392
 QY 299 MSLKRRHVSXSSGCMYHHLVDVNLTLWVE-HTDIEPASPPQIIRKALDL 351
 DB 393 ---NKSQSGVYSSTQAIVVSKIDSRLEQYTNALGETVASKP--MKPAASDL 440
 RESULT 2
 ID SNEI HUMAN STANDARD; PRT; 8797 AA.
 AC Q8NFF1; Q94890; Q8N9P7; Q8TCB1; Q8MWM6; Q8MWM7; Q8MXF6; Q96N17;
 AC Q9C0A7; Q9H525; Q9H526; Q9NS36; Q9NU50; Q9U06; Q9U07; Q9ULF8;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neepirin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic
 DE nuclear envelope protein 1) (Syn-1) (Myocyte nuclear envelope protein
 DE 1) (Myne-1) (Enaplin).
 GN SNEI OR MYNE1 OR KIAA0796 OR KIAA1756 OR KIAA1262.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), CHARACTERIZATION, AND
 RP MUTAGENESIS OF 8758-LEU--CYS-8763.
 RC TISSUE=Heart, Placenta, Skeletal muscle, Spleen, and Testis;
 RX MEDLINE=21652858; PubMed=11792814;
 RA Zhang Q., Skepper J.N., Yang F., Davies J.D., Heyl L., Roberts R.G.,
 RA Weisberg P., Ellis J.A., Shanahan C.M.;
 RT "Neepirin, a novel family of spectrin-repeat-containing proteins that
 RT localize to the nuclear membrane in multiple tissues.";
 RL J. Cell Sci. 114:4485-4498 (2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.
 RC TISSUE=Heart, Spleen, and Testis;
 RX MEDLINE=22296983; PubMed=12408964;
 RA Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
 RT "The neepirins are giant actin-binding proteins, orthologous to
 RT Drosophila melanogaster muscle protein MSP-300.";
 RL Genomics 80:473-481 (2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.
 RA Braune S., Abraham S., Padmakumar V., Tunggal B., Nossel A.A.,
 RA Korenbaum E.;
 RT "The longest isoform of enaplin/Syne-1, a nuclear envelope associated
 RT protein, binds actin cytoskeleton via the alpha-actinin-like actin-
 RT binding domain.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
 RA Zhang Q., Shanahan C.M.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Almeida J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M.,
 RA Tracey A., Williams S.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 1-856 FROM N.A.
 RC TISSUE=Kidney;
 RA Gough L., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.;
 RT "Golgi localization of syn-1.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.
 RC TISSUE=Adrenal gland, and Testis;Ovariochondria;
 RA Niimiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Katuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,

RA Kakenori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Takeuchi M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
RA Nagai K., Isegai T.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 443-8797 FROM N.A. (ISOFORM 5).
RC TISSUE=Brain;
RX MEDLINE=21082923; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.",
RL DNA Res. 7:347-355(2000).
RN [9]
RP SEQUENCE OF 743-8797 FROM N.A. (ISOFORM 6).
RC TISSUE=Brain;
RA Amorge W., Winkler U., Newes H.-W., Weil B., Wiemann S.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirotsawa M., Nomura N.,
RA Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.",
RL DNA Res. 6:337-345(1999).
RN [11]
RP SEQUENCE OF 6922-8797 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kishimi H., Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.",
RL DNA Res. 5:277-286(1998).
RN [12]
RP REVISIONS.
RC TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.,
RT "Construction of expression-ready cDNA clones for KIA clones: manual
RT curation of 330 KIA cDNA clones.",
RL DNA Res. 9:99-106(2002).
RN [13]
RP SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=21659781; PubMed=11801724;
RA Mielow J.M.K., Kim M.S., Davis D.B., McNally E.M.,
RT "Myo-1, a spectrin repeat transmembrane protein of the myocyte inner
RT nuclear membrane, interacts with lamin A/C.",
RL J. Cell Sci. 115:61-70(2002).
RN [14]
RP SEQUENCE OF 8406-8797 FROM N.A.
RA Ma F.-R., Zhu L.-P.,
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the maintenance of nuclear organisation and
CC structural integrity. Probable anchoring protein which cheters the
CC nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton
CC by interacting with the nuclear envelope and with F-actin in the
CC cytoplasm.
CC -1- SUBUNIT: Interacts with MUSK, with F-actin via its N-terminal
CC domain, and with LMNA in vitro (By similarity).
CC -1- SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The
CC largest part of the protein is cytoplasmic, while its C-terminal
CC part is associated with the nuclear envelope, most probably the
CC outer nuclear membrane. In skeletal and smooth muscles, a
CC significant amount is found in the sarcomeres.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Name=1;

```

CC      IsoId=Q8NF91-1; Sequence=Displayed;
CC      Name=2; Synonyms=Beta;
CC      IsoId=Q8NF91-2; Sequence=VSP_007130;
CC      Name=3; Synonyms=Alpha;
CC      IsoId=Q8NF91-3; Sequence=VSP_007132, VSP_007144;
CC      Name=4;
CC      IsoId=Q8NF91-4; Sequence=VSP_007134, VSP_007139, VSP_007140,
CC      VSP_007144;
CC      Name=5;
CC      IsoId=Q8NF91-5; Sequence=VSP_007135, VSP_007136;
CC      Note=No experimental confirmation available;
CC      Name=6;
CC      IsoId=Q8NF91-6; Sequence=VSP_007137, VSP_007138;
CC      Note=No experimental confirmation available;
CC      Name=7;
CC      IsoId=Q8NF91-7; Sequence=VSP_007141, VSP_007142;
CC      Note=No experimental confirmation available;
CC      Name=8; Synonyms=Beta 2;
CC      IsoId=Q8NF91-8; Sequence=VSP_007131;
CC      Name=9; Synonyms=Alpha 2;
CC      IsoId=Q8NF91-9; Sequence=VSP_007133, VSP_007143, VSP_007144;
CC      TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal
CC      and smooth muscles, heart, spleen, and peripheral blood
CC      leukocytes.
CC      -1 DOMAIN: The KlsrAicht domain, which contains a transmembrane
CC      domain, mediates the nuclear envelope targeting.
CC      -1 SIMILARITY: Belongs to the naspin family.
CC      -1 SIMILARITY: Contains 1 actin-binding domain.
CC      -1 SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC      -1 SIMILARITY: Contains 12 HAT repeats.
CC      -1 SIMILARITY: Contains 1 KlsrAicht domain.
CC      -1 SIMILARITY: Contains 31 spectrin repeats.
CC      -1 CAUTION: Ref.5 (CAB55865, CAB55866, CAC16280 and CAC16281)
CC      sequences differ from that shown due to erroneous gene model
CC      prediction.
CC      -1 CAUTION: Ref.7 (BAB71097) sequence differs from that shown due to
CC      a chimeric cDNA.
CC      -1 CAUTION: Ref.14 sequence differs from that shown due to two
CC      frameshifts in positions 8412 and 8784.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by, and for commercial
CC      entities require a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).
CC      or send an email to license@isb-sib.ch.
CC      -----
CC      EMBL, AY061755, AAL33798.1; -
CC      EMBL, AY061756, AAL33799.1; -
CC      EMBL, AF495910, AAN60442.1; -
CC      EMBL, AF555142, AAN03486.1; -
CC      EMBL, AY184203, AAO27771.1; -
CC      EMBL, AY184206, AAO27774.1; -
CC      EMBL, AL049548, CAB55865.1; ALT_SEQ.
CC      EMBL, AL049548, CAB55866.1; -
CC      EMBL, AL078582, CAB87586.1; -
CC      EMBL, AL136079, -; NOT_ANNOTATED_CDS.
CC      EMBL, AL138832, CAC16280.1; ALT_SEQ.
CC      EMBL, AL138832, CAC16281.1; ALT_SEQ.
CC      EMBL, AL135708.1; -; NOT_ANNOTATED_CDS.
CC      EMBL, AL154041, -; NOT_ANNOTATED_CDS.
CC      EMBL, AL589963, -; NOT_ANNOTATED_CDS.

```

```

Db      6943 YAHIEHYLOKXGKFKIDINCKQITVDVFNQSVL-----QISSQVSEKRDCKTDPAEQ 6996
Qy      159 GLFHHVPLVANIIGSEQLGYTVSGCMS--TGFSRAVQTHSSKFEEDGSLKEVHKINE 217
Db      6997 GAMNNSWQLOGL-VTERK--QLTGLLSMSEYENNNQCKLTWETPEKXKLOOHRIGD 7053
Qy      218 MYASIQEELKSTICKXVESEQAVDLVQVNLKKEIEKRGKQIQAREKNIQKDPEN 277
Db      7054 Q-ASVQNALKD-CODLED-----LIK-----AKEKEVEKIEQNG 7085
Qy      278 IFGLQALRTFFPNSPEFLHSCVMSLKRRHVSXSSCNVNHLDVVDNLTLMEVHTDIPBASP 337
Db      7086 LALIQ-----NKEKRVSSIVSTL-RELGGTWMALDH--MVQGLKTLIK----- 7126
Qy      338 ASTPQIIRK-AID-----LDRWQFKSRLLDTQDKRSKANTGSSNQDKASKMSPEP 390
Db      7127 SYLDQWSSHKVAFDKINSYLMARVSLSRFRL-----TQSLRAVQVVDNLQNL 7176
Qy      391 DEEIECKX 398
Db      7177 QDDLEKQE 7184

```

RESULT 3

AKA9 RABIT STANDARD; PRT; 1087 AA.

```

AC Q28628;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE A-kinase anchor protein 9 (protein kinase A anchoring protein 9)
DE (PKRA9) (A-kinase anchor protein 120 kDa) (AKAP 120) (Fragmant).
GN AKAP9 OR AKAP120.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Gastric parietal cell;
RX MEDLINE=97220389; PubMed=9148752;
RA Dransfield D.T., Yeh J.L., Bradford A.J., Goldentring J.R.;
RT "Identification and characterization of a novel A-kinase-anchoring
RT protein (AKAP120) from rabbit gastric parietal cells."
RL Biochem. J. 322:801-808(1997).
CC -1- FUNCTION: Binds to type II regulatory subunits of protein kinase
CC A. May be a scaffolding protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in gastric parietal cells.
CC -1- DOMAIN: RII-binding site, predicted to form an amphipathic helix,
CC could participate in protein-protein interactions with a
CC complementary surface on the R-subunit dimer.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U26360; AAC35413.1; ALT_INIT.
KW Coiled coil.
FT NON TER 1
FT DOMAIN 559 572 PKA-RII SUBUNIT BINDING DOMAIN.
FT DOMAIN 5 461 COILED COIL (POTENTIAL).
FT DOMAIN 614 773 COILED COIL (POTENTIAL).
FT NON TER 1087 1087
SQ SEQUENCE 1087 AA; 124756 MW; 90916BEC0CA89FF02 CRC64;

```

Query Match 5.8%; Score 122; DB 1; Length 1087;
 Best Local Similarity 19.8%; Pred. NO. 3.4; Indels 94; Gaps 13;
 Matches 68; Conservative 59; Mismatches 122;

```

Qy      79 EVNEQALKILSNVKNVGVYKFRHSQDITFERRLHKYLQEHFNSQDVLFIILTPS 138
Db      205 EVQLQERAPADIKREKEITNL-----EQQLQFRELLENKNEVQQLMQL----- 251
Qy      139 IITESCSTHRL-----EHLGYKQKGLFRRVPLVANIIGMSQGLGYTVSGCMSGTGSR 193
Db      252 -IQKKESTRRLQLEQENLTFQDE-----MKTGLPAIKESDAVSPQDQ 294
Qy      194 AVQTHSSKFEEDGSLKEVHKINEMYASIQEELKSTICKXVESEQAVDLVQVNLKKE 253
Db      295 VLFGRKAQIIIE--KEVEIDRLNEQIIKIQQQLKTTD-----NKVIEKKEILLRD 343
Qy      254 IEKRGKQIOA--AREKNIQKDPENIFLQALRTFFPNSPEFLHSCVMSLKNR----- 304
Db      344 LE-----AQIECLMSDQERAKNREEL-----EQNLNVEIKLQOELANIDQK 386
Qy      305 -----HVSXSSCNVNHLDVVDNLTLMEVH-TDIPBASPASTPQIIRKALDLD----- 353
Db      387 TSVDPSLSREADSLKHQLDKVIATKALAEHOVETNEEMAVTKNVLKKTENFRKNQLTG 446
Qy      354 -----RWQFKSRRLDTQDKRSKANTGSSNQDKASKMSPEP 391
Db      447 LSLKREKREKMERIQSVPEKSVMSVGLSKDK-----PMD 483

```

RESULT 4

CENF HUMAN STANDARD; PRT; 3210 AA.

```

ID CENF HUMAN
AC P49454; Q13171; Q13246;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE CENF-F kinetochore protein (Centromere protein F) (Nucleosome
DE antigen).
GN CENPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95348175; PubMed=7542657;
RA Liao H., Winkler R.J., Mack G., Rattner J.B., Yen T.J.;
RT "CENF-F is a protein of the nuclear matrix that assembles onto
RT kinetochores at late G2 and is rapidly degraded after mitosis."
RL J. Cell Biol. 130:507-518(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95379848; PubMed=7651420;
RA Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B.,
RA Jones D., Yang-Feng T.L., Lee W.-H.;
RT "Characterization of a novel 350-kilodalton nuclear phosphoprotein
RT that is specifically involved in mitotic-phase progression."
RL Mol. Cell. Biol. 15:5017-5029(1995).
RN [3]
RP SEQUENCE OF 2194-3210 FROM N.A.
RX MEDLINE=95336446; PubMed=7612011;
RA Li Q., Ke Y., Kapp J.A., Peritt N., Medsger T.A. Jr., Joshi H.C.;
RT "A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal
RT domain sufficient for nuclear localization."
RL Biochem. Biophys. Res. Commun. 212:220-228(1995).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95370296; PubMed=7642639;
RA Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;
RT "The C terminus of nucleosome targeting and dimerization."
RL J. Biol. Chem. 270:19545-19550(1995).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=98437347; PubMed=9763420;

```

RA Chan G.K.T., Schaar B.T., Yen T.J.:
 RT "Characterization of the kinetochore binding domain of CENP-E reveals
 interactions with the kinetochore proteins CENP-F and HUB1.";
 RL J. Cell Biol. 143:49-63(1998).
 [6]
 RN FARNESYLATION.
 RP MEDLINE=20459117; PubMed=10852915;
 RX Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L.,
 RA Bishop W.R., Kirschmeier P.:
 RT "Farnesyl transferase inhibitors block the farnesylation of CENP-E
 and CENP-F and alter the association of CENP-E with the
 RT microtubules.";
 RL J. Biol. Chem. 275:30451-30457(2000).
 CC -1- FUNCTION: Probably required for kinetochore function, involved in
 chromosome segregation during mitosis. Interacts with
 CC retinoblastoma protein (RB), CENP-E and HUB1.
 CC -1- SUBUNIT: Homo- or heterodimer.
 CC -1- SUBCELLULAR LOCATION: Nuclear matrix (but not in the nucleolus);
 CC reorganization to the kinetochore/centromere (coronal surface of
 CC the outer plate) and the spindle during mitosis.
 CC -1- DEVELOPMENTAL STAGE: Gradually accumulates during the cell cycle.
 CC -1- PTM: Hyperphosphorylated during mitosis.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U19769; AAA8289.1; -;
 DR EMBL; U30872; AAA82935.1; -;
 DR EMBL; U25725; AAA8689.1; -;
 DR PIR; PC4035; PC4035.
 DR Gene; HGNC:1857; CENPF.
 DR GK; P49454; -;
 DR MIM; 600236; -;
 DR GO; GO:0005699; C:kinetochore; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0005819; C:spindle; TAS.
 DR GO; GO:0000667; P:DNA replication and chromosome cycle; TAS.
 DR GO; GO:0007088; P:regulation of mitosis; TAS.
 DR Chromosomal protein; Nuclear protein; Centromere; coiled coil;
 KM Microtubule; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;
 KM Lipoprotein; Prenylation.
 KM DOMAIN 14 197 COILED COIL (POTENTIAL).
 FT DOMAIN 273 769 COILED COIL (POTENTIAL).
 FT DOMAIN 823 1328 COILED COIL (POTENTIAL).
 FT DOMAIN 1642 1746 COILED COIL (POTENTIAL).
 FT DOMAIN 1862 2987 COILED COIL (POTENTIAL).
 FT DOMAIN 2207 2568 2 X 177 AA TANDDEM REPEATS.
 FT REPEAT 2207 2386 1.
 FT REPEAT 2389 2568 2.
 FT REPEAT 2389 3032 3.
 FT DOMAIN 3015 3032 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT LIPID 3207 3207 K->N (in dbSNP:7289).
 FT VARIANT 3202 3202 /FTID=VAR_014839.
 FT CONFLICT 16 16 T->A (IN REF. 2).
 FT CONFLICT 250 250 L->Q (IN REF. 2).
 FT CONFLICT 272 272 G->D (IN REF. 2).
 FT CONFLICT 611 611 MISSING (IN REF. 2).
 FT CONFLICT 1494 1589 MISSING (IN REF. 2).
 FT CONFLICT 1611 1611 V->A (IN REF. 2).
 FT CONFLICT 1811 1811 V->L (IN REF. 2).
 FT CONFLICT 2242 2243 ER->DG (IN REF. 3).
 FT CONFLICT 2335 2335 L->Q (IN REF. 3).
 FT CONFLICT 2492 2492 D->N (IN REF. 2).
 FT CONFLICT 2545 2561 ELINERVAALINDQEAACK->SSMRWQPCIMTKKPVSS
 (IN REF. 3).
 SQ SEQUENCE 3210 AA; 367569 MW; 11D63324960E8334 CNG64;
 Query Match 5.88; Score 122; DB 1; Length 3210;

Best Local Similarity 20.7%; Pred. No. 13;
 Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;
 QY 36 EVKGEAKNS-ITDSQMDVVEVYTIQKYI-----PCYQSFSPYNSGEVNEQALKKI 88
 DB 817 EADQSPKXSAIIQWRVLSLE--FSLSQKQNSDLDQKCELVQI--KGIENLMK-- 869
 QY 89 LSNVKKVWGVGKRRRSDDQIMFRE-RLAHKNQGEH-----FSNQDLVFIILTPSITTES 143
 DB 870 AEQWQGSFVA-----ETSORISKLQEDTSAHONVAVETLSALEKKELOLDNDKVTBQ 924
 QY 144 C-----STRLEHSLYKQKGLFRRVPIVAVTNGSEQLGYKTVSGSCMSTGSPAVQ 196
 DB 925 AEIQELKSNHLLBDSIKELQL-----LSETLSLEKEMSSHISANKKEIE 970
 QY 197 THSKFPBEDQSLKEVAKINEMVSLQBELKICKYEDSQAQDKVQVNRKREIK 256
 DB 971 ---ELTQENGTLEIN-----ASLNQEKNTLQKSESPANYIDEREKSISELSDQKQ 1020
 QY 257 RGAQIQAAERK-NIQKDPENIFLCOALRTPFPENSE---FLNSCVMSLNRRHYSKSCN 312
 DB 1021 EKLLQRCBETGNAYVDLSQKYAAQE-----KNSKLEGLNCTSLCENRKXELBQLK 1075
 QY 313 ---YNEHLVDVNDUTLWVEHTDIPASPASTPQITKAKALDDDRNQPKSRLDTPDKR 369
 DB 1076 EAPAKHQEFITKLAFAEERN-----QWLMLELTVQQLRSEMTDNQN-N 1120
 QY 370 SKANTGSSNQ-----PKASCKMSPETD--EIEIKM 397
 DB 1121 SKSRAGLKGQETMLTKEQNKMKQKENVVDLQENQL 1156
 RESULT 5
 ID SCPI_MOUSE STANDARD; PRT; 993 AA.
 AC 062209; 009205; P70192; 062329;
 DT 15-0UL-1998 (Rel. 36, Created)
 DT 15-0UL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Synaptonemal complex protein 1 (SCP-1 protein).
 GN SYCP1 OR SCPI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA; TISSUE=Testis;
 RX MEDLINE=96004899; PubMed=7548215;
 RA Sage J., Martin L., Guzin F., Rassoulzadegan M.;
 RT "cDNA sequence of the murine synaptonemal complex protein 1 (SCP1).";
 RL Biochim. Biophys. Acta 1263:258-260(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss; TISSUE=Testis;
 RA Kerr S.M., Taggart M.H., Lee M., Cooke H.J.;
 RT Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-149 FROM N.A.
 RC STRAIN=C57BL/6;
 RA Sage J., Li Y., Martin L., Mattei M.-G., Guenet J.-L., Liu J.G.,
 RA Hoeg C., Guzin F., Rassoulzadegan M.;
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 95-787 FROM N.A.
 RC STRAIN=ICR; TISSUE=Testis;
 RA Tsuchida Y., Nishina Y., Nozaki M., Uchida K., Nishimura Y.;
 RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Major component of the transverse filaments of
 CC synaptonemal complexes (SCS), formed between homologous
 CC chromosomes during meiotic prophase.
 CC -1- SUBCELLULAR LOCATION: Nuclear. In tripartite segments of
 CC synaptonemal complexes, between lateral elements in the nucleus.

CC Found only where the chromosome cores are synapsed. Its N-terminus
 CC is found towards the centre of the synaptonemal complex while the
 CC C-terminus extends well into the lateral domain of the
 CC synaptonemal complex (By similarity).
 CC -1- DOMAIN: Consists of an alpha-helical stretch of 700 AA residues,
 CC flanked by N- and C-terminal globular domains. The C-terminal
 CC domain has DNA-binding capacity (By similarity).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z38118; CAA86262.1; -
 CC EMBL; L41069; AAC64514.1; ALT_INIT.
 CC EMBL; U62864; AAC53335.1; -
 CC EMBL; U62860; AAC53335.1; JOINED.
 CC EMBL; U62861; AAC53335.1; JOINED.
 CC EMBL; U62862; AAC53335.1; JOINED.
 CC EMBL; U62863; AAC53335.1; JOINED.
 CC EMBL; D88539; BAA13639.1; -
 CC PIR; S49461; S49461.
 CC MGD; MG110593.1; Sygpl.
 CC GO; GO:0000795; C:synaptonemal complex; IDA.
 CC InterPro; IPR008827; SCP-1.
 CC Pfam; PF05483; SCP-1; 1.
 CC Nuclear protein; Meiosis; Cell division; Phosphorylation;
 CC DNA-binding; Coiled coil.
 CC
 CC FT DOMAIN 12 ASP/GLU-RICH (ACIDIC).
 CC FT DOMAIN 104 97 COILED COIL (POTENTIAL).
 CC FT DOMAIN 114 815 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT DOMAIN 697 700 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT DOMAIN 898 901 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT DOMAIN 978 986 ARG/LYS-RICH (BASIC).
 CC FT CONFLICT 527 527 F -> L (IN REF. 2).
 CC FT SEQUENCE 993 AA; 115962 MW; 1AAFA790D64FAF66 CRC64;

Query Match 5.7%; Score 121; DB 1; Length 993;
 Best Local Similarity 18.4%; Pred. No. 3.6;
 Matches 89; Conservative 91; Mismatches 151; Indels 152; Gaps 22;

CC 21 OHNTDSDTSGFLGKVG-----EAKNSITSDMDVEVVTIDIOKYPICYGF 71
 CC 361 ELKAKATTTSFVTELEKATTCLEELRTQORLEKNEBQKLT-TVELQKSNLEEM 419
 CC DB 72 SFYNSGSEVQALKKILS-----NYKNVGVGMYKFRHSDQINTP---RELLH--- 118
 CC DB 420 TKFQNKREVELLEKNTLAEQKLDKQVEKLAELQEKQELTFLETRKEVHQDQ 479
 CC DB 119 -----KTLQEHFENO-----DIVELLPSIITSCSTHREHSLYKQKGLFRRVPL 166
 CC DB 480 EQVTVTTSQCHYKQVEKMTLEKXNTLEITASCMLLENKKFQVE----- 530
 CC DB 167 VVANIAGMSQGLGYKTVSGSCMSTGFSRAVQTHSKFP-----EEDGSLKEVHKINEMVYASL 222
 CC DB 531 -----ASDMALLEKKHQGDITINCKQEBRLKQLENEKEEMH 569
 CC DB 223 QEEIKSL-----CK-KVDSQAVD-----KLVVD-VNRLKREKR 257
 CC DB 570 RDELESVKERTIQGDQEVKCLDSEENARSIEVLLKKEKQMTLESKKNLKKQVEN- 628
 CC DB 258 RGAQIQAREKNIQKDPQENIFL-----COALRTFPNSEFLHSCWMLKNRHVSKS 310
 CC DB 629 -----KSKNTEIHEQENKTLKKSAEIKQNAVYEIKVSKLELESTKQRFPEEMT 680
 CC DB 311 CNYVHHLD--VVDNLTLMTVEHTDIPKSPASTPQIR-KHALLDDDWQKRRLLDTPD 367
 CC DB 681 -NYKEIEENKKISGKLGE-----VEKAKATVDAVAKLQKEITD--RCQHKIEMVYALME 733
 CC DB 368 KRS-----KANTG--SSNQDASKMSSPETD-----EELI 395

Db 734 KHKHQYKIVERDSEIGLYKNEQEOSSAKIALFTELNSIRNELVSLKKQLEIEKEKE 793
 QY 396 KMK 398
 Db 794 KTK 796

RESULT 6
 MACF_MOUSE STANDARD; PRT; 5327 AA.
 ID MACF_MOUSE
 AC Q9QXZ0: P97394; P97395; P97396;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Microtubule-actin crosslinking factor 1 (Actin cross-linking family
 DE 7).
 GN MACF1 OR MACF OR ACP7 OR ACP7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=BALB/c;
 RX MEDLINE=20069791; PubMed=10601340;
 RA Leung C.L., Sun D., Zheng M., Knowles D.R., Liem R.K.H.;
 RT "Microtubule actin cross-linking factor (MACF): a hybrid of dystronin
 RT and dystrophin that can interact with the actin and microtubule
 RT cytoskeletons";
 RL J. Cell Biol. 147:1275-1286(1999).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=97124842; PubMed=8954775;
 RA Bernier G., Mathieu W., De Repentigny Y., Vidal S.M., Kothary R.;
 RT "Cloning and characterization of mouse ACP7, a novel member of the
 RT dystronin subfamily of actin binding proteins";
 RL Genomics 38:19-29(1996).
 CC -1- FUNCTION: F-actin-binding protein which may play a role in cross-
 CC linking actin to other cytoskeletal proteins. Also binds to
 CC microtubules.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=2;
 CC IsoId=Q9QXZ0-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=Q9QXZ0-2; Sequence=VSP_000717;
 CC Note=Incomplete sequence;
 CC Name=3;
 CC IsoId=Q9QXZ0-3; Sequence=VSP_000718;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in lung, brain, spinal cord,
 CC skeletal and cardiac muscle, and skin.
 CC -1- SIMILARITY: Contains 1 actin-binding domain.
 CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -1- SIMILARITY: Contains 37 spectrin repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF150755; AAD32244.1; -
 CC EMBL; U67203; AAC52988.1; -
 CC EMBL; U67204; AAC52989.1; -
 CC EMBL; U67205; AAC52990.1; -
 CC HSSP; Q01082; 1BKX.

DR MGD; MG1:108559; Macfi.
 DR InterPro; IPR001589; Actbind_actinin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR003108; GAS2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF02187; GAS2; 1.
 DR Pfam; PF00435; spectrin; 27.
 DR Prodom; PD000012; EF-hand; 1.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00054; EH; 2.
 DR SMART; SM00243; GAS2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00150; SPEC; 36.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 DR PROSITE; PS50021; CH; 2.
 DR PROSITE; PS50002; SH3; FALSE_NEG.
 DR Actin-binding; Cytokeleton; Calcium-binding; Repeat; SH3 domain.
 KM Alternative splicing.
 FT DOMAIN 1 295 ACTIN-BINDING (BY SIMILARITY).
 FT 78 181 CH 1.
 FT DOMAIN 194 295 CH 2.
 FT REPEAT 314 355 SPECTRIN 1.
 FT REPEAT 591 623 SPECTRIN 2.
 FT REPEAT 680 784 SPECTRIN 3.
 FT REPEAT 786 800 SPECTRIN 4.
 FT DOMAIN 871 923 SH3.
 FT REPEAT 1250 1272 SPECTRIN 5.
 FT REPEAT 1287 1342 SPECTRIN 6.
 FT REPEAT 1458 1534 SPECTRIN 7.
 FT REPEAT 1593 1660 SPECTRIN 8.
 FT REPEAT 1817 1866 SPECTRIN 9.
 FT REPEAT 1934 2044 SPECTRIN 10.
 FT REPEAT 2262 2282 SPECTRIN 11.
 FT REPEAT 2376 2397 SPECTRIN 12.
 FT REPEAT 2400 2509 SPECTRIN 13.
 FT REPEAT 2557 2617 SPECTRIN 14.
 FT REPEAT 2620 2727 SPECTRIN 15.
 FT REPEAT 2730 2837 SPECTRIN 16.
 FT REPEAT 2840 2944 SPECTRIN 17.
 FT REPEAT 2946 2972 SPECTRIN 18.
 FT REPEAT 2986 3025 SPECTRIN 19.
 FT REPEAT 3086 3162 SPECTRIN 20.
 FT REPEAT 3195 3273 SPECTRIN 21.
 FT REPEAT 3276 3382 SPECTRIN 22.
 FT REPEAT 3385 3491 SPECTRIN 23.
 FT REPEAT 3494 3518 SPECTRIN 24.
 FT REPEAT 3603 3709 SPECTRIN 25.
 FT REPEAT 3722 3817 SPECTRIN 26.
 FT REPEAT 3869 3930 SPECTRIN 27.
 FT REPEAT 3933 4039 SPECTRIN 28.
 FT REPEAT 4042 4149 SPECTRIN 29.
 FT REPEAT 4152 4258 SPECTRIN 30.
 FT REPEAT 4261 4368 SPECTRIN 31.
 FT REPEAT 4371 4477 SPECTRIN 32.
 FT REPEAT 4480 4587 SPECTRIN 33.
 FT REPEAT 4594 4695 SPECTRIN 34.
 FT REPEAT 4698 4804 SPECTRIN 35.
 FT REPEAT 4807 4872 SPECTRIN 36.
 FT REPEAT 4917 4941 SPECTRIN 37.
 FT CA_BIND 4998 4998 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 5023 5034 EF-HAND 2 (POTENTIAL).
 FT DOMAIN 5173 5180 POLY-SER.
 FT DOMAIN 5252 5267 4 X 4 AA TANDEN REPEATS OF [GS]-S-R-[AR].
 FT VARSPLIC 1 MSSDETLTSSRSRSRSRSRSRSRSRSGLSPCPGQ
 FT 1 QAYEDVLERX (in isoform 1).
 FT /FTid=VSP_000717.

FT VARSPLIC 1 181 MSSDETLTSSRSRSRSRSRSRSRSGLSPCPGQ
 FT 1 TLFWNLPLHOKKRSQSDVLDPAERAVVAVVADRDVOKK
 FT 1 TETKVNKHLMKVAKINDYEDLRDGNLISLEVLGK
 FT 1 LPRKGRMFRRLNOVALDFLKRQOVKVININDITDG
 FT 1 NPKTLGLITLHFO -> MNSLICKVPEKSTIVPEK
 FT 1 AFISPKRVFRKMKRKKITLPASRREBLSTGYTER
 FT 1 ETLTKLTPALPKEPVGGAHPSPDILPGDSAPNSGVGD
 FT 1 GMIVQKESFQAEIOTAHLLLENSSVVGAMDSLEGMTV
 FT 1 IAHLLDNPARNCKSVLSQVFPRTASCRAVLPLDQGE
 FT 1 TAVEGGTLNHRHRSSTLPRTDYSETVDQDSGMSVG
 FT 1 GRTKSVSPADPTGSIKASVYASIIIPROSGPHTEPTVG
 FT 1 LYSCKGPIPMASQSDSVSGITVYSITLSSSGYSGDGLRNG
 FT 1 IREBDTEKSTISFSEEDGTLSE (in isoform 3).
 FT /FTid=VSP_000718.
 FT L -> P (IN REF. 2; AAC52990).
 FT Q -> H (IN REF. 2).
 FT CONFLICT 393 393
 FT CONFLICT 1882 1882
 SQ SEQUENCE 5327 AA; 607972 MW; 5DB4FF5A6514BFFA CRC64;
 Query Match 5.7%; Score 121; DB 1; Length 5327;
 Best Local Similarity 21.4%; Pred. No. 29; Mismatches 113; Indels 124; Gaps 19;
 Matches 80; Conservative 57; Mismatch 113; Indels 124; Gaps 19;
 QY 82 EQALKILS-----NVKGVVGVYFRSHSDQIMTFR-ERL-----LHKNLQE 123
 DB 937 EQSYQKVALMHQHLINT-KSLISWNYLRKOLDIVQYWSLEKRLAPGECHQVMAKULQA 995
 QY 124 HPSN--QDLVFLITPSEITTESCTHLEHSLYPOKGLFHRVPLVYANLGMSEQLGYKT 181
 DB 996 HYEDFLD-----SH-----DSALF-----SVADRLITEE 1020
 QY 182 VSGSCMTGFSRAVQVOTHSKFFEDGSLKEVHKINENYASLOEIKSICKVEDSEQAVD 241
 DB 1021 EVELAC-----KAFQHLKMSLENEDEKEFTLAKV---YIS---ELKNIRLLDECEGRLL 1068
 QY 242 KLVVDVRLKREIKRRGAQIOAAREKNIQDPOE-----NIFLQALRTFFP 289
 DB 1069 KOIOSPASKTDARDADITLRIAEQHTQEDDQHLNSDDIDATSMKCNVFPQOS-----P 1123
 QY 290 NSEFLHGC-----VMSLKNHVSKSGCNVNHHLDDVV-----NLTMVETHTI-----P 333
 DB 1124 SGGSATTLRSRLNLMVKRMHVGLSTVYLNKLTIVYRSMODALVKGVTIKLSQE 1183
 QY 334 EASPASTPQIIKHKALDLDPRQFKSRLLDTPDKRSKANTGSSNQDKASRMSSPETDEE 393
 DB 1184 EAVPADLSALESHRT--TLQHM-----LSDVCKDKNSVFSV-----LDSE 1220
 QY 394 IEKMKGFGEYGRSP 407
 DB 1221 ITKAKVAEQLRHP 1234
 RESULT 7
 MACF_HUMAN STANDARD; PRT; 5430 AA.
 AC Q9UPN3; Q75053; Q8WXY2; Q9H540; Q9UKP0; Q9ULG3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Microtubule-actin crosslinking factor 1, isoforms 1/2/3 (Actin cross-
 DE linking family protein 7) (Macrophin 1) (Tubaculin-alpha) (620 kDa
 DE actin-binding protein) (ABP620)
 GN MACP1 OR AC7 OR ABP620 OR KIAA0465 OR KIAA1251.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20001959; PubMed=10529403;
 RA Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
 RA Takahashi M., Ishigaki T., Hamaguchi M.;
 RT "Molecular cloning of macrophin, a human homologue of Drosophila
 RT kakapo with a close structural similarity to plectin and dystrophin.";

RL Biochem. Biophys. Res. Commun. 264:568-574(1999).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20026884; PubMed=10559237;
 RA Sun Y., Zhang J., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y.,
 RA Sutherland R., Saigal R., Griffin J.D., Ferland L.H., Chen L.B.;
 RT "Molecular cloning and characterization of human trabecular-alpha, a
 RT giant protein defining a new family of actin-binding proteins";
 RL J. Biol. Chem. 274:33522-33530(1999).
 RN (3)
 RP SEQUENCE OF 182-4812 FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=21833812; PubMed=11845288;
 RA Gong T.-W.L., Besirli C.G., Lomax M.I.;
 RT "MACF1 gene structure: a hybrid of plectin and dystrophin";
 RL Mamm. Genome 12:852-861(2001).
 RN (4)
 RP SEQUENCE OF 868-2350 FROM N.A.
 RX TISSUE=Brain;
 RC MEDLINE=20039619; PubMed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:337-345(1999).
 RN (5)
 RP SEQUENCE OF 1544-5057 FROM N.A.
 RX Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP SEQUENCE OF 3312-5430 FROM N.A.
 RX TISSUE=Brain;
 RC MEDLINE=22158633; PubMed=12168954;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones";
 RL DNA Res. 9:99-106(2002).
 RN (7)
 RP SEQUENCE OF 3734-5430 FROM N.A.
 RX TISSUE=Brain;
 RC MEDLINE=98116662; PubMed=9455484;
 RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
 RA Nakajima D., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones in size-fractionated cDNA libraries
 RT from human brain";
 RL DNA Res. 4:345-349(1997).
 RN (8)
 RP FUNCTION: F-actin-binding protein which may play a role in cross-
 RP linking actin to other cytoskeletal proteins. Also binds to
 RP microtubules (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=2;
 CC IsoId=G9UPN3-2; Sequence=Displayed;
 CC Name=1;
 CC IsoId=G9UPN3-1; Sequence=VSP_007341;
 CC Name=3;
 CC IsoId=G9UPN3-3; Sequence=Not described;
 CC Name=4;
 CC IsoId=G96PK2-1; Sequence=External;
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
 CC -1- SIMILARITY: Belongs to the plectin or cytolinker family.
 CC -1- SIMILARITY: Contains 1 actin-binding domain.
 CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -1- SIMILARITY: Contains 3 spectrin repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation in
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF029290; BAA63821.1; -;
 DR EMBL; AF141968; AAF06360.1; -;
 DR EMBL; AF325341; AAL39000.1; -;
 DR EMBL; AF325330; AAL39000.1; JOINED.
 DR EMBL; AF325331; AAL39000.1; JOINED.
 DR EMBL; AF325332; AAL39000.1; JOINED.
 DR EMBL; AF325333; AAL39000.1; JOINED.
 DR EMBL; AF325334; AAL39000.1; JOINED.
 DR EMBL; AF325335; AAL39000.1; JOINED.
 DR EMBL; AF325336; AAL39000.1; JOINED.
 DR EMBL; AF325339; AAL39000.1; JOINED.
 DR EMBL; AF325340; AAL39000.1; JOINED.
 DR EMBL; AB033077; BAA6565.1; -;
 DR EMBL; AL137853; CAC15920.1; -;
 DR EMBL; AB007934; BAA32310.2; -;
 DR PIR; T00079; T00079.
 DR HSSP; Q01082; IBKR.
 DR Genew; HGNC:13664; MACF1.
 DR GO; GO:0005856; C:cytoskeleton; NAS.
 DR GO; GO:0003780; F:actin cross-linking activity; NAS.
 DR GO; GO:0005509; F:calcium ion binding; NAS.
 DR GO; GO:0008017; F:microtubule binding; NAS.
 DR InterPro; IPR001589; Actbind_actin.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR003108; GMS2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00036; ehband; 2.
 DR Pfam; PF02187; GAS2; 1.
 DR Pfam; PF00435; Spectrin; 27.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00054; EFh; 2.
 DR SMART; SM00243; GAS2; 1.
 DR SMART; SM00150; SPEC; 36.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; FALSE-NEG.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00002; SH3; FALSE-NEG.
 KM Actin-binding; Cytoskeleton; Calcium; Calcium-binding; Repeat;
 KW SH3 domain; Coiled coil; Alternative splicing.
 FT DOMAIN 1 295
 FT 1 181
 FT 194 295 CH 2.
 FT 243 265 COILED COIL (POTENTIAL).
 FT 477 529 COILED COIL (POTENTIAL).
 FT 722 751 COILED COIL (POTENTIAL).
 FT 816 943 COILED COIL (POTENTIAL).
 FT 1013 1118 COILED COIL (POTENTIAL).
 FT 1164 1191 COILED COIL (POTENTIAL).
 FT 1399 1690 COILED COIL (POTENTIAL).
 FT 1780 1843 COILED COIL (POTENTIAL).
 FT 1975 2005 COILED COIL (POTENTIAL).
 FT 2039 2312 COILED COIL (POTENTIAL).
 FT 2385 2417 COILED COIL (POTENTIAL).
 FT 2544 2695 COILED COIL (POTENTIAL).
 FT 2760 2838 COILED COIL (POTENTIAL).
 FT 2911 3001 COILED COIL (POTENTIAL).
 FT 3130 3164 COILED COIL (POTENTIAL).
 FT 3244 3277 COILED COIL (POTENTIAL).
 FT 3418 3482 COILED COIL (POTENTIAL).
 FT 3596 3666 COILED COIL (POTENTIAL).
 FT 3786 3806 COILED COIL (POTENTIAL).
 FT 3852 3951 COILED COIL (POTENTIAL).
 FT 3967 4218 COILED COIL (POTENTIAL).
 FT 4084 4218 COILED COIL (POTENTIAL).
 FT 4343 4378 COILED COIL (POTENTIAL).

FT	DOMAIN	4408	4437	COILED COIL	(POTENTIAL)
FT	DOMAIN	4468	4498	COILED COIL	(POTENTIAL)
FT	DOMAIN	4907	4935	COILED COIL	(POTENTIAL)
FT	DOMAIN	5044	5067	COILED COIL	(POTENTIAL)
FT	REPEAT	314	355	SPECTRIN 1.	
FT	REPEAT	591	623	SPECTRIN 2.	
FT	REPEAT	680	784	SPECTRIN 3.	
FT	REPEAT	786	800	SPECTRIN 4.	
FT	DOMAIN	871	923	SH3.	
FT	REPEAT	1250	1272	SPECTRIN 5.	
FT	REPEAT	1287	1342	SPECTRIN 6.	
FT	REPEAT	1455	1534	SPECTRIN 7.	
FT	REPEAT	1547	1659	SPECTRIN 8.	
FT	REPEAT	1815	1891	SPECTRIN 9.	
FT	REPEAT	1932	2042	SPECTRIN 10.	
FT	REPEAT	2260	2280	SPECTRIN 11.	
FT	REPEAT	2392	2395	SPECTRIN 12.	
FT	REPEAT	2398	2507	SPECTRIN 13.	
FT	REPEAT	2510	2618	SPECTRIN 14.	
FT	REPEAT	2621	2728	SPECTRIN 15.	
FT	REPEAT	2731	2838	SPECTRIN 16.	
FT	REPEAT	2841	2945	SPECTRIN 17.	
FT	REPEAT	2987	3024	SPECTRIN 18.	
FT	REPEAT	3136	3163	SPECTRIN 19.	
FT	REPEAT	3187	3274	SPECTRIN 20.	
FT	REPEAT	3277	3383	SPECTRIN 21.	
FT	REPEAT	3386	3492	SPECTRIN 22.	
FT	REPEAT	3495	3601	SPECTRIN 23.	
FT	REPEAT	3604	3673	SPECTRIN 24.	
FT	REPEAT	3713	3819	SPECTRIN 25.	
FT	REPEAT	3832	3937	SPECTRIN 26.	
FT	REPEAT	3982	4043	SPECTRIN 27.	
FT	REPEAT	4046	4152	SPECTRIN 28.	
FT	REPEAT	4155	4262	SPECTRIN 29.	

Query	Match	Similarity	Score	ID	Length
Best Local	Similarity	21.0%	Pred. No. 30		
Matches	76	Conservative	57	Mismatches	119
				Indels	110
				Gaps	16
Query	82	EQALKKILS----	NYK-KNVVGMWYKFRHSDQIMTFR-ERL-----	LHKNIQEH	124
Db	937	EQGYCKVMAIMHQLHVTNKTSLISWNYLTKRDDIVQWNMLEKLSASAPGEGCHQIMKNLOAH			996
Qy	125	FSN--QDLYFLLTBPILITFESGSTRRLHSLYKQKGLFHRVPLVYANLGMSEQLGYKV			182
Db	997	YEFPLD-----SRDSVLFPSVADRLLREEV-----			1022
Qy	183	SGSCMSGTGFSRAVQHTSSKFEEQDLSLEVKINEMYASLQEEILSKYCKVEDSEQAYDK			242
Db	1023	-EAC-----KRFQHKMKSMEHNEKETLVAK--MTIS--ELKXNIRLRELYEGRVYK			1066
Qy	243	LYKDVNRLKREIEKRGGAQIQAREKNIQKDPQENIFLCOALRT----	FFPNSFLH--		295
Db	1070	RIGSLASSRTDDAWQDNALRIAEQHEQEDLQO-----LRSDLDAYSMKCDSEPLDS			1122
Qy	296	-----SCWMSLKNR-----HVSQSGCNVYHHLDVYDNLTLWMEHNDPEAS--	PAST		340
Db	1123	PSSSSVPTLRSENLINLVECMHNVGLSTVYLANKLTQVDVYVRSIQDAELLYKYEYIKLSQ			1182
Qy	341	FOIIRKALDLDPRWQFKASRLDITQDKRSXANTGSSNODKASWSSPETDEIEIKMGF			400
Db	1183	EEVVLADLSALEHMTLRHMLSDYDKNSVFSV-----LDEELIAKAYV			1222
Qy	401	GE	402		
Db	1228	AE	1229		

[illegible]

```

Db      173 ERKEFLSQEQRKKEKKAIE-----RISEIKSIHSLEKLSSEVRNLSH 224
Qy      165 PLVAVNLGMSQGLYTVSGCMSTGFSRAVQTHSSKF-----FEEDGSLKEVHKINEMYA 220
Db      225 -----KELSEHKRLSLRQESVLAQVRGLBEKLR 256
Qy      221 SLOEELKSTCKKVEDSQ-----ANDKLVQVNRKLEIKERG----- 259
Db      257 ELERQKVEVERLEDEKKAVERKEPKAERYSLKLEIKQLRVEKREBGDLTRE 316
Qy      260 -----AQICAAEKEN-----IQKDPENIFLCOALRTPFPNSEFLHSCVMSLKNRHVSKS 309
Db      317 AAGIQQLKKAEDNSLLEITRIE-----LERELRF-----EKSHRLLETLPK----- 364
Qy      310 SCVNHLDVVDNLTMVHTDIPKASPASTPQIIR-----HKALDLDNRQPKRSKL 363
Db      365 -----MDRMQGIKALEKKNL-----TPDKVKEMVDLAKAKEBEKEITEKXKLLI 410
Qy      364 DTQDKSKANTGSSNQDKA-----SKMSGP-----ETDERIEKMGKGFEXSR 405
Db      411 -----AKSSSLKTRAQKLKAAVEIKSAERTCPVCGRELDDEHRK-NIMAEYTR 458

RESULT 9
ZIP1_YEAST STANDARD; PRT; 875 AA.
AC 1111;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Synaptonemal complex protein Zip1.
DN ZIP1 OR YDR285W OR D9819.9.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=BR1824-3B;
RX MEDLINE=93161412; Pubmed=7916652;
RT Sym M. Engbrecht J.A. Roeder G.S.;
RT "Zip1 is a synaptonemal complex protein required for meiotic
RT chromosome synapsis."
RT Cell 72:365-378(1993).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Ravetto A., Fulcon L., Gattung S., Greco T., Kirsten J.,
RA Kuubaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Riken L., Riles L., Taich A., Trevasakis E., Vignati D.,
RA Wilcox L., Wolfdan P., Vaudin M., Wilson R., Waterston R.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Required for meiotic chromosome synapsis and cell cycle
RL progression. May act as a molecular zipper to bring homologous
RL chromosomes in close apposition. Zip1 may encode the transverse
RL filaments of the synaptonemal complex.
RL -1- SUBCELLULAR LOCATION: SYNAPSMD MEIOTIC CHROMOSOMES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; 106487; AAA5239.1; -
CC EMBL; U51031; AAB64474.1; -
CC PIR; S70115; S70115.

```

```

DR      Germonline; 140777; -.
DR      SGD; S0002693; ZIP1.
DR      GO; GO:0000795; C:synaptonemal complex; IDA.
DR      GO; GO:0007126; P:meiosis; IMP.
DR      GO; GO:0007129; P:synapsis; IMP.
KW      Nuclear protein; Meiosis; Coiled coil.
FT      DOMAIN 177 333 COILED COIL (POTENTIAL).
FT      DOMAIN 397 438 COILED COIL (POTENTIAL).
FT      DOMAIN 456 752 COILED COIL (POTENTIAL).
FT      COMPLET 55 55 T -> A (IN REF. 1).
SQ      SEQUENCE 875 AA; 100035 MW; 674F12625CD9D9D CRC64;

Query Match      5.6%; Score 117.5; DB 1; Length 875;
Best Local Similarity 18.0%; Pred. No. 5;
Matches 85; Conservative 80; Mismatches 135; Indels 171; Gaps 20;

Qy      23 LNTSDTEGFLGKVK-----GEAKNSITDSQMDVYVYTTIDIQKI 65
Db      110 IENDTD-EDFEITEVRESEGVAKETKESHGDPNDSETTLKDSKME---YTWNGK-A 163
Qy      66 PCYOLFSPYNSGGEVNEQAL-----KRLSNVKNVGVWYKFRHSQDQMTFERELHK 119
Db      164 PLHT--STNNSSTSNVDYLAFTNTORICSNLKQELQ-----KQGDNKK-----LKV 210
Qy      120 NLQEHFSNQDLVFLLLTPSITTESCTHRLHSLYKPKQGLFHRVPLVANLGMSEQLG- 178
Db      211 RLQSVASNSDKI-----NEKVGK 228
Qy      179 YKTVSGCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMY-----ASLOEELK 227
Db      229 YK---SLEF-LERLITLTHSHKNOBETKLRDNRHOLYQRIISGFKTSINLNTIN 283
Qy      228 SICKKVEDSEQAVDKLVQVNRKLEIKERGAQIQAREKN---IQKDPENIFLCOAL 284
Db      284 DLGKKKKAADALMKKKEIRYLKRELDCCG-QLSEKIKNSLLIQEMGRREEMTKSI 342
Qy      285 RTFPNSSEFLH-----SCVMSLKNRHVSKSCVNNHLDV-DNLTMVHTDIPK 335
Db      343 ENFSEDAHHLDPNNKEERHDLFERKQK-----HFDVAKDTLNGLRITVVELS 395
Qy      336 SPASTPQIIRKALDLDNRQFK----- 358
Db      396 S--NTETWLKQGYVDIKENLEQKMSKDEWAKTINELSTQKGLINGVQELTSSGNI 453
Qy      359 -----KSLRLDTQDGRSAANTGSSNQDKASMSSEPTDELEIKK 398
Db      454 QTAIVSEMNNTROELDDASQTAKYASLENLVAYRAEIVQSNYEERIK 504

RESULT 10
SBCC_CIOAB STANDARD; PRT; 1163 AA.
AC 097FKI;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nuclease sbccD subunit C.
DN SBCC OR CAC2736.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1488;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VM B-1787;
RX MEDLINE=21359325; Pubmed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson K., Lee H.W., Dubois C., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Koonin E.V., Doucet-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RA bacterium Clostridium acetobutylicum."
RT J. Bacteriol. 183:4823-4838(2001).

```


Matches 96; Conservative 62; Mismatches 146; Indels 153; Gaps 21;
QY 20 FQHLNTDSDTEGFLGCVKGAANKSITD--SQMDVEVYITDID-----KXIPCYQ 69
DB 1742 FQSLMSEKDS-----LSEEVQDLKHQ:EDVVSQKQANLEATEKEDNCNTVTEGTSQIP--- 1794
QY 70 LRFSEYSGSEVNVQ-----ALKILSNKKNVGVKFKRRSDQIMFR 113
DB 1795 -----GSTEQDSLSMSTRPTGSESVPSAKSNPAVSKDPSHDEINNTLQIDQIK 1846
QY 114 ERLL-----HKNLQEHFSNODLVFL-----LTPSITTESC 144
DB 1847 ERLAGLEEKQKKKESQTLLENKNTLLSQISTKQDELKMLQEVYTKMLNQIQOELLS 1906
QY 145 STRLRLSHLYPKQKGLFHRPLVYVNLGSEQIGYTVGSCMSGTSFSAVQTHSSKFFE 204
DB 1907 RVTKLKETAEEEDKDDLEERLMOJLNLGNS-----IGNYQDV----- 1944
QY 205 EDGSLKEVHKINMYASLOEELKSIQKVEDSEQAVDKLVKVNRLKREIERKRGAGQIOA 264
DB 1945 TDAQIK-----NGL-----LSEEMKMLKKCVSELEEEKQQLVKETKVESIRKEVLEKIQ 1996
QY 265 ARF-----KNIQD-----POENIFLQALRTFFPNSFFLHSCVM 239
DB 1997 AQKEPNKSHAKELQELKKEQOEYKQLOKDCIRYQEKI---SALERTYKALEFVQT--E 2051
QY 300 SLKNRRYSSSCNYNHLDVYDNLTLMEHTIDPEASPASTPQIIRKHALDLDDEMOFAR 359
DB 2052 SQQDLDTTK-----ENLAQAVHRKKAQKQELAS-----FKYL-LDDT-QSBA 2091
QY 360 SRLDITQDKRSKANTSSNODKASKMSPEPTDEIEIK 396
DB 2092 ARVL-ADNMLKKELOSNKESVSKMK--QKDEDLER 2125
RESULT 12
RA50_PRRHO STANDARD; PRT; 879 AA.
ID RA50_PRRHO STANDARD; PRT; 879 AA.
AC 058687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR PH0929.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Furushashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuhira Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -1- SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL/ AP000004; BAA30025.1; -
DR PIR/ C71083; C71083.
DR HAMAP/ MF 00449; 1.
DR InterPro/ IPR003593; AAA_ATPase.
DR InterPro/ IPR003439; ABC_transporter.
DR InterPro/ IPR007517; Rad50_zn_hook.
DR InterPro/ IPR003405; SMC_C.
DR InterPro/ IPR003395; SMC_N.
DR Pfam/ PF04423; Rad50_zn_hook; 1.
DR Pfam/ PF02483; SMC_C; 1.
DR Pfam/ PF02483; SMC_N; 1.
DR SMART/ SM00382; AAA; 1.
DR DNA_repair/ Hydrolyase; ATP-binding; Coiled coil; Complete proteome.
KW NP_BIND 30 37 ATP (By similarity).
FT DORAIN 141 744 COILED COIL (POTENTIAL).
SQ SEQUENCE 879 AA; 103673 MW; FDE330FD1BDB929 CRC64;
Query Match 5.5%; Score 116; DB 1; Length 879;
Best Local Similarity 20.4%; Pred. No. 6.3; Indels 36; Gaps 9;
Matches 65; Conservative 65; Mismatches 153; Indels 36; Gaps 9;
QY 45 ITDSQMDVEVYITD---IQKXIPCYQLFSFYNSSGSEVNEQALKILSNKKNVGVK 101
DB 448 LTESHRKADLARKSLSELSIEKEL-----QEKALERDRLRFRVNEHLSLSS 497
QY 102 FRHSDDIMTFRRRLHKNLQEHFSNODLVLLTPSI---ITSCSTRLHSLYKPK 157
DB 498 LKTIADQIIEIRRELSKINLEDLKRDKEVEYELKSESNKLGVESEIKKEVNEINLYKNE 557
QY 158 KGLFHRPLVYVNLGMS-----QLGYKTVSGSCMSTGSPRAVQTHSSKFFEDSLKE 211
DB 558 STKL-EIIDKAKKLEIIEDRLRLRSLFKTID---ELSGIRLEKTHNNTYIAKAEKE 613
QY 212 VHKINMYASLOEELKSIQKVEDSEQAVDKLVKVNRLKREIERKRGAGQIOAREKNIQ 271
DB 614 LRDLEELKDEREELDLAFELAKIETDIKVTSQLTELQKRPQKK---YEEKREK-NM 669
QY 272 KDPOENIFLQALRTFFPNSFFLHSCVMSLKKNHVSQSCNYNHLDVYDNLTLMEHTD 331
DB 670 KLSWEINGLSTKLLELERRRDEIKSTIEKLKEKREKESHAKM-----LEKINATIRIE 724
QY 332 IPEASPASTPQIIRKHALD 350
DB 725 ELRGKIKYKALIKERALN 743
RESULT 13
KTN1_HUMAN STANDARD; PRT; 1357 AA.
ID KTN1_HUMAN STANDARD; PRT; 1357 AA.
AC Q86UP2; Q13999; Q14707; Q15387; Q86W57;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinectin (Kinectin receptor) (CG-1 antigen).
GN KTN1 OR CGI OR KIAA0004.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC Tissue=Lymphoid;
RX MEDLINE=95306853; PubMed=7787243;
RA Fuetterer A., Kruppa G., Kraemer B., Lemke H., Kroecken M.;
RT "Molecular cloning and characterization of human kinectin";
RL Mol. Biol. Cell 6:161-170(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=94314220; PubMed=6039706;
RA Print C.G., Leung E., Harrison J.E.B., Watson J.D., Kisaanzen G.W.,
RT "Cloning of a gene encoding a human leukocyte protein characterised by
RT extensive heptad repeats."
RL Gene 144:221-228 (1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wang H.-C., Chen W.-F., Su Y.-R.;
RT "Identification of a variant of Hmo sapiens kinecin mRNA."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.,
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1A0001-K1A0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1."
RL DNA Res. 1:27-35(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX PubMed=12508121;
RA Hellig R., Eckenberg R., Petit J.-U., Fonknechten N., Da Silva C.,
RA Catolico L., Levy M., Barbe V., De Berardinis V., Ureña-Vidal A.,
RA Pelleterier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Chuand C.,
RA Brunele T., Tallon O., Friedlander L., Samson G., Brothier P.,
RA Cure S., Segurens B., Aniere F., Saman S., Crespeau H., Abbast N.,
RA Alich N., Boscus D., Dichtot R., Dore M., Dubois I., Friedmann C.,
RA Guyonoux M., James R., Madan A., Malreje-Estrada B., Mangnot S.,
RA Martins N., Menard M., Octas S., Ratcliffe A., Shaffer T., Traak B.,
RA Vacheire B., Bellemere C., Belser C., Beznard-Comet M.,
RA Barthelemy D., Bouvard M., Briez-Silla S., Combette S.,
RA Dufosse-Laurent V., Perron C., Leclaplatte C., Louesse C.,
RA Magdelent G., Patreau E., Petit E., Stréval-Trukniewicz P., Trybou A.,
RA Vega-Czarny N., Bataille E., Bluet E., Bordelats I., Dubois M.,
RA Dumont C., Guerin T., Hatfay S., Hammadi R., Muanga D., Pellouin V.,
RA Robert D., Wunderle E., Gauguet G., Roy A., Sainte-Marthe L.,
RA Verdier J., Verdier-Discala C., Hillier L.M., Fulton L., McPherson J.,
RA Matsuda F., Wilson R., Scarpelli C., Gyapay G., Mincker P., Saurin W.,
RA Oetler F., Waterson R., Hood L., Weissensbach J.,
RT "The DNA sequence and analysis of human chromosome 14."
RL Nature 421:601-607(2003).
RN [6]
RP SEQUENCE OF 1-870 FROM N.A. (ISOFORMS 1/2).
RX TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shmamen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Marx S.I., Wang J., Hsieh F.,
RA DiCicco L., Marzula K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Teshigahara S., Cantino P., Prange C.,
RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek U.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.C., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherbakov Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywicki M.T., Skalska U., Smalov D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 191-195; 395-405; 545-554; 747-761 AND 811-823.
RX MEDLINE=21966647; PubMed=11973345;

RA	TRAN H. Parkov R., Tran S.D., Hampton B., Burgess W.H., Yamada K.M.;
RT	"Integrin clustering induces kinectin accumulation.";
RL	J. Cell Sci. 115:2031-2040(2002).
RN	[8]
RP	CHROMOSOMAL LOCATION.
RX	MEDLINE=9616023; PubMed=8575822;
RA	Print C.G., Morris C.M., Spur N.K., Rooke L., Kriksen G.W.;
RT	"The CG-1 gene, a member of the kinectin and ES/130 family, maps to
RL	human chromosome band 14q22.";
RL	Human Genetics 43:227-229(1996).
CC	-1- FUNCTION: Receptor for kinesin thus involved in kinesin-driven
CC	vesicle motility. Accumulates in integrin-based adhesion complexes
CC	(IAC) upon integrin aggregation by fibronectin.
CC	-1- SUBUNIT: Parallel homodimers formed between the membrane-bound and
CC	the cytosolic form, and also between 2 cytosolic forms (By
CC	similarity).
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Vesicle membrane
CC	protein anchored to the endoplasmic reticulum.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event-Alternative splicing; Named isoforms=2;
CC	Comment=Additional isoforms seem to exist;
CC	Name=1;
CC	Isoid=Q86UP2-1; Sequence=displayed;
CC	Name=2;
CC	Isoid=Q86UP2-2; Sequence=VSP_007981, VSP_007982;
CC	-1- TISSUE SPECIFICITY: High levels in peripheral blood lymphocytes,
CC	testis and ovary, lower levels in spleen, thymus, prostate, small
CC	intestine and colon.
CC	-1- SIMILARITY: Belongs to the kinectin family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; Z22551; CAB0271.1; -;
DR	EMBL; L25616; AAB65853.1; -;
DR	EMBL; AY624265; AAP20418.1; -;
DR	EMBL; D13629; BAA02794.1; -;
DR	EMBL; AL138499; -; NOT ANNOTATED CDS.
DR	EMBL; BC050555; AA50555.1; ALT_TERM.
DR	PIR; S32763; S32763.
DR	PIR; I53799; I53799.
DR	Genew; HGNC:6467; KTN1.
DR	MM; 600381; -;
DR	GO; GO:0005789; C:endoplasmic reticulum membrane; TAS.
DR	GO; GO:0005687; C:integral to plasma membrane; TAS.
DR	GO; GO:0005624; C:membrane fraction; TAS.
DR	GO; GO:0006899; P:nonelective vesicle transport; TAS.
DR	GO; GO:0007018; P:microtubule-based movement; ISS.
DR	InterPro; IPRO2011; Spectrin.
KM	Endoplasmic reticulum; Signal-anchor; Transmembrane; Coiled coil;
FT	DOMAIN 1 6
FT	TRANSEM 7 29
FT	DOMAIN 30 1357
FT	DOMAIN 330 1356
FT	CARBOHYD 172 172
FT	CARBOHYD 435 435
FT	CARBOHYD 772 772
FT	CARBOHYD 904 904
FT	CARBOHYD 1055 1055
FT	CARBOHYD 1088 1088
FT	CARBOHYD 1263 1263
FT	CARBOHYD 1329 1329
FT	VARSPIC 1031 1059
FT	VARSPIC 1232 1259
FT	VARSPIC 1232 1259
FT	Missing (in isoform 2).
FT	/FtId=VSP_007982.

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grympey B.,
RA Wellens I., Vanstreels B., Rieger W., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
RA Galibert F., Ayes S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: Belongs to the THO2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z69239; CAA3223.1; -
CC EMBL: Z54285; CAA31079.2; -
CC DR: PIR: T38055; T38055.
CC DR: GeneDB: Spocbe; Spac104.14; -
CC DR: GO: GO:0016591; C:DNA-directed RNA polymerase II, holoenzyme; ISS.
CC DR: GO: GO:0006403; P:RNA localization; ISS.
CC DR: GO: GO:0006366; P:transcription from Pol II promoter; ISS.
CC DR: GO: GO:0006350; P:transcription; ISS.
CC KW Hypothetical protein.
CC SQ SEQUENCE 1628 AA; 188831 MW; 85A30FB43D2CAED0 CRC64;

Query Match 5.5%; Score 115; DB 1; Length 1628;
Best Local Similarity 20.0%; Pred. No. 16;
Matches 87; Conservative 75; Mismatches 196; Indels 76; Gaps 16;

QY 18 LAFOHNTDSDTEGFLGVEYGEAKN-----SIFDSQMDVDEVYTTIDIQYIPC 67
DB 1119 MSFLLEIFNSQLPSFIPTMTQRADNFGRIYEVLYDITSWYRDKILYERCLANGALPG 1178
QY 68 YOLFSPYNSGGEVNEQALKILSNVKNV--GWYKFRHSDQIMTFERLLHKNLQEHF 125
DB 1179 FRLY-----WSDEONDDPLSAVLPYNKFLVLFSSKWHKY-----LTSYFSCSLSTEWMI 1228
QY 126 SNGDLV---FLLTPSIIITESGSTRLEHSLYPKGLFHRVPLVYANLGMSEOLGYKT 182
DB 1229 YNSVITILEKLPGLPFIIESGSLKRAERLNDKDEK---REDLKYTLALGYFAKLSKOP 1284
QY 183 SSGSCWSTGFSRAVQTHSSKFFE--EDGS:KEVKINEMAYASLOELKSIQCK----- 232
DB 1285 EWSFNS-FSGTVRPNSEKLRPQOLSVATSAVDKTSASISEQAKIDKQVALNP5A 1343
QY 233 ---VEES-----EQAVDLVADVNRILKREIEKRGADIOAREKNIQKPOENIFLCQ 282
DB 1344 PEFVDPSTPSDVAASETDNNKLVENKAVERVEARSSANERKKEERKTTPEGN--RR 1400
QY 283 ALRTFFPNSSEFLNSCWMLNRR-----VSKSSCNYNHLLDVNDLTLMEVHTDIPAS 336
DB 1401 ALRTTRPTMEDIGRSDSKLRREDQSRDPTQSRSTFTENN---DNLRSVSRHTR-REPO 1454
QY 337 PASTPQIIRKALDLDNRQ-----FKRSLD-----TQDKRSKANTGSSNODKASKM 385
DB 1455 QAOQLNARREHESQKSDRMRQNGNVNRPVSNNSNTNVSREKSSERANRTSDNKRDEV 1514
QY 386 SSPETDEIEIKMG 399

DB 1515 TEGDKXNRQDISG 1528
Search completed: April 16, 2004, 10:14:02
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comogen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:20 ; Search time 44 Seconds

(without alignments)
894.144 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109

Sequence: 1 MGEESTAVLSGFVGLALF.....TDEIERKKKGFGRYSRPTF 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR_78:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	132	6.3	1738	2	T14867	interactin - slime
2	129.5	6.1	531	2	A55887	caldesmon, non-mus
3	126.5	6.0	600	2	A45112	major paraflagella
4	123.5	5.9	825	2	S62042	probable membrane
5	121	5.7	993	2	S49461	synaptonemal compl
6	121	5.7	1825	2	T42725	actin binding prot
7	121	5.7	1885	2	T30847	actin binding prot
8	121	5.7	2033	2	T30849	actin binding prot
9	119.5	5.7	820	2	C81252	probable NADH2 deh
10	119	5.6	1837	2	T41023	probable nuclear p
11	119	5.6	2401	2	T26676	cholesterol protein
12	118.5	5.6	886	2	H69379	conserved hypochet
13	118.5	5.6	2253	2	T30336	nuclear/mitotic ap
14	117.5	5.6	875	2	S70115	Z1P1 protein - yea
15	117.5	5.6	1163	2	G97236	ATPase involved in
16	117.5	5.6	3259	1	A56539	giantin - human
17	117	5.5	3225	2	I52300	giantin - human
18	116	5.5	879	2	C71083	conserved hypochet
19	116	5.5	4717	2	T41581	hypothetical colle
20	115.5	5.5	1231	2	T18532	serine/threonine pr
21	115.5	5.5	1300	2	I53799	CG1 protein - huma
22	115	5.5	1233	2	T14157	serine/threonine p
23	114.5	5.4	1628	2	T38055	hypothetical prote
24	114.5	5.4	1078	2	T18352	protein p120 - Myc
25	114.5	5.4	2269	2	T28677	thoptery protein -
26	114	5.4	946	2	S28061	SCP1 protein - rat
27	114	5.4	1790	2	S67593	transport protein
28	114	5.4	3973	2	B71612	hypothetical prote
29	113.5	5.4	754	2	S48020	kinesin-related pr

30	113.5	5.4	755	2	T41912	structural phospho
31	113.5	5.4	1356	2	S32763	kinectin I - human
32	113	5.4	804	2	G90571	hypothetical prote
33	113	5.4	1526	2	T41522	myosin ii - fiesio
34	113	5.4	1875	2	S38173	myosin-like protei
35	113	5.4	2783	1	A41948	alpha-fetoprotein
36	112.5	5.3	837	2	UN0282	antigen 332 - mala
37	112.5	5.3	879	2	S22028	paramyosin, standa
38	112.5	5.3	1313	2	F96673	hypothetical prote
39	112.5	5.3	1979	1	S03166	myosin heavy chain
40	112	5.3	1398	2	S56814	microtubule-intera
41	112	5.3	1640	2	D86798	prophage p13 prote
42	112	5.3	1690	2	T13030	microtubule bindin
43	111.5	5.3	636	2	G36717	hypothetical prote
44	111.5	5.3	886	2	T01125	hypothetical prote
45	111.5	5.3	1038	2	I38935	bone morphogenetic

ALIGNMENTS

RESULT 1

T14867 interactin - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: T14867

R:Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.

J. Cell Biol. 142, 735-750, 1998

A:Title: Interactin, an actin-binding protein of the alpha-actinin superfamily in Dicty

ts.

A:Reference number: Z18248; MUID:98365468; PMID:9700162

A:Accession: T14867

A:Status: preliminary; translated from GB/EMBL/DBEt

A:Molecule type: DNA

A:Residues: 1-1738 <RIV>

A:Cross-References: EMBL:AF057019; NID:93549260; PID:93549261; PIDN:AAC34582.1

C:Genetics:

A:Gene: abpd

A:Introns: 173/2; 1680/1

Query Match 6.3%; Score 132; DB 2; Length 1738;
Best Local Similarity 18.4%; Pred. No. 2.1; Indels 138; Gaps 18;
Matches 78; Conservative 79; Mismatches 129

QY	23	LNTDSDTEGFLGKGEANNSITDSQMDV---EYVYTIID--QKYPICYQ-----LF 71
DB	466	LSIWQATNSLMEKI--GILNMDLTDIPQDIKEKDEIANKIESEKMLKCFODFVALQ 524
QY	72	SFYNSGEVNEQ--ALKILSNVKKVGVGVYFRHSDDIMTFRRLLAKNLOEHSNQ 128
DB	525	SRYSLTIEQTSQLODRKQINELQEDDKFIETSSNSQSLDNQVVIDQLTNE--KQ 581
QY	129	DIVFLLTTPSITTESCTHLSHLYKQGLFHRVPLVVAANTGMSHQLYKTVSGSCWS 188
DB	582	SITQLQDQDIKEX-----EFOFEKQ--LISQDISITTN----- 615
QY	189	TGFRANVTSSKX-----FEEDGSL-----KEYKIKEMVASLOEIKSTCKY 233
DB	616	-----IOEYQDKNNLQOEFNTQCTLNQOETRLTQQLVQINTDVNEKQYLOS--EI 666
QY	234	EDSEQAVDKLVQVNRILKREIERKGAQIOAAREKNIQKDPORNIPLQALRTFFPNSF 293
DB	667	KDNQTNELQNKQSEKDKIEKLSNQEQEQDEK----- 701
QY	294	LHSCVMSLKNRHSXSSCNVNHLDVVDNLTVAVEHPTIDPEASPASTPQIIRKALDLD 353
DB	702	-----LNNLLLEIKEDC--LIERNQQLLEN--IDLNS 731
QY	354	RMQ-----FKRSRLDTQDKRSKANTSSNQDASKSSSETDEBIKEMK-----GFG 401
DB	732	KYQQLLEFNFKLSKSEKENQNLQSKQDERFNQNLN--DEKLEKEKQLOSIDEFN 788

QY 402 EYGR 405
 Db 789 QYKQ 792

RESULT 2

A:Species: non-muscle - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
 C/Accession: A55887
 R/Yamashiro, S.; Yamakita, Y.; Yoshida, K.; Takiguchi, K.; Matsunura, F.
 J. Biol. Chem. 270, 4023-4030, 1995
 A>Title: Characterization of the COOH terminus of non-muscle caldesmon mutants lacking the
 A/Reference number: A55887; PMID:95181370; PMID:7876150
 A/Accession: A55887
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-531 <YAM>
 A/Cross-references: GB:U018419; NID:9622966; PIDN:AA68521.1; PID:9622967
 A/Note: authors translated the codon GCC for residue 68 as Val
 C/Superfamily: caldesmon
 C/Keywords: phosphoprotein

Query Match 6.1%; Score 129.5; DB 2; Length 531;
 Best Local Similarity 24.0%; Pred. No. 0.68; Indels 93; Gaps 21;

Matches 85; Conservative 54; Mismatches 122; Indels 93; Gaps 21;

QY 35 GEVKGSAKNSITDSQMDVEVYTTIDIQKIPCYQLSFYNSG-----EVNEQALK 86
 Db 143 GEEKGSRSG--RYEMETEVTIT-----SYQKNSYQDAEDKKKEKEEKEK 192
 QY 87 KILSNKKNVGVYKFRH---SDQIMTERRLHKNLOEHSNODVFLITPSITBS 143
 Db 193 G--GNGENQIDKEKIKKKEPEVKNFDR--KKGFTE-VKQNGEFM----- 237
 QY 144 CSTHRL--HSLYKPOKG-----LFRVPLVNLGMSDQLGKYTVSGCMSTGFSR 193
 Db 238 --THKIKOTENAFSPRSGRASGDKEAGAPQVEGKRLIE--LRRRGTESEFEK 292
 QY 194 AVQTHSKFFEDGSLKEVHAKINEMKASIQEELKICKVEDSEQAVDKLVQVNLKRE 253
 Db 293 LKCKQOEALD---LEELKKKEERKVLSEBQRKQEDRKAREE--EKKRLKEE 346
 QY 254 IEXRRGAQIQAEKNIQKPOENT-----FLCQALRTFFP-----NSEFLHSCV 298
 Db 347 IERRRA---EAAERK--QKPEFGDSEDKKPFKC-----FTKGSGLKEERAEFL---- 392
 QY 299 MSIKRNVKSSGNNVHLDVNTLTLMVE-HTDIPASPASTPQIIKHALDL 351
 Db 393 ---NKSQKSGVSKTHQAAVVKIDSRLEQYTNALIEGFKAKP--MKPAADL 440

RESULT 3

A:Species: Trypanosoma cruzi
 C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
 C/Accession: A45112
 R/Beard, C.A.; Sabotio, J.L.; Tewari, D.; Kriegstein, K.G.; Henschen, A.H.; Manning, J.

J. Biol. Chem. 267, 21656-21662, 1992
 A>Title: Evidence for two distinct major protein components, PAR 1 and PAR 2, in the par
 A/Reference number: A45112; PMID:93016117; PMID:1400477
 A/Accession: A45112
 A/Status: preliminary
 A/Molecule type: mRNA; protein
 A/Residues: 1-600 <BEA>

A/Cross-references: GB:M97548; NID:9162178; PID:9162179
 A/Experimental source: Esmeraldo clone 3
 A/Note: sequence extracted from NCBI backbone (NCBIN:116802, NCBI:116803)

Query Match 6.0%; Score 126.5; DB 2; Length 600;
 Best Local Similarity 20.6%; Pred. No. 1.2;

Matches 80; Conservative 67; Mismatches 135; Indels 107; Gaps 18;

QY 19 AFQHLNTSDPTEGFLGEVGEAKN---SITDSQMDVEVYTTIDIQKIPCYQLSFYN 75
 Db 276 SFOETSAIKAKRLKRCEDDLKYLHDAIQKADMEADAKKPAQK----- 323
 QY 76 SSGEVNEQALKILSNYKKNVGVYKFR-----RRSDQIMTERRLHKNLOEHSFN 127
 Db 324 -----EKSEKFIQENLDRODEAMRRIOELERVLOLGTETFEERKRIEENREERKY 377
 QY 128 QDLVFLITPSITTESGSTR--LEHSLYKPOKGFLHVRVPLVNLGMSDQLGKYTVSGS 185
 Db 378 EYQGF-----DVGQHKULLEISV-----NCDLAKRCIGMBEL---VAEG 417
 QY 186 CMSTGSPRAVQTHSKFFEDGSLK-EVH-KINEMKASIQEELKICKVEDSEQAVDKL 243
 Db 418 C-----SAIKSRHDKNNEELGDLRLQVHQEYVEAFRRILYKTLGQLVYKKEKLEIDRN 471
 QY 244 VK-----DYNRLKELEKRRGAQIQAEKNIQ--KDPQENIFLCQALRTFF 288
 Db 472 IRTTHIQLEPALETFPNAKGSDAKKELYKRAQVEELEMLDKD---WAQALEMFG 526
 QY 289 PNSEFLHSCVMSLKNRHSKSGNNVHLDVVD--NLV--LWVEHTDIPASPASTPQI 343
 Db 527 PTERDAL-----NAGIEFVHPAEVEDGMLTRSKNVEY-----RAHL 564
 QY 344 IKHKAIDL-DDRMOFKRSRLDTQDKRSK 371
 Db 565 AKQEEVXIAERBELKSKTKLQSQYRGK 593

RESULT 4

S62042
 Probable membrane protein YPL032c - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein P7102.17
 C/Species: Saccharomyces cerevisiae
 C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 06-Feb-1998

R/Dietrich, F.S.; Allen, E.; Araujo, R.; Aparicio, A.; Carpenter, J.; Cherry, J.M.; Chu
 H.; Lin, A.; Lin, D.; Marathe, R.; Mittipati, S.; Namath, A.; Oefner, P.; Petel, F.X.;
 submitted to the EMBL Data Library, December 1995
 A/Reference number: S62042
 A/Accession: S62042
 A/Molecule type: DNA
 A/Residues: 1-825 <DIE>
 A/Cross-references: EMBL:U44030; NID:91171408; PID:91171425; MIPS:YPL032c
 C/Genetic8:

A/Gene: SGD:SVL3
 A/Cross-references: SGD:S0005953; MIPS:YPL032c
 A/Map position: 16L
 C/Keywords: transmembrane protein
 F,243-259/Domain: transmembrane #status predicted <TM>

Query Match 5.9%; Score 123.5; DB 2; Length 825;
 Best Local Similarity 19.2%; Pred. No. 2.9; Indels 141; Gaps 19;

Matches 98; Conservative 86; Mismatches 183; Indels 141; Gaps 19;

QY 1 MEGESTAVLSGFLGALAFQHLNT-----SDTEGFLG-----EYKGAKNSTID 47
 Db 71 LSSKSSAVVDIIMSAFSLQELSLASKLTIIDNTKFLSSGFIQLPEPKLSMES 130
 QY 48 SQMDVAVVYTTIDIQKIPCYQLSFYNSGVEY-----E 82
 Db 131 PHVAVFSILTDLDIRQIGPMH--FKHPPSAKNTIYLGSSKSTERYSGVITLITFE 188
 QY 83 QALKKILSNYKKNVGVYKFRHSDQIMTERRLHKNL-----QEHFS--NODVFLLL 135
 Db 189 KLFKALFNSNKKINLCNNSI-EPLSQQWKLAISICDPLLIMEQENPSLDQIIAKFL 248
 QY 136 TPSITTSK-----STRLE-----HSLYKQKGLFHRVP----- 165
 Db 249 ISGLVETIITVAKTMGARLNSHDNENSLSLWKNSYHSNKPALVYHQTPLNID 308

```

QY 166 -LVANLGMSEQLGYKTVSGSCSTGFSRAVQTHS--SKF-----EEDSLKEVHKINEM 218
DB 309 ILLLTQITLLADDFGKITPTLFEFLVLSQFERLNSGSKRMFTRSEKQIOLISLOKSQKN 368
QY 219 VASLQBELKSTCKYKDESDQAVDKLVK---DYNFLKEIEKRGAGIQAAERKNIQKDP 274
DB 369 ESALTQITQITSLQGOISKURQELLMQAKQHEMETNELKEKHQVYALKQAQA--QAQAQQA 426
QY 275 QENIFLCOALRTFFNFSEFHSQWMLKRRHVSQSCYVNHLLDVNDLTLMEHTDIBE 334
DB 427 QTSI---EALTTEATNQ-----SDNEYKATGTPNLR--DIEDVALSVNIGDSFV 473
QY 335 ASP---ASTPQI-----IKKAKLDDRMQFKRSRL 362
DB 474 RSPPPVSSQPMNSPLSHSQTFGNNGTNDKLLQERELQKKELELQERLEFQKRA 533
QY 363 LDTQPKRSKANTGSSNQDKAKSSSPETDE 392
DB 534 LQQQ-----RPNNSNNSIPRKPSPFQLOQ 557

```

RESULT 5

synapcnemal complex protein 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_rev1sion 20-Feb-1995 #text_change 05-Nov-1999
C/Accession: S49461; S59599

R/Juilen, S.; Luc, M.; Francois, C.
submitted to the EMBL Data Library, October 1994

A/Description: Cloning and sequencing of the murine SCP1 cDNA.
A/Reference number: S49461

A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 1-993 <JUL>

A/Cross-references: EMBL:Z38118; NID:g1360015; PIDN:CAA6262.1; PID:g558603
R/Sage, J.; Martin, L.; Guzin, F.; Rasseoulzadegan, M.
Biochim. Biophys. Acta 1263, 258-260, 1995

A/Title: cDNA sequence of the murine synapcnemal complex protein 1 (SCP1).
A/Reference number: S59599; MUID:96004899; PMID:7548215

A/Accession: S59599

A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 1-993 <SAG>

A/Cross-references: EMBL:Z38118; NID:g1360015; PIDN:CAA6262.1; PID:g558603

Query Match 5.7%; Score 121; DB 2; Length 993;
Best Local Similarity 18.4%; Pred. No. 5.4;
Matches 89; Conservative 91; Mismatches 151; Indels 152; Gaps 22;

```

QY 21 QHLNDSDEGFLGAEVKG-----EAKNSIDSGMDVAVYTTDIDQKYPQOLF 71
DB 361 EELNAAKTTTHSFVVELCAATCTTEELLRTQORLEKNEDQKIL-TVELQKSNLEEM 419
QY 72 SFYNSGGEVNCALKKILS-----NVKNVVGWYKFRHSQDQMTF---RESLH--- 118
DB 420 TFKNNKEVELBELKNILAEQDKLDEKQYKLAELQEKQELTFLTEREKVNDLQ 479
QY 119 -----KVLQEHFSQ-----DLVFLLLPSIITSGSTRLEHSLYKPKQGLPHRYPL 166
DB 480 EGVVTKTSEQHYLQVEEMKTELEKEKLVKNTELTASCDMLLEKFKVQ----- 530
QY 167 VVANLGMSEQLGYKTVSGSCSTGFSRAVQTHSSKF---EEDSLKEVHKINEMVASTL 222
DB 531 -----ASDWALEKKHQEDILNCKQBERLLKQINLEKEMHL 569
QY 223 QBELKSI-----CK-KYEDSEQAVD-----KLVKD-VNRLKRELEKR 257
DB 570 RDELSTVAKKEPTIQGDEVKCKLQKSEENARSIECVLKKERQMKLESKCNLKKQVEN- 628
QY 268 RGAQIARERKNIQDQENIFL-----COALTFFPNSEFLHSQWMLKRRHVSQSCS 310
DB 629 -----KSKNIEELHQENKTLKKKSSAELIKQINAYIKYKLELELESTKQCFEEMTN 680

```

```

QY 311 QNNHND--VNDNLTLMEHTDIPASPASTPQIIR-KKALDDRMQFKRSRLDTPQ 367
DB 681 -NQKELENKKISEGKLGE---VEKATYDEAVKLOQKEDL--RCQKLAEMVALME 733
QY 368 KRS-----KANTG---SSNQDKAKSSSPETDE-----EETL 395
DB 734 KKHQYDKIYEERDSEGLYKQNEQSSAKIALETELSNINRELVSLKQLEIEKEKE 793
QY 396 KAK 398
DB 794 KLR 796

```

RESULT 6

T42725

actin binding protein ACF7, neural isoform 1 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 11-Jan-2000 #sequence_rev1sion 11-Jan-2000 #text_change 03-Nov-2000
C/Accession: T42725

R/Bernier, G.; Mathieu, M.; De Repentigny, Y.; Vidal, S.M.; Kohary, R.
Genomics 38, 19-29, 1996

A/Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin sub
A/Reference number: Z20900; MUID:97124842; PMID:8544775

A/Accession: T42725

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-1825 <BER>

A/Cross-references: EMBL:U67203; NID:g1675221; PID:g1675222; PIDN:AACS2988.1

A/Gene: ACF7
A/Map position: 4
C/Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein;
C/Keywords: actin binding

Query Match 5.7%; Score 121; DB 2; Length 1825;
Best Local Similarity 21.4%; Pred. No. 12;
Matches 80; Conservative 57; Mismatches 113; Indels 124; Gaps 19;

```

QY 82 EQLKKILS-----NVKNVVGWYKFRHSQDQMTF-ERL-----LHKNLQE 123
DB 880 EQGYQKVMALMQHLINT-KSLISWYTLRKDDTVQWGLEKRLSLAPGCHQVMKNLQA 938
QY 124 HFSN--QDLVFLLLTISITSGSTRLEHSLYKPKQGLPHRYPLVANLGMSEQLGYKT 181
DB 939 HYEDFLQD-----SH-----DSALP-----SVADRLLIEE 963
QY 182 VSQSCMSTGFSRAVQTHSSKFEEEDSLKEVHKINEMVASTLOBELKSTCKYEDSEQAVD 241
DB 964 EYKAC-----KHPQLMKSLNEDKEKERTLAKV---YIS---ELKNILLLLEECQRL 1011
QY 242 KLVQVYNRLKRELKRGAGIQAAERKNIQKQPOE-----NIFLQALRTFFP 289
DB 1012 KOQSPASSKRTBDAQDITTLRLAQEHQTOEDLQHLRSDDLAI SMKCNVFLQOS-----P 1066
QY 290 NSEFLSC-----VMSLKNRHVSQSCYVNHLLDVVD-----NLLTMEHTDI---P 333
DB 1067 SSSSATTLSSELNLTMEVKNKDHVYGSLTYLNTKLTIDVVRSMQDELIVKGEITLQSE 1126
QY 334 EASPASTPQIIRKHALDDRMQFKRSRLDTPQDKRSKANTGSSNQDKAKSSSPETDEE 393
DB 1127 EAVPADLSALSHRT--TLQHW-----LSDYDKNSVSV-----LDBE 1163
QY 394 IEKMGGEYSRSP 407
DB 1164 ITKAKTYAEQLRHP 1177

```

RESULT 7

T30847

actin binding protein ACF7, neural isoform 2 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 22-Oct-1999 #sequence_rev1sion 22-Oct-1999 #text_change 03-Nov-2000

[illegible]

Db 372 SDFVLVAAEMMLRIYAPILSYIKYNALVW-NAGSULIFIEEDMDGMAISNFIETIAK 322
 Qy 172 GMSFOLGYKYVSGSCMSGTGFEFRAVQTHSSKRFEDSGSLKEVHK-INENYASLOBELKIC 230
 Db 430 GDEEILVFLLOKFSQDPRG---IKTHLAEPFVASEN-KELFEESINE-----EWEVEYI 477
 Qy 231 KKVVESEQAVDKVDV--NLLKKEIEKRRRAQIQAREKNIQDPCENIFLCAQLRTFF 268

```

Db      478 EKEBEGNE-IQKEVKKVPPKVKKILIVQSV--FAKNGIDEDKLEDLLKKANFTLV 533
QY      289 PNSEF 293
Db      534 AGSDF 538

RESULT 10
T41023
probable nuclear pore complex-associated protein - fission yeast (Schizosaccharomyces po
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T41023
R/Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrett, B.G.
submitted to the EMBL Data Library, June 1998
A/Accession: Z21965
A/Reference number: Z21965
A/Molecule type: DNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1837 <MUR>
A/Cross-references: EMBL:AJ023860; PIDD:CA19588.1; GSPDB:GN00068; SPDB:SPCC162.08C
A/Experimental source: Strain 972h-; cosmid C162
A/Genetic:
A/Genes: SPDB:SPCC162.08C
A/Map position: 3

Query Match      5.6%; Score 119; DB 2; Length 1837;
Best Local Similarity 20.4%; Pred. No. 16;
Matches 86; Conservative 90; Mismatches 162; Indels 84; Gaps 18;

QY      27 SDTEGFLGVEKGEAKNSITDSQMDVEVYTTIDIQKIPCYQLFSPYNSGSEVNEQA-L 85
Db      1147 SSKLDYILG---ENQKLIHQFDLSQOITV-LQG-----NSENINISALT 1191
QY      86 KKLISNVKKNVGVWYFRRHSDQIMTFRRL-----LHKQLQEHFSNODLVFLLI-- 135
Db      1192 EAVQDNDLRELIV--SYLRHEKEIMONKXELTLDNRGNQVKSQSTVDSLOELNLT 1248
QY      136 -----TP-----SIITESCSTHRLH--SLYKPKGLFHRVPLVANIAG-- 172
Db      1249 QSLPVNDQDTPIIIGSQGVQLLYESNSVLRKDNQAKIGIOE-LKEVEKLIASNL 1307
QY      173 -----MSEQLGYTVSGSCMSTGFSR--AVQTHSSKFEEDGS-LKEVKK---INEM 218
Db      1308 QTEINELKKEIGAKTASLIMKEYNRWKLRFQSVLNTKERYVDPTQLEIKKNCCEALERE 1367
QY      219 YASLOELKSIQKVEDSEQAVDKLVKDVNRLKREIEK--RGAQIQARREKNIQKDPE 276
Db      1368 KOELKTKLOETAKETDTFKQVNSLNEVEENLKGEVEQANTKTRLAAMNEKCEWLKKS 1427
QY      277 NIFLQALRTFPNSEFLHSQVMSLKNRVSKSCNYNHLDVVDNLTLMEHTDIPKAS 336
Db      1428 SL-----TFPAH-LKQELTNKKELTSSKNAENEAQKEIESLKDSNHQJESGA 1474
QY      337 PASTPQIKKALDLDNRWQFKRSRLDTPDKRSKANTSSNQDRAKMSSETDEIEK 396
Db      1475 SSQAEITKQEPQLKSEKRETEKELADSKNEHLQSEAVALDGTETISLE--KEIHE 1532
QY      397 MK 398
Db      1533 LR 1534

RESULT 11
T28676
rhoptery protein - Plasmodium yoelii (fragment)
C/Species: Plasmodium yoelii
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C/Accession: T28676; A45521
R:Simha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A/Title: Comparison of two members of a multigene family coding for high-molecular mass

```

```

A/Reference number: Z20507; MUID:97077455; PMID:8920022
A/Accession: T28676
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2401 <SIN>
A/Cross-references: EMBL:U36927; NID:91041784; PIDD:91041785; PIDD:AB41263.1
R:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A/Title: Identification of the gene for a Plasmodium yoelii rhoptery protein. Multiple c
A/Reference number: A45521; MUID:91101660; PMID:2270106
A/Accession: A45521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 2260-2401 <KE>
A/Cross-references: GB:M34281

Query Match      5.6%; Score 119; DB 2; Length 2401;
Best Local Similarity 19.9%; Pred. No. 22;
Matches 94; Conservative 82; Mismatches 167; Indels 130; Gaps 24;

QY      24 NTSDPTBSFLGVEKGEAKNSITDSQMDVEVYTTIDIQKIPCYQLFSPYNSGSEVNEQ 83
Db      344 NMETET-----VKSHLKNIEITNNKLSLSET-----LIDIIKXI-----YGEITNE 381
QY      84 ALKKILSNVKNVGVWY----KFRHSDQIMTFRRLHKNLQEHFSNODLVFLLTPSI 139
Db      382 -LNTLEDFPKKKEKGLSKIDVAKENQVQNVKSNIL--EIKKHYDQ-----INIDN 432
QY      140 ITESCSHRL---EHSLYPKQGLFHRVPLVANIQMSQGLGYTVSGSCMSTGFSRAV 195
Db      433 IKEKAKQNDQFKEHMKTIIPNEMKIQKPSIEIKI-MKQEFISKVKNVNFDPKYYEKV 491
QY      196 QTHSSKFEEDGSK-----EVKK-----INEMYASLOELKSI--CKYVEDS 236
Db      492 ESEHNTFELTNKKTVEVSDEIKYENKRNDSLSLNETKSLSESYQNTNLTKKVDY 551
QY      237 EQA---VDKLVKDVNRLKREIEKRGAIQARREK---IQKDPOENIFLQ--ALRTF 287
Db      552 IKVCINTVELITNCHNQTLKDLNQNIKTIKETNSIDKIYTPKFENILIDKXTELET 611
QY      288 FP-----NSEPL-----HECVMSLKNRVH--SKSS 310
Db      612 FTGISLNHNSNNKELLTYFDLKNLGNKKNKMLYQFNEKEKAVDIDKGNVDINKIV 671
QY      311 CN-----YNHLDVVDNLTLME--HTDIPKASPASTPQI--IKHALDLDNRWQF 357
Db      672 SNIEITITSYININEDTENEIGKSIELNLTQVLEKVKAVTNLNEIKELKQYDFQDFG 731
QY      358 KRSRLDTPDKRSKANTSSNQ--DKA-----SKMSSETDE--EIEKKK 398
Db      732 KKNIKYPDENKIKNDIDITLNQIKDKSIETLTKKNSNNHIDEIKQIDKLR 784

RESULT 12
H69378
conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C/Accession: H69378
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: H69378
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-866 <KLE>
A/Cross-references: GB:AE00103; GB:AE000782; NID:92689355; PIDD:AB90211.1; PIDD:9264955
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

```

```

Query Match      5.6%; Score 118.5; DB 2; Length 886;
Best Local Similarity 19.7%; Pred. No. 6.7;
Matches 93; Conservative 82; Mismatches 140; Indels 157; Gaps 24;

QY 11 SGFVGLAFQHLNTD-----SDTEGFLGKVEKAGNSITDSQMDVVEVYTIIDQX 63
DB 67 SGVSL-SLTFSS-LINGDYYTISRKNSGSLITGKEIVGSGNTTW-----VER 112
QY 64 YIPCYQLP-SFYNSGSEVN-----EQALKKI-----LSNVKQNVGMYK-FRRHS 106
DB 113 HLCRAVHFGATVYRQGEIDSLIRDESEKRIIRQITRLEDYENMKNKGVIRMLERBK 172
QY 107 DQIMTF--PERLLHKLQEHFNSQDLVFLILPSTITSCSTHRLHS:YKPOKGLFHRV 164
DB 173 ERKLEFLSQDEQIKRQKEKKAET-----RISEELKSIESLRKLESEVRULBSRL 224
QY 165 PLVAVNLGMSQQLGYXTVSGSCWSTGFSRAVQTHSSKF---FEEDGSLKEVHKINEMYA 220
DB 225 -----KELSEHKRIESLRKQESSVLQEVRLGEKLR 256
QY 221 SLQELKSIQKVEDSEQ-----AVDKLVQVNRKREIERKRG----- 259
DB 257 ELERQKKEVERTEDEKAKAVEKELPKAERYSLIKLSEINQALRQVEKRGDITRE 316
QY 260 -----AQIQARERKN-----IQDPOENIFLQALRTFFPNSEFLHSCVMSLKNRVSXS 309
DB 317 AAGIQQLKKAEDNSLSEITKRIE--LERELERF--EKSHRLLETIKPK----- 364
QY 310 SCYNHHLDVYDNLTMVEHTDIPKASPASTPQIIR-----HKALDDRRQFRRSL 363
DB 365 -----MDRMQGIKAKLEKKNL-----TPDKVEMKTDLSKAKEEKEITEKIKKLI 410
QY 364 DTQDKSKANTGSSNODKA-----SKMSSP-----ETDEIEKMKFGESYR 405
DB 411 ---AKSSLSKTRGAQLKKAVEELKSAERTCPVGRLEDEHRR-NIMAEYTR 458

RESULT 13
T30336
nuclear/mitotic apparatus protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T30336
R:Merdes, A.; Vecchio, J.D.; Cleveland, D.W.
Cell 87, 447-458, 1996
A>Title: A complex of NuMA and cytoplasmic dynein is essential for mitotic spindle assem
A:Reference number: Z20828; MUID:97053784; PMID:8898198
A:Accession: T30336
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2253 <MER>
A:Cross-references: EMBL:Y07624; NID:91514670; PIDN:CAA6905.1; PID:91514671
C:Genetics:
A:Gene: NuMA

Query Match      5.6%; Score 118.5; DB 2; Length 2253;
Best Local Similarity 18.3%; Pred. No. 22;
Matches 77; Conservative 89; Mismatches 164; Indels 91; Gaps 16;

QY 1 MEGESTAVLSGFLVGLAFQHLNTDSDTEGFLGKVEKAGNSITDSQMDVVEVYTIID 60
DB 851 LGGRSKYL-----IEAKASSETSSQLEKINQEGELSA--ANACIKREAEKELTVALH 905
QY 61 I--QKIPCYQLPFSFYNSGSEVNQA-LKKILSVYKQNV-----VQMYFRHSDQIMT 111
DB 906 SAERKLIAYO-----GESERLSHLETLNNAKQDLQCLAELEDEKTKKAEFPAYV 957
QY 112 FRERLLHKLQEHFNSQDLVFLILPSTITSCSTHRLHSLYKPOKGL-----FHRVPL 166
DB 958 ---KVLKQNSERLASLESELKNSLAVYKERKCEKSLSGVEHLTKROLDSQKHEAL 1014
QY 167 VVAVNLGMSQQLGYXTVSGSC-----MSTGFSRAVQTHSSKFPEEDGSLK----- 210

```

```

DB 1015 AQKNIEIKQILNKEKATSLDAIKSEMGAQLQKAVQDTHSEFALQNEJRSRIDLLAKE 1074
QY 211 -EVHKINEMYASIQEEL---KSIQCKVEDEQAV---DKLVQVNRKREIERKGAQI 262
DB 1075 GEVERLNKEAALQOEIQQOQOTITKLTBEETALAKKQVALQOEKIKQOVATGAERK 1134
QY 263 QAAREKNIQDPOENIFLQALRTFFPNSEFLHSCVMSLKNRVSXSQYNHLLDVVN 322
DB 1135 EMATKSVISEKRI---ECLEODIQNQKRDLSCT---QEGRQSK----- 1174
QY 323 LTMVEHTDIPKASPASTPQIIRHKALDDRRQFRRSLIDQDKRSKANTGSSNODKA 382
DB 1175 -----LQESQGLQALADLEKCKQKEQELICEAQNKAEEKTLAS--EKA 1217
QY 383 S 383
DB 1218 S 1218

RESULT 14
S70115
Z1P1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D9819.9; protein YDR285w
C:Species: Saccharomyces cerevisiae
C>Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: S70115; A45173; S30868
R:Fulton, L.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of S. cerevisiae cosmid 9819.
A:Reference number: S70114
A:Accession: S70115
A:Molecule type: DNA
A:Residues: 1-875 <FUL>
A:Cross-references: EMBL:U51031; NID:91332635; PID:91332639; MIPS:YDR285w
R:Sym, M.; Engbrecht, J.A.; Roeder, G.S.
Cell 72, 365-378, 1993
A>Title: Z1P1 is a synaptonemal complex protein required for meiotic chromosome synapsi
A:Reference number: A45173; MUID:93161412; PMID:7916652
A:Accession: A45173
A:Molecule type: DNA
A:Residues: 1-54; N/A; 56-875 <SYM>
A:Cross-references: EMBL:L06487; NID:9173240; PIDN:AAA35239.1; PID:9173241
A>Note: sequence extracted from NCBI backbone (NCBIP:124844)
C:Genetics:
A:Gene: SGD:Z1P1
A:Cross-references: SGD:S0002693; MIPS:YDR285w
A:Map position: 4R

Query Match      5.6%; Score 117.5; DB 2; Length 875;
Best Local Similarity 18.0%; Pred. No. 7.6;
Matches 85; Conservative 80; Mismatches 135; Indels 171; Gaps 20;

QY 23 LATDSDTGFLGKFK-----GEAKNSITDSQMDVVEVYTIIDQYI 65
DB 110 IENDTD-BDFETTEFREYSEGVAKETKESHDPDSDSETTLDSQKHE-----YTMNGK-A 163
QY 66 PCYQLFSFYNSGSEVNQAL-----KKILSVKQNVGMYKFRHSDQIMTFERLLHK 119
DB 164 PLHT--SLNNSSTSDVLTLEAFNTQKICSNLQOELD-----KQOQDNK-----LKV 210
QY 120 NIQEHFNSQDLVFLILPSTITSCSTHRLHSLYKPOKGLFHNVPVAVNLGMSQQLG- 178
DB 211 RLQSYASNSDKI-----NEKVGK 228
QY 179 YKTVSGSCWSTGFSRAVQTHSSKFPEEDGSLKEVHKINEMT-----ASIQEELK 227
DB 223 YK-----SCLFT-LGRIRATILSHKNNQETKLDLRQNHQLQYRRISGFRTSIEINIKTIN 283
QY 228 SICKVEDEQAVDVKLVQVNRKREIERKGAQIQAAAREKN---IQDPOENIFLQAL 284
DB 284 DLGKRRKQADALMKKQKIEIYLRKELDDCG-QLSEKIKNSSLIQEMGNREEMISII 342

```

QY 285 RTFFPNSSEFLH-----SCVMSLKNRHYKSSCNVNHLLDVV-DNLTLMVHTDIPBA 335
DB 343 ENFSESEKKAHLLQFNKFEERVHDLPEKDLQK-----HFDVAKDTLVNGLNRTVELS 395
QY 336 SPASTPQIIRKALDDDRMQRK----- 358
DB 396 S--NTETMLKQYEDIKENIQCKSSSKDMAXTINELSVTKGLIMGVQOEILLTSSGNI 453
QY 359 -----RSRLDTQDKRSKANTGSSNODKASKSSPPTDEIEIKK 398
DB 454 QTLVSEMNNTROGLDDASQTAKNTASLENLVKAYKAEIVGSNEYERIK 504

RESULT 15

G97236
ATPase involved in DNA repair [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: G97236
R/Nolling, U.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A/Reference number: A96900; MIMD:21359325; PMID:21359325
A/Accession: G97236
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1163 <KUR>
A/Cross-references: GB:AE01437; PIDN:AAK80682.1; PID:q15025772; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CMC736

Query Match 5.6%; Score 117.5; DB 2; Length 1163;
Best Local Similarity 19.0%; Pred. No. 11;
Matches 87; Conservative 70; Mismatches 146; Indels 155; Gaps 19;

DB 47 DSGMDVEVYITDIDQITPCYQLFSPYSSGSEVNEQALKILSNVKNVGVGMYKFRHS 106
DB 488 DPEKDVLLTFQEKLNDSKQAKKISEYNS-----LKASLRVE-----NS 529
QY 107 DQIMPRERLHNLOEHSPSNODLVFLTPSIITESCSTHRLHSLYK-----PQK 158
DB 530 EQVLTQKXEMTK-LEDXISK-----VNKIESLETENMAVHLREKLKSGEACFVC 579
QY 159 GLFHRVPLVYANIGMSEQLGYTVSGSCMT-----GFSRAVQTHSSKFFEDGSL--- 209
DB 580 GSYVHL-----KEGFKEVDLKALETLSLEGFKKRKEENEIVMCEASIKYE 628
QY 210 -KEVHKINEMYASLOEELKSI CKVEDSEQAVDKLVQVNRLLRE-----IEKR 257
DB 629 ENNIKKLINSINNLSGEFKEV--SLESMEKFNVLKEKNKPNLEKIQLODNDIKDLSERS 686
QY 258 RGAQIOAAREKNIQKDPENIF-----LCQALRTP-----PNSE 292
DB 687 NKLEIVYQKEKTEVKQCEKRIVDLKSLEAEAKKEFNEVATTIENLKAEIKIQDFPEWKE 746
QY 293 FL-----HSCVMSLKN---RHVSKSSCNVNHLLDVVNDLTMVHTDIPASPAS 339
DB 747 ILEKERVVEABGEIKDLRLNLRHTEKE-----QLMDKCSRLKEELSKNPAELKE 798
QY 340 TPQI-----IKHKALEDDDRMQRK-----SRLLDTQDKRSK--- 371
DB 799 KDKIINEXIELIKNKVGLDNLVELKEIKIEGTIKIEQYNLCDKKMEIEDKXKCSDE 858
QY 372 -----ANTGS-----SNODKASKSSPPTDEIEIKK 398
DB 859 IIKTHSNSSLKDKRKVNDIDKLNKLTMEKEFENIEKAK 896